

Cell and Molecular Biology
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Week 10
Central Dogma of Molecular Biology (Part 2)
Lecture - 38
Transcription (Part 1)

Hello everybody, this is Dr. Vishal Trivedi from the Department of Biosciences and Bioengineering, IIT Guwahati. So in today's lecture, we are going to discuss some more aspects related to the central dogma of life. So what we have discussed so far is the DNA-dependent DNA synthesis. DNA-dependent DNA synthesis is a process where you can synthesize a new copy of DNA. And once you have synthesized the new copy of DNA, that new copy of the DNA is responsible for the synthesis of the RNA molecule, and this process is called transcription.

RNA is going to be synthesized in exactly the same sequence as the DNA molecule. So, in today's lecture, we are going to discuss transcription. So, as the name suggests, transcription means deriving information from other molecules. So, in this case, you are actually taking the information from the DNA molecule and utilizing this information or utilizing the nucleotide sequences that are present on the DNA.

You are synthesizing the different types of RNA molecules: you are synthesizing the ribosomal RNA molecule, you are synthesizing the transfer RNA, and you are also synthesizing the messenger RNA molecule; this process of synthesizing the different types of RNA molecules from the DNA is called transcription. So, every cell contains three different types of RNA molecules: transfer RNA (tRNA), ribosomal RNA (rRNA), and messenger RNA (mRNA). Synthesis of the RNA from the DNA template with the help of an enzyme called DNA-dependent RNA polymerase is known as transcription. It occurs unidirectionally in which the chain is synthesized from 5 prime to 3 prime, and the segment that is transcribed from the DNA is known as the transcription unit. So, unlike the replications, if you recall, the replication is a bidirectional process, which means it can be run from the left side to the right side or from the right side to the left side.

But in the case of transcription, it is unidirectional and runs only in the direction of 5' to 3', and the particular segment that is going to be synthesized or transcribed from the DNA is known as the transcriptional unit. In eukaryotes, you have the monocistronic transcriptional unit, which occurs when the coding sequence is present for only one polypeptide. Whereas in the case of prokaryotes, the polycistronic transcriptional unit occurs in which the coding sequence is present for more than one polypeptide sequence. So, what you see here is actually one individual transcriptional unit. When you transcribe

the DNA, you are going to get one transcriptional unit where you will have the promoters, the RNA coding sequence, and the terminators.

So, during the transcription, you are going to synthesize three different types of RNA molecules: the ribosomal RNA molecule, the tRNA molecule, and the messenger RNA molecules. Transcription, as you have seen when we were discussing replication, also. That replication also has discrete steps like initiation, elongation, and termination. Similarly, in the transcription, we also have the discrete steps when the transcription is going to start and when the transcription is going to stop, so that it actually gives you a synthesized RNA, which is called the transcriptional unit. So let us see what the different steps are in the transcription.

So, in transcription, you are going to have all the transcriptional units. So this is one of the transcriptional units that you are going to have. So in this, you are going to have a starting point, you are going to have the upstream sequences, and you are going to have downstream sequences. So, what is the starting point? So, it is the first base pair from which transcription starts, and it is called the transcription start site. RNA polymerase moves from the start point along the template and synthesizes the RNA up to the terminator sequence, which means that if this is the gene that is responsible for or is going to be utilized for transcription, Then you are going to have a promoter sequence, a coding sequence, and a termination sequence.

And in this, you are going to have the starting point, which is going to be somewhere here, and from here, actually, the first base pair of the DNA is going to transcribe, and that is how you are going to have the RNA, which is responsible for the coding sequence. And then the RNA will go to the termination site, and that is how it is actually going to give you a synthesis of the RNA that is responsible for this particular sequence. Then, along with this start site as well as the end site, you are actually going to have the upstream and downstream sequences. So in the upstream, it is a non-template nucleotide at the five prime end or in the minus direction and sequence. These are the sequences before the starting point.

So these are the upstream sequences that are actually going to facilitate the binding of RNA polymerase, and that's how they are going to help in terms of the transcription of this particular sequence. Then you are going to have the downstream sequences, so downstream sequences are actually going to be present in the plus direction, and these sequences are after the start point. Since the DNA is double-stranded, you can actually have the two different templates that can be utilized for the transcription side. In this one, you have blue-colored DNA and black-colored DNA. So ideally either of these DNAs can be utilized for the transcriptions.

