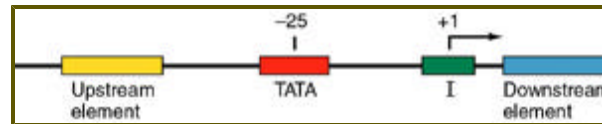


Eukaryotic Class II Promoters and Control Elements

(Reading: Chapter 10, pages 281-289, Class II promoters only; pages 293-295)

Just as prokaryotes, eukaryotic DNA has sequences that dictate the beginning of transcription. These are called promoters. Since there are three polymerases, you will not be surprised to hear that there are three kinds of promoters. Since we are focusing on the activity and products of RNA polymerase II, we will examine the structure of the class II promoters.

Figure 10.25 shows the kinds of structures found in many class II promoters:

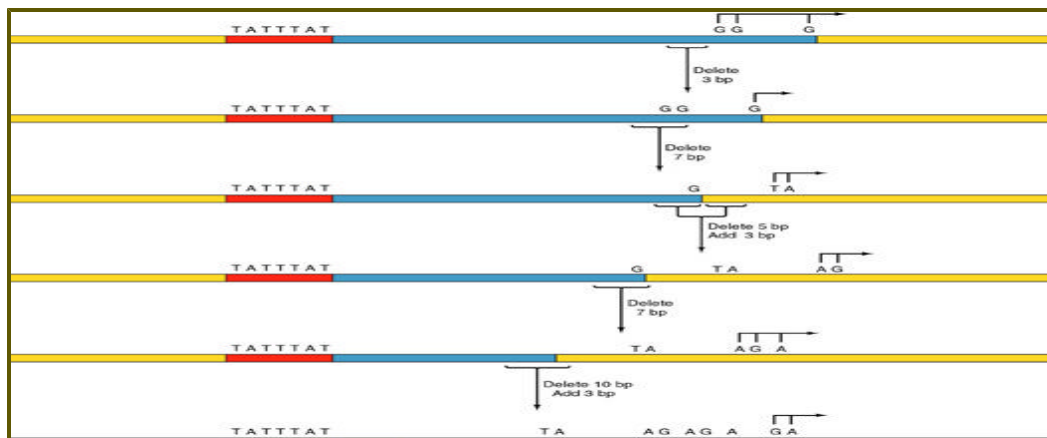


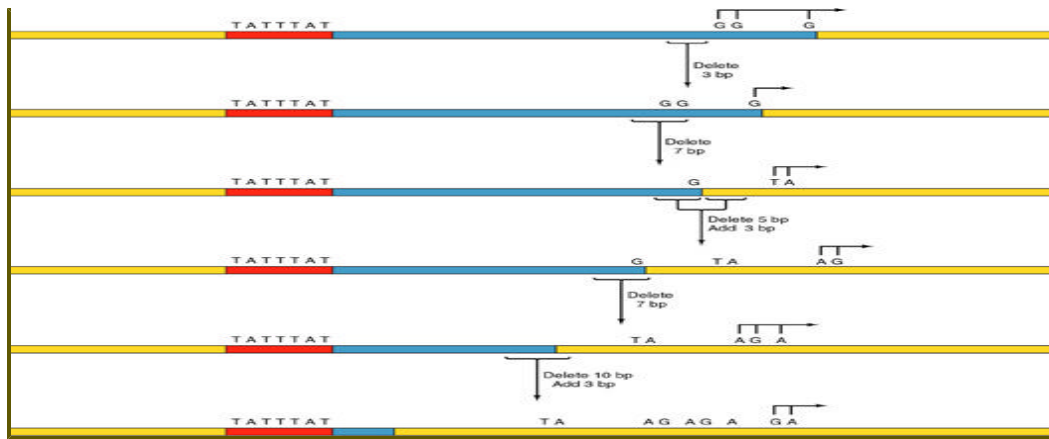
The start point for transcription is at +1. This region contains what is called an initiator sequence. Upstream from that we find the TATA box at -25 and beyond that the upstream elements. In addition, there can be downstream elements. Not all class II promoters contain all of these elements.

The TATA Box:

The sequence region at -25 from the start has the consensus sequence 5'-TATAAAA-3' (the sequence is that found in the non-template strand of the DNA), and is commonly called the TATA box. It is very similar to the -10 sequence of prokaryotes, called the Pribnow box.

