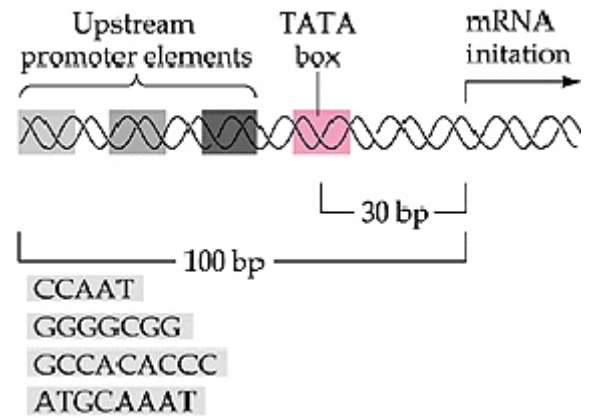


# TRANSCRIPTION

Griffiths et al, 7th: p. 300-306, Brooker 2<sup>nd</sup>: p 311-, Griffiths 9<sup>th</sup>: 295-315  
 rvsd 2/19/93, 2/17/95, 2/19/97, 18 Feb 00, 14 Feb 01, 15 Feb 02, 23 Feb 04, 20 Feb 06, 20Feb08, 20Feb09, 23Feb09, 18Feb11



Where is RNA synthesized?

pulse chase expt with hot uracil showed: (P 297)

**RNA first appears in nucleus, then in cytoplasm.**

Is one strand of DNA used?

Marmur: SP8viral DNA separated on CsCl<sub>2</sub> gradient:( p 300)

**separated DNA strands, cooled rapidly**

**mRNA hybridizes (binds) only to one strand.**

Template strand is termed the **sense strand**.

**TRANSCRIPTION:** (p 300) <http://www.youtube.com/watch?v=WsofH466lqk>

Two regions of homology in all promoters (consensus sequences):

at -35 and -10 (-10 is Pribnow box: TATAAT):

- initiation**      -35: **RNA holoenzyme polymerase** (tetramer, 2  $\alpha$ , 2  $\beta$ ) scans DNA, stops at promoter  
**Promotor:** p 302
- 10: Then **sigma** (promoter recognition, initiation factor) in holoenzyme, unwinds DNA at -10 region forming open promoter complex. The sigma dissociates once elongation begins. (p 307)
- elongation**      5' to 3', similar to DNA synthesis (note the untranslated 5' length upstream fr AUG)
- termination, two types:** (p 303 , 304)
- 1) GC rich region in RNA forms **hairpin loop**, followed by U rich region dissociates
  - 2) **rho** factor for release (NusA protein) attaches to *rut* site, (rho utilization site) pulling RNA off the polymerase using ATP hydrolysis to drive rxn

three types of ribosomal RNA by sucrose gradient: 5S, 16S, 23S

**EUKARYOTIC RNA** (p 304)

2/23/94, 2/23/96, 24 Feb 97, 20 Feb 08

**in eukaryotes, three RNA polymerases,**

polymerase I synthesizes r RNA

**polymerase II synthesizes** mRNA (monocistronic) produce RNA transcripts  
 (once called heterogeneous nuclear RNA)

polymerase III synthesizes tRNA

**Initiation:** TATA-binding protein binds to TATA box, recruits other transcription factors

RNA polymerase II binds to start site.

**Carboxyl Tail Domain (CTD):**

a protein tail which is phosphorylated, facilitates post transcriptional processing

**Co-transcriptional processing:** (p 308)

**cap at 5' end:** begin with guanosine, methylated to form 7 methylguanosine via triPO<sup>4</sup> bond

**tails added to 3' end:** poly A after transcription (stabilizes transcript)

RNA splicing to remove internal portions of transcript

Split genes: **introns** intervening sequences must be removed and

**exons** coding regions must be joined to produce message

**small nuclear ribonucleoprotein (snRNP)** particles perform editing ("ribozyme activity")

**Lariat model** uses a snRNP to recognize --AGGU---AGGU-- (start, stop) to clip out (p 311)

**exon shuffling** allows interchange of domains in proteins, more rapid evolution of proteins (p 309)