So when you talk about the transcription, you see that the DNA has double-stranded structures. So, during transcription, only one strand is transcribed. So that the transcribed sequence is identical to one of the strands of the DNA, and this strand that is going to be utilized for transcription is called the coding or sense strand, whereas the other complementary strand is known as the template or anti-sense strand. So, which means if this is the double-stranded DNA, you can have the two strands; you can have a strand running from the 5' to 3' and the other strand running from the 3' to 5'. And what you see here is that the only one of the strands, as I said, when the transcription is unidirectional, it can be run for both the templates above the DNA strands, but it will only be in a single direction.

So transcription is always in the direction of 5 prime to 3 primes. which means it is actually going to utilize the 3 prime to 5 prime sequence as non-coding strands, or it is also called the template strands. Whereas it is going to synthesize the RNA that matches the DNA sequence present from the 5 prime to 3 prime, this strand is called the coding strand, which means this strand is also called the sense strand. The other strand is also called the antisense strand; these are the different names for the different types of strands. For example, the strand that is going to be used for synthesizing the RNA is called the non-coding strand or the template strand; this is also called the template strand, so this is going to serve as a template, right? And the RNA that is going to be synthesized is going to be called the coding strand.

So this is going to be because the nucleotide sequence of this RNA is going to match the sequence that is present in the DNA. And that is why this strand is going to be called the coding strand or the sense strand. Now, the transcription can happen in the is the universal. So, transcription can happen in the eukaryotic cell or transcription can happen in the prokaryotic cell. So, it can happen in a prokaryotic cell.

So, in both cells, the steps of transcription are almost identical: you have initiation, elongation, and termination, but the different types of factors responsible for eukaryotic and prokaryotic transcription are different. The places where eukaryotic or prokaryotic transcription is taking place are also different, and the machinery that participates in eukaryotic or prokaryotic transcription is also different. So, let us, before going into the discussion about the transcription in prokaryotes or transcription in eukaryotes, see the differences between the transcription of eukaryotic and prokaryotic organisms. So transcription is different in terms of the machinery involved, the places where it is going to take place, and the different types of steps. So what is the difference between transcription in eukaryotic and prokaryotic cells? So, the first difference is that for prokaryotic transcription, it is polycistronic, which means the single RNA is going to

transcribe for the different types of polypeptide chains.

So, whereas in the case of eukaryotes, it is going to be monocistronic. Then the second is, as you know, that the bacteria do not have a nucleus, so everything that is happening is inside the cell; right, it is within the same cell or within the cytosol. So that's why the site of transcription in the case of prokaryotes is the cytosol, whereas the site of transcription in the case of eukaryotes is. The DNA is present inside the nucleus. So transcription is going to occur for the eukaryotic cell inside the nucleus, and once the RNA is synthesized, it is transported outside the nucleus, where it participates in protein synthesis.

Since there is no nucleus, we can actually have the coupled transcription and translation process, which means that as soon as this RNA is synthesized, it is utilized for the protein production machinery, and that is how it actually starts producing the protein. So, this is called the coupled transcription and translational process, which means it is actually going to be called the co-translational process. This means that as soon as the transcription starts, it also allows the protein production machinery to attach to these RNA molecules, and that is how it actually begins the translation. Whereas, in eukaryotic cells, that is not the case; transcription is occurring inside the nucleus. So, once the transcription is over, the nucleus is going to transport the synthesized messenger RNA as well as all other RNA species, and then these RNA species are going to go into the cytosol, and that is how it is actually going to do the translation.

So, transcription is going to occur in the nucleus. Whereas the translation is going to occur inside the cytosol. So, that is why these two processes are not linked to each other, they are not going to occur simultaneously. In the case of prokaryotes, you require a single type of RNA polymerase for all types of RNA molecules. Whereas, in the case of eukaryotes, you require three different types of RNA molecules or RNA polymerase for the synthesis of all types of RNA molecules.