The role of the TATA box appears to be the correct positioning of the polymerase to begin transcription. This is most clearly demonstrated, I think, by the experiment outlined in Figure 10.28:



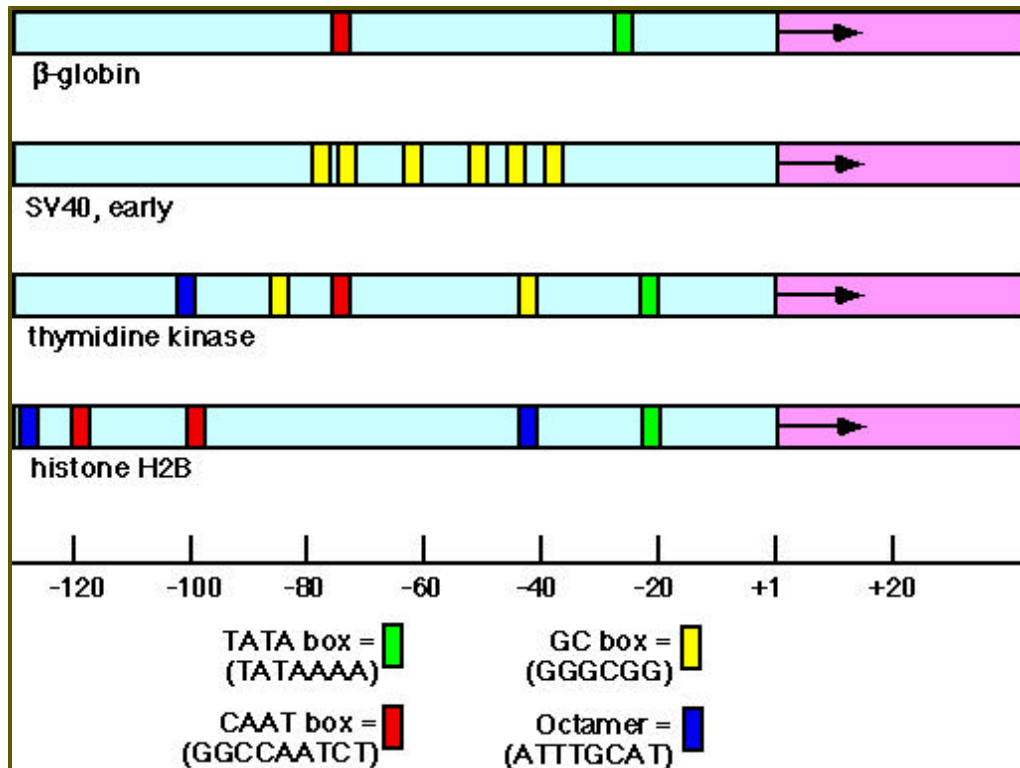


In this experiment, the region between the TATA box and the original start point of transcription was progressively shortened by making small deletions. Each time a deletion was made, the beginning point of transcription was shifted further downstream from the original. This experiment indicates that transcription always begins about 30 bases downstream from the TATA box.

Some genes do not have TATA boxes. Such genes, including the so-called "housekeeping" genes that are always expressed (constitutively "on") in a cell, have other elements that are involved in control, including the upstream elements.

Upstream Elements:

There are a number of upstream elements. Your book mentions two: the GC box (GGGCGG) and the CAT box (CCAAT). Here is a figure I've prepared that shows the relative position of these, as well as one other (the octamer), in representative eukaryotic promoters:



These upstream elements operate by binding certain transcription factors that will be the subject of our next module (Module 10).

Initiator Sequence:

Not all eukaryotic genes have initiator sequence elements at their start point. When they do, they appear to have the consensus sequence PyPy**A**N(TorA)PyPy, where Py means a pyrimidine, N means any base and the A is the start point (+1). Such sequences can function as very simple promoters, although at a low rate of transcription.

Downstream Elements:

There is not consensus sequence here. These elements are only known by the fact that experimental alteration of them changes the transcription of the genes that contains them. It is only important that you know they exist.

The promoters tell the polymerase where to start. However, there are other sequences that affect the rate of transcription. These are called enhancers or silencers.

Enhancers and Silencers:

The rate of transcription in prokaryotes can be altered by binding of proteins to specific sequences (remember cAMP-CAP binding). In eukaryotic cells there are sequences that influence the rate of transcription by interaction with specific proteins.

Sequences that increase the rate of transcription are called enhancers. They can be located near the transcription unit in question or quite distant from it. Here is the control region for a virus, SV40, shown in Figure 10.38:



The two 72 bp regions are the enhancer elements. Notice the GC boxes and the TATA box. In this case, the enhancer elements are located near the transcription unit. Later, we will see examples where the enhancer is quite a distance (kilobases) away.

Silencers, as their name suggest, decrease the rate of transcription or, in some cases, prevent a region from being transcribed at all. We'll come to an example of this when we look at the yeast mating system later on.

In summary, then, eukaryotic transcription has the basic features of prokaryotic transcription except that the enzymes and the sequences are more complex and varied.

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