

Source: [KBhBIO101ProteinSynthesis](#)

1 | DNA Transcription

The process of DNA transcription is done by the RNA Polymerase Enzyme. In short summary, DNA transcription begins by ripping apart hydrogen bonds using DNase enzyme * Read one side (“template strand”, a.k.a. noncoding strand) of the double helix, recognizing each nucleotide * 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.

Starting Transcription * Series of utility “factors” proteins begin to assemble to call the attention of RNA polymerase. (#how + #when does this happen? #ASK) * RNA polymerase binds to the Sigma Subunit => form a holoenzyme to unwind DNA * Sigma subunit informs the enzyme where to find a promoter (beginning of binding) * “Enhancer” gene sequences help bind with activator proteins to help attract RNA polymerase II

Promoters

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

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 Eukaryotes
 - Pol I genes — transcription stopped through termination factor by unwinding 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

1.0.1 | Before we continue, two words

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