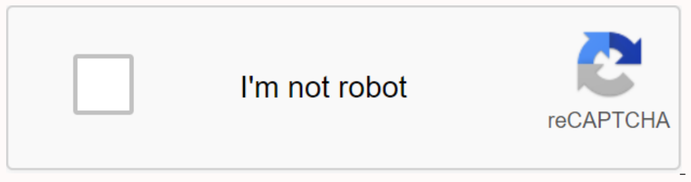

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Transcription process in eukaryotes pdf

By the end of this section, you will be able to do the following: List of steps in eukaryotic transcription Discussing the role of RNA polymerase in transcription Compare and contrast the three RNA polymerases Polymerases Explain the importance of transcription factors Prokaryotes and eukaryotes is basically carried out in the same way transcription process, with several key differences. The most important difference between prokaryote and eukarote transcription is due to the membrane nucleus and organelles of the latter. With the genes associated with the nucleus, the eukariotic cell must be able to transport its iRNA into the cytoplasm and must protect its iRNA from degradation before it is translated. The Ucariotes also use three different polymerases, which each transcribe different subgroups of genes. Ucarion mRNAs are usually monogenic, which means that they determine a single protein. Unlike prokaryotic polymerase, which can bind to a DNA template on its own, the ucariotes require several other proteins called transcription factors to first bind to the promotor region and then help recruit the appropriate polymerase. The characteristics of the synthesis of eukaryotic iRNA are significantly more complex than those of prokaryotes. Instead of a single polymerase consisting of five subdivisions, eukaryotes have three polymerases, each composed of 10 subunits or more. Each ucariotic polymerase also requires a separate set of transcription factors to bring it to the DNA template. RNA polymerase I is located in the nucleocle, a specialized nuclear structure in which ribosomal RNA (rRNA) is transcribed, processed and assembled into ribosomes (Table 15.1). RRNA molecules are considered structural RNAs because they have a cellular role but are not translated into protein. RRNAs are components of the ribosoma and are essential for the translation process. RNA polymerase I synthesizes all rRNAs from the tandem duplicate set of 18S, 5.8S and 28S ribosomal genes. (Note that the designation S applies to Svedberg units, non-charged value that α characterises the rate at which particle sediments during centrifugation. , SCCS polymerase Table II and small nuclear RNAs have moderately sensitive 15.1 RNA polymerase II and synthesize all nuclear pre-MRNAs encoding the protein. Ucarion pre-mRNAs undergo extensive processing after transcription, but before translation. For the sake of clarity, the discussion of this transcription and translation module in eukaryotes will use the term mRNAS to describe only mature, processed molecules that are ready to be translated. RNA polymerase II is responsible for transcribing majority of the ucariotic genes. RNA polymerase III is located in the core. This polymerase transcription of various structural RNAs, which includes 5S pre-rRNA, transfer pre-RAs (pre-tRNAs) and small nuclear preliminarys. RNAs play a key role in translation; they serve as adaptor molecules between the template and the growing polypeptide chain. Small nuclear RNAs have a variety of functions, including splicing pre-mRNAs and regulating transcription factors. A scientist who characterizes a new gene can determine which polymerase transcriminaps it by testing whether the gene is expressed in the presence of α-amanitin, an oligopeptide toxin produced by the muhomor mushroom and other species of amanies. Interestingly, the α-amanitin affects three polymerases very differently (Table 15.1). RNA polymerase I is completely insensitive to α-amanitin, which means that polymerase can transcribe DNA in vitro in the presence of this poison. RNA polymerase III is moderately sensitive to the toxin. In contrast, RNA polymerase II is extremely sensitive to α-amanytin. The toxin prevents the development of the enzyme by DNA and thereby inhibits transcription. Knowledge of the transcription of polymerase can give clues to the general function of the researched gene. Since RNA polymerase II transcripts most of the genes, we will focus on this polymerase in our follow-up discussions about eukaryotic transcription factors and promoters. Eukaryotic promotions are much larger and more complex than prokaryotic organizers. However, both have a sequence similar to -10 sequences of prokaryotes. In eukaryotes, this sequence is called the TATA box, and has the consensus TATAAA consensus of the encoding direction. It is located on -25 to -35 bases relative to the place of commencement (+1) (Figure 15.10). This sequence is not identical to the E. coli -10 box, but retains an A-T rich element. The thermostableity of A-T bonds is low, and this helps the DNA template to develop locally in preparation for transcription. Instead σ a simple factor that helps to connect prokaryotic RNA polymerase to its promotor, eukaryotes assemble a complex of transcription factors needed to dial RNA polymerase 2 polymerase gene system. Transcription factors that are associated with the organizer are called basal transcription factors. These basal factors are called TFII (for transcription factor/polymerase II) plus an additional letter (A-J). The main complex is TFIID, which includes a TATA-binding protein (TBP). Other transcription factors are systematically placed on the DNA template, each of which further stabilizes the complex before starting the procedure and contributes to the recruitment of RNA polymerase II. Figure 15.10 A generalised promoter of a gene transcribed from RNA polymerase II is displayed. Transcription factors recognize the organizer. RNA polymerase ii then binds and forms the transcription initiation complex. Scientist shrinks