Then, in the case of prokaryotes, there is no need to have any transcription factors for initiation, which means that the RNA polymerase present in the prokaryotic system is fully independent in terms of initiating transcription, whereas in the case of eukaryotes, it requires transcription factors for initiation. So, this is a very important step because it actually gives more control over the process of transcription. In the case of prokaryotes, whenever the RNA polymerase wants, it can actually go and start the transcription. Whereas in the case of eukaryotes, it is not so. Even if the RNA polymerase is present, if the required transcription factor is not present, transcription cannot be started.

So, that is why eukaryotic transcription is going to be more tightly controlled compared

to prokaryotic transcription. Then, as far as the structure of the polymerase is concerned, the polymerase in the case of the eukaryotic and prokaryotic systems is made up of 5 different subunits, whereas in the case of RNA polymerase, RNA polymerases are made up of 10 to 15 subunits in eukaryotic cells. So these are a few of the classical differences in the transcriptional process between the prokaryotic and eukaryotic systems. So if you take home the message, what are the three important points? What are the differences between transcription in prokaryotes and eukaryotes? The number one is the location. So, the location of transcription in the case of prokaryotes is the cytosol, whereas the location is going to be the nucleus in the case of eukaryotes.

The transcription and translation are going to work together or simultaneously in the case of prokaryotes, whereas they are going to be separate in the case of eukaryotes. Number 3 is that it is going to be more controlled in the case of eukaryotes, so transcription depends on the transcriptional factors. So, that is why it is going to be more finely controlled in the case of eukaryotes, whereas it is less controlled because it does not require the transcription factors. So, we are going to start discussing the transcription in prokaryotes and then we are going to discuss the transcription in eukaryotes. So, when we want to start the discussion about transcription in prokaryotes, first we have to discuss the machinery.

So, in the case of prokaryotes, the only machinery that we require is RNA polymerase, right? So, in prokaryotes, a single type of RNA polymerase is present, which is responsible for the synthesis of all types of RNA. Eubacterial RNA polymerase is termed the holoenzyme, and it is a multisubunit protein that contains the five subunits. You have the 2 alpha subunits, 2 beta subunits, and 2 sigma subunits, which means you have the 2 beta subunits beta and beta prime; you have the 2 alpha subunits alpha and alpha. And you also have a sigma factor. So, alpha is required for the assembly of the core enzyme, beta and beta prime are going to perform all enzymatic and catalytic functions, and sigma is actually required or sigma is a factor that is responsible for the recognition of the promoter sequence.

So, the promoter is the upstream sequence that indicates where to bind, and then it actually starts the synthesis of the RNA polymer. So, it actually going to initiate the RNA transcriptions. Two alpha and two beta are going to be formed together, and that is all going to form as a core enzyme. When the core enzyme actually mixes with the sigma factor, it forms the holoenzyme. which means the RNA polymerase in prokaryotes is actually going to be present always as a core enzyme, which means it is going to have the four subunits: alpha, alpha, beta, and beta prime.

But as soon as the sigma factor comes and joins, it actually forms the holoenzyme, and

this holoenzyme is functionally active. So, it is going to start with the transcription. So, it is going to start the transcription. So, as soon as the sigma factor is not going to combine with the core enzyme, the holoenzyme is not going to form, and that is why it is not going to participate in the transcriptional activities. Now, the second thing is about the promoter, right? So, prokaryotic promoters are.

Promoters typically consist of a 40 base pair region located near the 5' prime end of the transcriptional start site. So remember that when we are showing you the typical transcriptional unit, we have the coding sequence and then upstream to the coding sequence is the region of the promoter. The promoter region consists of the -6, -2, -6 base pair consensus sequence elements, which are called the Pribnow box or the -35 region and the -10 region. Then the Pribnow box is a 10 base pairs upstream of a start codon, and it is a consensus sequence of T A T T T A. Whereas the -35 region has a consensus sequence that is called the TTGA CA.

So this is what you are going to have: you are going to have a -10 region, and then you are going to have the -35 region. In the -10 region, you are going to have the Pribnow box, which is going to have a consensus sequence called TA, TAAT. Whereas this is going to be the starting point, this will be the +1 site, and above this, in the -10 region, you are going to have the Pribnow box, and in the -35 region, you are going to have the sequences. So, these are the optimal sequences that are present in the promoter of prokaryotic genes, and they are actually going to be responsible for facilitating transcription.

