

(7)
- All 64 codons deciphered by the 1960's ; 61/64 for AA's, 3 for "STOP"

- AUG → methionine or start

→ redundancy but not ambiguity

Reading Frame - reading the symbols in the correct groupings.

↳ the Genetic Code is Universal
(A few tiny exceptions) !!

TRANSCRIPTION Details ...

- RNA Polymerase pulls the 2 strands of DNA apart and builds RNA nucleotides in a strand complementary to the template DNA strand.

→ goes in 5' to 3' direction

→ no "primer" needed

Promoter → the DNA sequence where RNA polymerase attaches and initiates transcription.

Terminator → sequence that signals end of transcription; differences between pro and eukaryotes.

"Downstream" and "Upstream"

i.e. promoter is "upstream" from the terminator.

Transcription Unit → the section of DNA that is transcribed into an RNA molecule.

Detail → bacteria have one type of RNA polymerase for everything
 → eukaryotes have 3 types
 → RNA polymerase II for mRNA synthesis.

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3 stages of Transcription

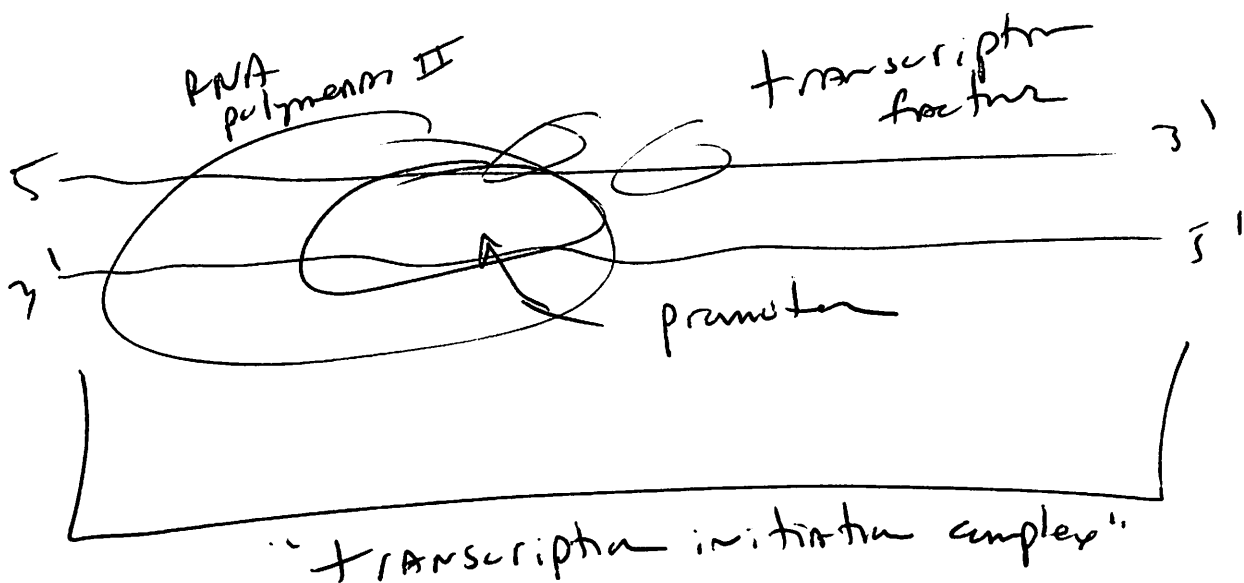
(1) INITIATION

(2) ELONGATION

(3) TERMINATION

Initiation — direct binding of RNA polymerase to promoter in bacteria

→ proteins called Transcription Factors mediate in eukaryotes



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★ in eukaryotic cells, proteins called "transcription factors" mediate the initiation of transcription by RNA polymerase II

Eukaryotic Promoters -

include a TATA Box which is a nucleotide sequence containing TATA (as read from the non-template strand), about 25 nucleotides upstream from the start point.

→ transcription factors, one able to "recognize" the TATA box, must bind to the DNA before RNA polymerase II can bind correctly.

→ RNA polymerase II then unwinds the DNA and transcription begins at the start point on the template strand.

⇒ PROTEIN - Protein interactions control eukaryotic transcription (11)

- 10-20 DNA nucleotides unzipped at a time
- RNA nucleotides are added to the '3 end' of the growing RNA molecule
- the rate is about 40 nucleotides/second
- several RNA polymerases can transcribe the same gene in succession.

Termination

No
MODS
necessary

Bacteria - terminator sequence in DNA transcribes a RNA termination sequence which causes the RNA polymerase to detach.

Eukaryotes - RNA polymerase II transcribes the POLYADENYLATION SIGNAL SEQUENCE which codes (AAUAAA) in the pre-mRNA.
- 10-35 nucleotides downstream from this signal the RNA transcript gets cut from DNA.

RNA Processing (eukaryotes)

- both ends of the primary transcript get altered; intron sections get cut out and remains spliced together.

5' end - synthesized first
 - gets a cap (modified G)
 - 5' cap
 - modified before exit
 - 50-250 Adenines get added
 - downstream from P.S.S.

- called Poly-A tail

Purposes of CAP and TMC:

- (1) facilitate export of mRNA from nucleus
- (2) protect the mRNA from degradation
- (3) help ribosomes attach to the 5' end of the mRNA in the cytoplasm.

UTRs - 5' UTRs and 3' UTRs

→ parts of the mRNA that will not be translated but play a role in ribosome binding

UNTRANSLATED REGIONS!

→ Diagrams on p277 Review!!

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RNA Splicing

27,000 molecules (avg) get reduced to about 1,200 that actually code !!

INTRONS - intervening SEQUENCES

EXONS - expressed into amino acid SEQUENCE (except UTR's)

(exit the nucleus)

→ these terms apply to both the RNA and the DNA sequences that code for them.

★ the eventual mRNA exits with a continuous CODING SEQUENCE

Alternative RNA splicing

→ A single gene can give rise to 2 or more polypeptides depending on how it is spliced.

★ the # of different proteins an organism produces can be much greater than its # of genes

↑ BIG IDEA ↑

Spliceosomes

- made of proteins + RNA's (big!)
- binds to short nucleotide sequences along intron
- intron then released and degraded
- then the flanking exons are joined.

⇒ sRNA's catalyze these events
and participate in recognition

!! BIG a NEW IDEA !!

catalytic RNA

★ Ribozymes - RNA molecules that function as enzymes

⇒ some introns act as ribozymes and catalyze their own excision

So... all biological catalysts are not proteins after all.

How is this possible?

(1) RNA (single-stranded) can base-pair with itself, creating three-dimensional structures.

SHAPE (conformation) plays key role in catalytic activity !! (like proteins)

(2) Some of the bases in RNA contain functional groups that can participate in catalysis (just like proteins)

(3) RNA can hydrogen bond with RNA or DNA, enabling very specific base pairing and precise cuts.

SHAPE
Functional Groups
Hydrogen Bonding

Bringing it all together !!

Recommendations - Re-read 14.4 Tuesday and Wednesday night,
Re-read 14.5 Thursday night