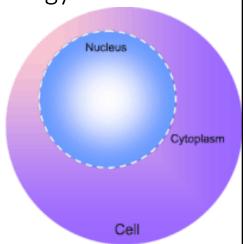
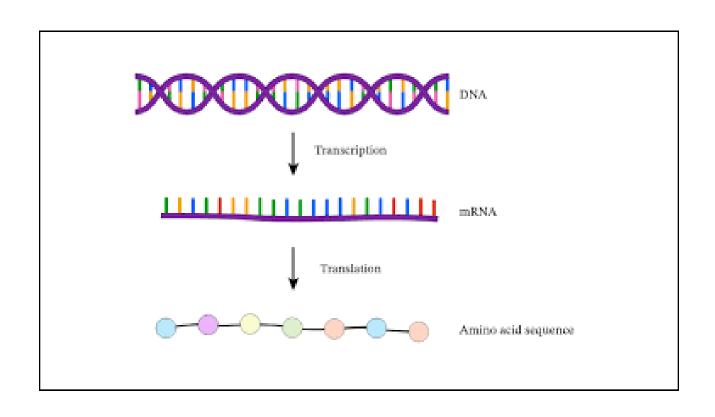
# Central dogma of molecular biology

- The central dogma of molecular biology describes the two-step process,
- 1. Transcription : synthesis of an RNA copy of a segment of DNA
- 2. Translation: Synthesis of proteins from RNA



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DNA 5' — ATG GGC TAC CCC TGC CTG — 3'

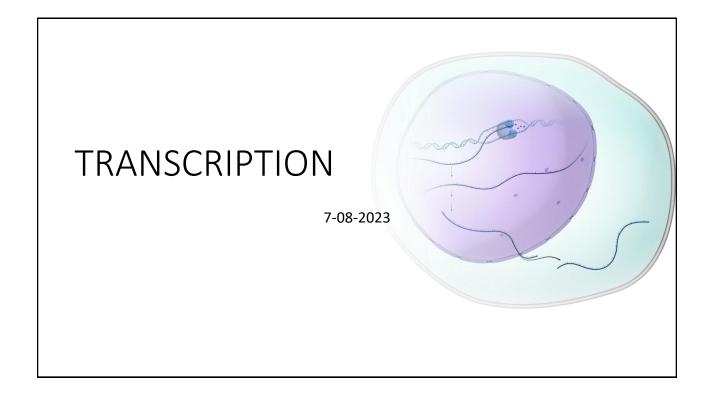
3' — TAC CCG ATG GGG ACG GAC — 5'

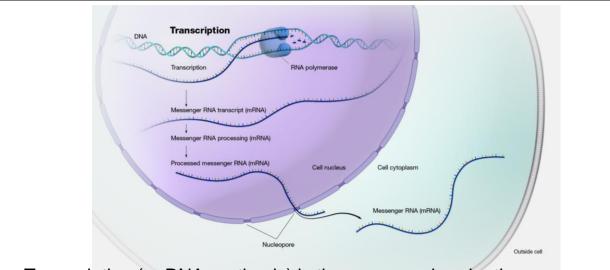
transcription

mRNA 5' — | AUG | GGC | UAC | CCC | UGC | CUG | — 3'

