Source: KBhBIO101ProteinSynthesis

1 | DNA Transcription

The process of DNA transcription is done by the RNA Polymerase Enzyme. DNA transcription begins by ripping apart hydrogen bonds using DNAse enzyme, then the RNA polymerease reads one side (the "template strand", a.k.a. noncoding "antisene" strand that runs from 3' to 5') of the double helix, recognizing each nucleotide

1.1 | Starting Transcription

1. Series of utility "factors" proteins begin to assemble at the promoter which signals transcription to call the attention of RNA polymerase.
2. RNA polyamerase binds to the Sigma Subunit => form a holoenzyme to unwind DNA — creates a **transcription bubble**
3. Sigma subunit informs the enzyme where to find a promoter (beginning of binding)
4. "Enhancer" gene sequences help bind with activator proteins to help attract RNA polymerase II

Promoters Promoters are the signaling devices that mark the be

- Polymerase Enzyme starts at a promoter (typically found upstream of the 5' start site) and ends at a terminator
    - Box of TATTAA highlights transcription rate and the start site
    - TFIIA cofactor in RNA recognizes TATTAA box, TFIIB recognizes C/CG/CG/CGCCC upstream
- Stronger promoters/enhancers => "enhance" "more." i.e. tumor viruses strengthen promoters for cell growth

1.2 | Transcribing

1.3 | Finishing Transcription

- Pluck the correct corresponding nucleotide out of the nucleus
    - G->C
    - C->G
    - A->**U**
    - T->A
- Prokaryotes lack membrane-bound nucleus (or any organelle)

Definition 1 · **Gene** information that successfully encodes a functional protein or a functional catalytic RNA

RNAs could also be catalysts!

- "Promoter"s denotes beginning of a gene. "Terminator"s denotes the end of gene.

Terminators

- Found in the end of the template sequence
- Two types in prokaryotes

    - Rho-independent terminators — roll back onto itself, causing the RNA to terminate and mRNA to be release
    - Rho-dependent terminators — activate cofactor named rho + unwind the transcribed RNA-DNA hybrid
- In Eukarotes
    - Pol I genes — transcription stopped through termination factor by unwindng the transcribed RNA-DNA hybrid
    - Pol II genes — don't stop until the end, but a polymerase has a "cleavage" mechanism that clips the end out using a poly(A) tail consensus sequence

1.3.1 | Before we continue, two words

- *Non-coding sequence*: metadata for DNA for the processors
- *Coding sequence*: DNA content for amino-acid production