the eukariotic in front of a bacterial gene and inserts a gene in a bacterial chromosome. The bacterium will copy the gene? Some eukaryotic stimulators also have a preservative CAAT box (GGCCAATCT) approximately -80. Further at the beginning of the TATA box, eukaryotic promoters may contain one or more GC-rich boxes (GGCG) or octamer boxes (ATTTGCAT). These elements bind cell factors that increase the efficiency of transcription and are often identified in more active genes that are constantly expressed by the cell. Basal transcription factors are crucial for the formation of a DNA template predestination complex, which subsequently recruits RNA polymerase II to initiate transcription. The complexity of eukaryotic transcription does not end with polymerase and promoters. An army of other transcription factors, which are associated with upstream enhancers and silencer, also help regulate the frequency with which pre-iRNA is synthesized by a gene. Amplifiers and silencers affect the efficiency of transcription, but are not necessary for transcription. The processes of bringing RNA polymerase I and III into the DNA template include slightly less complex collections of transcription factors, but the common theme is the same. The preserved promotional elements for genes transcribed from polymers I and III differ from those transcribed by RNA polymerase II. RNA polymerase I transcribes genes that have two GC-rich promoster sequences in the area -45 to +20. These sequences are sufficient to start transcription, but the organizers with additional sequences in the region from -180 to -105 upstream at the place of initiation of the procedure will further improve the start. Genes that are transcribed from RNA polymerase III have upstream promoters or stimulators that appear in the genes themselves. Eukaryotic transcription is a strictly regulated process that requires different proteins to interact with each other and with the DNA chain. Although the process of transcription in eukaryotes involves a greater metabolic investment than in prokaryotes, it ensures that the cell transcribes exactly the pre-mRNAs it needs for protein synthesis. The evolution of genes can be a familiar concept. Mutations can occur in genes during DNA replication, and the result may or may not be beneficial to the cell. By changing an enzyme, structural protein or any other factor, the mutation process can transform functions or physical characteristics. However, eukaryotic stimulators and other gene regulatory sequences can also develop. For example, think of a gene that over many generations has become more valuable to the cell. Perhaps the gene encodes a structural protein that cells need to synthesize in abundance for a certain function. If so, it would be useful for the cell for this gene promoter to recruit transcription factors more efficiently and gene expression. Scientists studying the evolution of promotor promotor sequences In part, this is because it is difficult to conclude exactly where the ucarriotic promotor begins and ends. Some stimulators occur in genes; others are located very upwards or even downstream of the genes they regulate. However, when the researchers limited their study to sequences of the human main promoter, which were defined experimentally as sequences that connect the predestination complex, they found that promoters developed even faster than protein-encoding genes. It is not yet clear how the development of a promotor can correspond to the evolution of humans or other complex organisms. However, the evolution of a promoter to make more or less of a gene product is an intriguing alternative to the evolution of the genes themselves. After the formation of the pre-release complex, polymerase is released from other transcription factors, and elongation is allowed to prokaryotes, as well as in prokaryotes with polymerase synthesizing pre-iRNA in the direction of 5' to 3'. As discussed before, RNA polymerase II transcribes the main share of eukaryotic genes, so in this section we will focus on how this polymerase achieves prolongation and termination. Although the enzyme process of prolongation is essentially the same in eukaryotes and prokaryotes, the DNA template is significantly more complex. When ukaryotic cells are not divided, their genes exist as a diffuse mass of DNA and proteins called chromatin. DNA is tightly packed around loaded histone proteins at repeated intervals. These DNA-histone complexes, collectively called nucleosomes, are regularly distributed and include 146 nucleotides DNA hack about eight histones as a thread around a spool. To obtain a synthesis of polynucleotide, the transcription apparatus must move out of the way every time it encounters the nucleosome. This is achieved through a special protein complex called FACT, which means facilitating chromatin transcription. This complex distances histumes from the DNA template as polymerase moves along it. After pre-mRNA is synthesized, the FACT complex replaces histoni to recreate nucleosomes. Termination of transcription is different for different polymers. Unlike prokaryotes, the prolongation of RNA polymerase II in eukaryotes is carried out from 1000 to 2000 nucleotides after the end of the transcribing of the gene. This pre-iRNA tail is subsequently removed by splitting during the processing of iRNA. On the other hand, RNA polymerases I and III require termination signals. Genes transcriminates from RNA polymerase I contain a specific 18-nucleotide sequence that is recognized by the term protein. The termination process in RNA polymerase III involves an iRNA hairpin similar to a ro-independent termination of transcription in prokaryotics. they are prokaryotes.