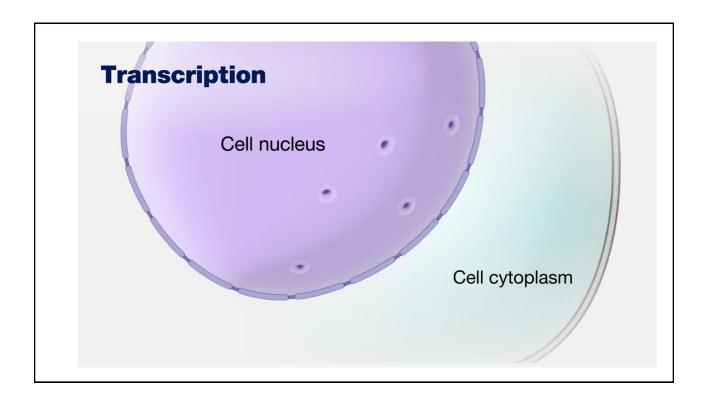
translation

protein N-terminus met gly tyr pro cys leu C-terminus M G Y P C L
```



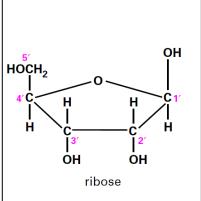


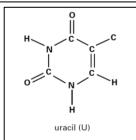
 Transcription (or RNA synthesis) is the process whereby the information held in the nucleotide sequence of DNA is transferred to RNA.



### Structure of RNA molecule

- Ribonucleic acid is a polymer made up of monomeric nucleotide units.
- RNA has a chemical structure similar to DNA, but with two major differences:
- 1. The sugar in RNA is a ribose sugar instead of deoxyribose.
- 2. The Purines are adenine, guanine and the pyrimidines are cytosine and uracil.



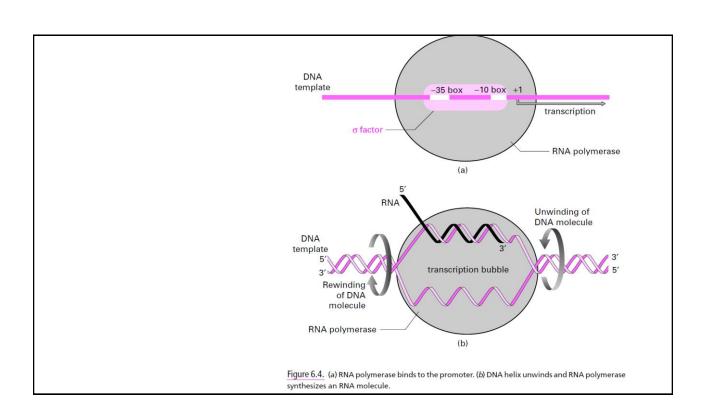


- Transcription takes place in three steps: initiation, elongation, and termination.
- The mRNA made is complementary to a strand of DNA.

#### **Step 1: Initiation**

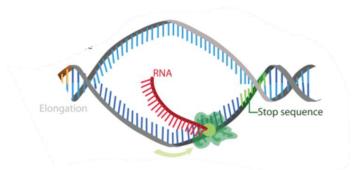
- **Initiation** is the beginning of transcription.
- It occurs when the enzyme **RNA polymerase** binds to a region of a gene called the **promoter**.
- This signals the DNA to unwind so the enzyme can "read" the bases in one of the DNA strands. The enzyme is now ready to make a strand of mRNA with a complementary sequence of bases.





### **Step 2: Elongation**

- Elongation is the addition of nucleotides to the mRNA strand.
- RNA polymerase reads the unwound DNA strand and builds the mRNA molecule, using complementary base pairs.
- During this process, an uracil (U) in the RNA binds to an adenine (A) in the DNA.



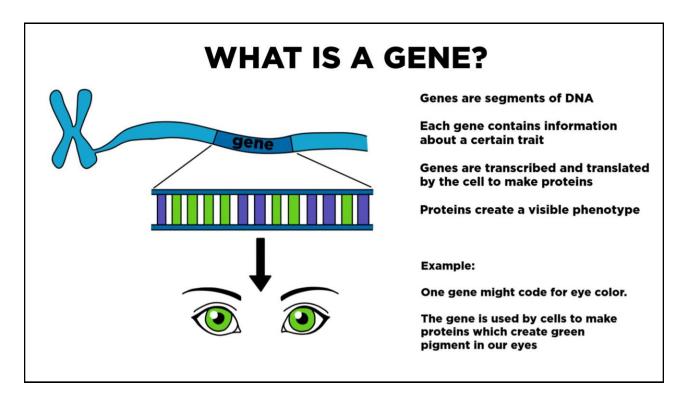
#### **Step 3: Termination**

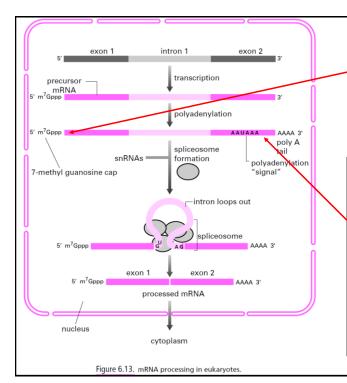
• **Termination** is the ending of transcription, and occurs when RNA polymerase crosses a **stop** (**termination**) **sequence** in the gene. The mRNA strand is complete, and it detaches from DNA.



# Processing of mRNA

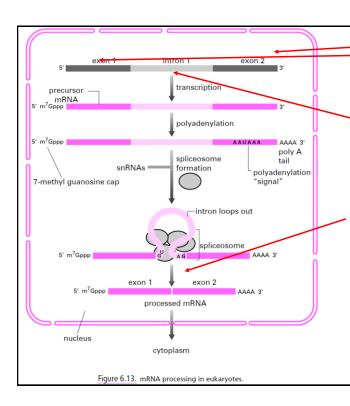
- The eukaryotic pre-mRNA undergoes extensive processing before it is ready to be translated.
- The three most important steps of pre-mRNA processing are the
- 1. addition of stabilizing and signaling factors at the 5' and 3' ends of the molecule
