

## Transcription is the DNA-directed synthesis of RNA: a closer look

- Messenger RNA is transcribed in the nucleus of the cell from the template strand of a gene (DNA).
- **RNA polymerase** separates the DNA strands at the appropriate point and bonds the RNA nucleotides as they base-pair along the DNA template.
- Like DNA polymerases, RNA polymerases can add nucleotides only to the 3' end of the growing polymer.
  - Genes are read 3' → 5', creating a 5' → 3' RNA molecule (elongates 5' to 3' direction).
- Specific sequences of nucleotides along the DNA mark where gene transcription begins and ends.
  - RNA polymerase attaches and initiates transcription at the **promotor**, “upstream” of the information contained in the gene, the **transcription unit**.
  - The **terminator** signals the end of transcription.
- Bacteria have a single type of RNA polymerase that synthesizes all RNA molecules.
- In contrast, eukaryotes have three RNA polymerases (I, II, and III) in their nuclei.
  - RNA polymerase II is used for mRNA synthesis.
- Transcription can be separated into three stages: initiation, elongation, and termination.
- The presence of a promotor sequence determines which strand of the DNA helix is the template.
  - Within the promotor is the starting point for the transcription of a gene.
  - The promotor also includes a binding site for RNA polymerase several dozen nucleotides upstream of the start point.
  - In prokaryotes, RNA polymerase can recognize and bind directly to the promotor region.
- In eukaryotes, proteins called **transcription factors** recognize the promotor region, especially a **TATA box**, and bind to the promotor.
- After they have bound to the promotor, RNA polymerase binds to transcription factors to create a **transcription initiation complex**.
- RNA polymerase then starts transcription.

- As RNA polymerase moves along the DNA, it untwists the double helix, 10 to 20 bases at time.
- The enzyme adds nucleotides to the 3' end of the growing strand.
- Behind the point of RNA synthesis, the double helix re-forms and the RNA molecule peels away.
- Transcription rate is approximately 60 nucleotides per second
- A single gene can be transcribed simultaneously by several RNA polymerases at a time.
- A growing strand of RNA trails off from each polymerase.
- The congregation of many polymerase molecules simultaneously transcribing a single gene increases the amount of mRNA transcribed from it.
- This helps the cell make the encoded protein in large amounts.
- Transcription proceeds until after the RNA polymerase transcribes a terminator sequence in the DNA.

### **Eukaryotic cells modify RNA after transcription**

- Enzymes in the eukaryotic nucleus modify pre-mRNA before the genetic messages are transferred to the cytoplasm.
- At the 5' end of the pre-mRNA molecule, a modified form of guanine is added, the **5' cap**.
  - Helps protect mRNA from hydrolytic enzymes.
  - Functions as an “attach here” signal for ribosomes.
- At the 3' end, an enzyme adds 50 to 250 adenine nucleotides, the **poly(A) tail**.
  - In addition to inhibiting hydrolysis and assisting with ribosome attachment, the poly(A) tail also seems to facilitate the export of mRNA from the nucleus.
- The mRNA molecule also includes nontranslated leader and trailer segments.
- The most remarkable stage of RNA processing occurs during the removal of a large portion of the RNA molecule during **RNA splicing**.
- Most eukaryotic genes and their RNA transcripts have long noncoding stretches of nucleotides.
  - Noncoding segments, called **introns**, lie between coding regions, called **exons**.
  - The final mRNA transcript includes **exons** that are translated into amino acid sequences, plus the leader and trailer sequences.

- RNA splicing removes introns and joins exons to create an mRNA molecule with a continuous coding sequence.
- RNA splicing appears to have several functions.
  - First, at least some introns contain sequences that control gene activity in some way.
  - Splicing itself may regulate the passage of mRNA from the nucleus to the cytoplasm.
  - One clear benefit of split genes is to enable one gene to encode for more than one polypeptide.
- **Alternative RNA splicing** gives rise to two or more different polypeptides, depending on which segments are treated as exons.
  - Early results of the Human Genome Project indicate that this phenomenon may be common in humans.
- The presence of introns increases the probability of potentially beneficial crossing over between genes.
  - Introns increase the opportunity for recombination between two alleles of a gene.
    - This raises the probability that a crossover will switch one version of an exon for another version found on the homologous chromosome.
  - There may also be occasional mixing and matching of exons between completely different genes.
  - Either way, exon shuffling could lead to new proteins through novel combinations of functions.