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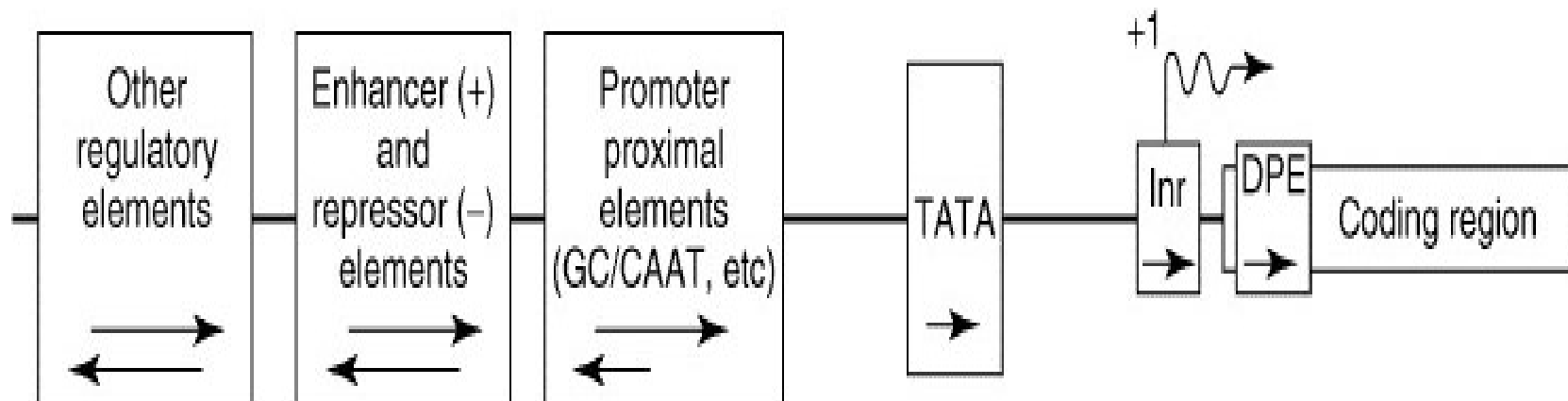
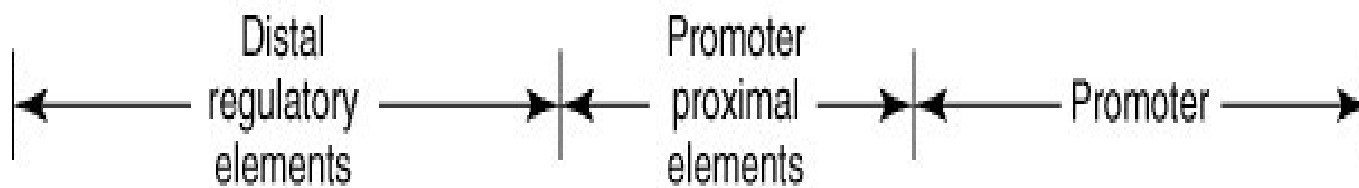
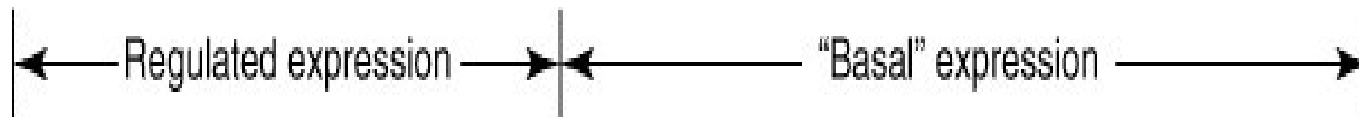
FACULTY OF ENGINEERING & TECHNOLOGY
DEPARTMENT OF BIOTECHNOLOGY

Prokaryotic versus Eukaryotic Transcription

Promoter regions

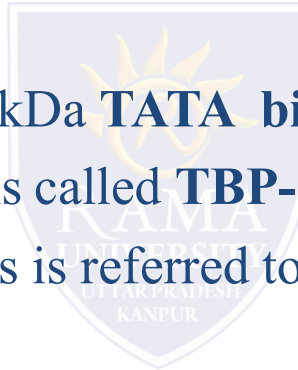
- Eukaryotic promoters are more complex.
- Two types of sequence elements are promoter-proximal and distal regulatory elements.
- There are two elements in promoter proximal, One of these defines **where transcription is to commence** along the DNA, and the other contributes to the mechanisms that control **how frequently** this event is to occur.
- Most mammalian genes have a TATA box that is usually located 25–30 bp upstream from the transcription start site.