- 2. removal of intervening sequences that do not specify the appropriate amino acids.





**5' Capping: A cap** is added to the 5' end of the growing transcript by a phosphate linkage. This addition protects the mRNA from degradation.

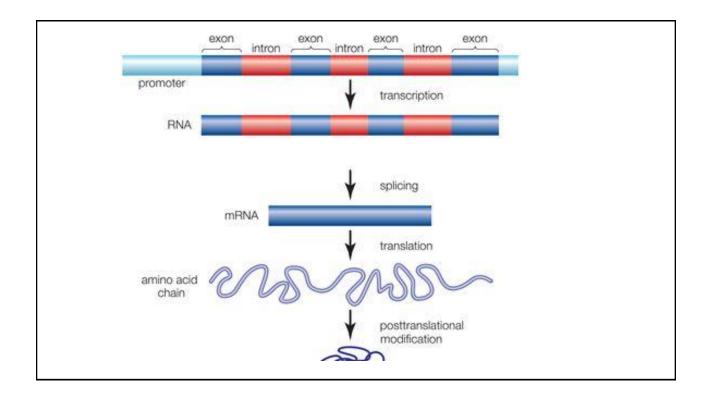
3' Poly-A Tail: Once elongation is complete, an enzyme called poly-A polymerase adds a string of approximately 200 A residues, called the poly-A tail to the pre-mRNA. This modification further protects the pre-mRNA from degradation and signals the export of the cellular factors that the transcript needs to the cytoplasm.



**Pre-mRNA Splicing:** Eukaryotic genes are composed of **exons**, which are protein-coding sequences (ex-on signifies that they are *ex*pressed)

intervening sequences called introns (intron denotes their intervening role) which are removed from the pre-mRNA during processing. Intron sequences in mRNA do not encode functional proteins.

The process of removing introns and reconnecting exons is called splicing



## Steps of mRNA processing

- 1. **5' Capping: A cap** is added to the 5' end of the growing transcript by a phosphate linkage. This addition protects the mRNA from degradation.
- 2. 3' Poly-A Tail: Once elongation is complete, an enzyme called poly-A polymerase adds a string of approximately 200 A residues, called the **poly-A tail** to the pre-mRNA. This modification further protects the pre-mRNA from degradation and signals the export of the cellular factors that the transcript needs to the cytoplasm.
- 3. **Pre-mRNA Splicing**: Eukaryotic genes are composed of **exons**, which correspond to protein-coding sequences (*ex*-on signifies that they are *ex*pressed), and *int*ervening sequences called **introns** (*int*ron denotes their *int*ervening role), which are removed from the pre-mRNA during processing. Intron sequences in mRNA do not encode functional proteins.

All of a pre-mRNA's introns must be completely and precisely removed before protein synthesis. If the process errs by even a single nucleotide, the reading frame of the rejoined exons would shift, and the resulting protein would be dysfunctional. The process of removing introns and reconnecting exons is called **splicing**