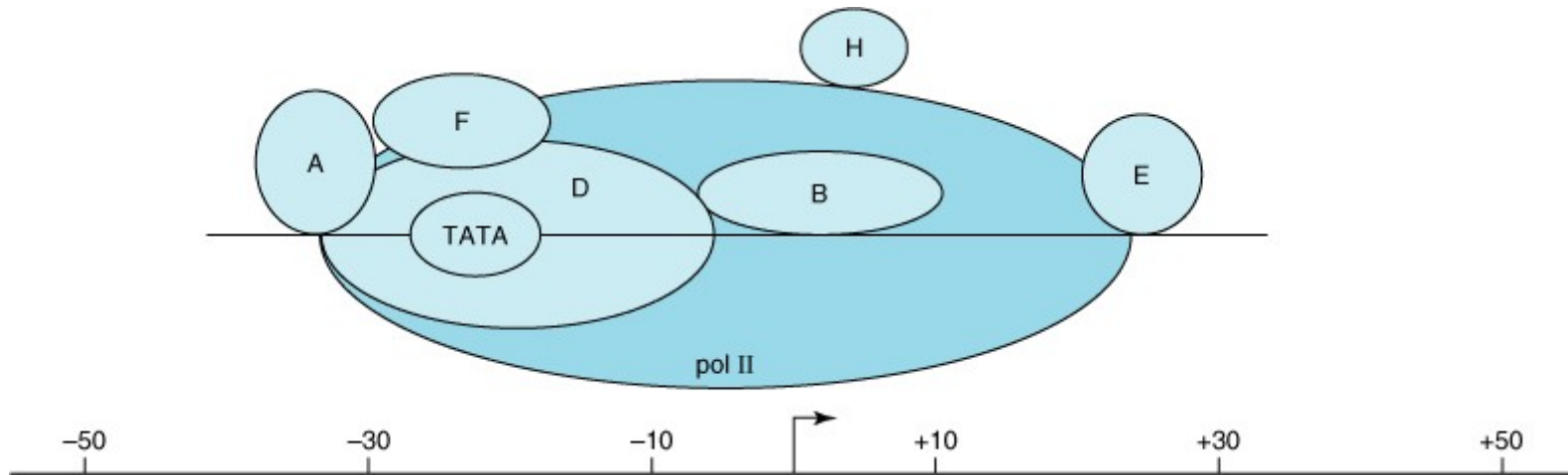
- The consensus sequence for a TATA box is TATAAA, though numerous variations have been characterized.
- Sequences farther upstream from the start site determine how frequently the transcription event occurs.
- Typical of these DNA elements are the GC and CAAT boxes, so named because of the DNA sequences involved.
- Each of these boxes binds a specific protein.
- Distal regulatory elements enhance or decrease the rate of transcription.
- They include the enhancer/ silencer regions and other regulatory elements.



Promoter identification

- In contrast to the situation in prokaryotes, eukaryotic RNA polymerases alone are not able to discriminate between promoter sequences and other regions of DNA
- The TATA box is bound by 34 kDa **TATA binding protein (TBP)**, which in turn binds several other proteins called **TBP-associated factors (TAFs)**.
- This complex of TBP and TAFs is referred to as **TFIID**





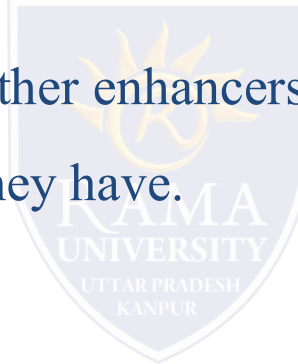
- Formation of the basal transcription complex begins when TFIID binds to the TATA box.
- It directs the assembly of several other components by protein-DNA and protein-protein interactions.
- The entire complex spans DNA from position -30 to +30 relative to the initiation site.

- Binding of TFIID to the TATA box sequence is thought to represent the first step in the formation of the transcription complex on the promoter.
- Another set of proteins—co activators—help regulate the rate of transcription initiation by interacting with transcription activators that bind to upstream DNA elements



Enhancers and Repressors

- A third class of sequence elements can either increase or decrease the rate of transcription initiation of eukaryotic genes
- These elements are called either enhancers or repressors (or silencers), depending on which effect they have.



- They have been found in a variety of locations both upstream and downstream of the transcription start site and even within the transcribed portions of some genes.



- In contrast to proximal and upstream promoter elements, enhancers and silencers can exert their effects when located hundreds or even thousands of bases away from transcription units located on the same chromosome.
 - **Hormone response elements** (for steroids, T_3 , retinoic acid, peptides, etc) act as—or in conjunction with— enhancers or silencers
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Termination of transcription

- The signals for the termination of transcription by eukaryotic RNA polymerase II are very poorly understood.

Processing of primary transcript

- mRNA produced as a result of transcription is not modified in prokaryotic cells. Eukaryotic cells modify mRNA by RNA splicing, 5' end capping, and addition of a polyA tail.
 - Most eukaryotic RNAs are synthesized as precursors that contain excess sequences which are removed prior to the generation of mature, functional RNA.
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