Now, once we are talking about the process, transcription in prokaryotes would be a four-step process. In the first step, you are going to have the template binding. In step two, you are going to have the chain initiation. In step three, you are going to have the chain elongations. And in step four, you are going to have the terminations.

So, in step one, you are going to have the binding of RNA polymerase to the template DNA and the chain initiation. So, the DNA duplex should be opened so that the RNA polymerase can approach the single-stranded DNA templates. The efficiency of the initiation is inversely proportional to the melting temperature T_m , and the AT rich has a lower T_m due to the double hydrogen bonding stabilizing it more than the triple bond in the GC rich region. So, the place where it is actually going to be able to melt the DNA more nicely or more easily is where you are going to have the AT rich sequences because AT is going to have 2 hydrogen bonds, whereas GC is going to have 3 bonds.

So, there are 3 hydrogen bonds. So, because of that, if the initiation is that the unit is going to be opened up by the RNA polymerase very easily, they can utilize the DNA as a

template if the DNA has more of the A or T sequences. The efficiency of initiation is inversely proportional to the melting temperature, and the AT-rich region is going to have the lower T_m because of the double hydrogen bonding stabilization compared to the GC-rich region. Therefore, the AT-rich region is better for the melting of duplexes and easier to create the open promoter complex than the GC-rich region. RNA polymerase has a sigma factor that recognizes the promoter sequence to which the RNA polymerase holoenzyme binds and forms a complex known as a closed complex. So, initially, it will go and bind to the region where it is easy to melt the DNA, within the promoter region, and then it is actually going to unwind the DNA, and that is how it is actually going to form the closed complex.

And the sigma factor that is present in the holoenzyme is responsible for recognizing the promoter sequence, or it is actually recognizing the sequence where it is easy to melt. So, in fact, the sigma factor is released when the chain reaches nearly up to 10 bases, leaving the core enzyme for elongation. So, as soon as the chain is going to enter or as soon as the RNA polymerase enters the initiation step and goes for the 10 nucleotides, then the sigma factor is going to be removed, and that has a very good advantage because you can have the sigma factor recognize the promoter. So, as soon as the sigma factor recognizes which is a part of the RNA polymerase. is going to recognize the promoter and when the transcription is going to start.

So, you can imagine that transcription is going to start and will continue for 10 nucleotides. Once the 10 nucleotides are over, the sigma factor is going to be released. So, the sigma factor is going to be released, and now this sigma factor is free. This vector sigma factor can assemble with another RNA polymerase, right? So, it can actually assemble with another RNA polymerase, and that is how it can help the other RNA polymerase molecule recognize another gene or another promoter, and that is how it can actually channelize the machinery for maximum outcome. So, you do not have to synthesize the many types of sigma factors.

You can actually work with one or two sigma factors to recognize the different types of promoters, and that is why you can utilize the factors more optimally. Now, once the binding of the RNA polymerase and the chain initiation has been done, it is actually going to enter into the next phase. So, in the next phase, it is actually going to have the binding of RNA polymerase to the chain initiation correctly, as we have already discussed. Then we are actually going to form the open complex. So, within the step, once the closed complex is converted into an open complex by melting the short region of DNA, like the 10 minus 10 base pair regions.

The RNA polymerase binds at the promoter region and unwinds it to cover the minus 55

to plus 1 region, which means the 55 to 50 to 55 base pairs. And it start the initiation here one template strand available for incoming nucleotide for the base pairing and the synthesis of RNA occurs. So, what happens is that the RNA polymerase will assemble with the sigma factor and then it is actually going to bind to the template. And, it is actually going to start melting the minus 10 regions, and once it starts melting the minus 10 regions, it will then bind the promoter region. So, when it is going to bind the promoter region, it is going to start the initiation steps.

The minus 10 region of the template is essential for recognition. The promoter regions are double-stranded in the closed complex and single-stranded in the open complex. So, once it melts the DNA, it is actually going to form the open complex, which means that in that open complex, one of the templates of the DNA is going to be available as a template, the other strand, so that the RNA polymerase will take that information, the nucleotide information from that template strand, and then it starts synthesizing the RNA. See, RNA polymerase has two binding sites for the nucleotides. It has the initiation sites, and it has the elongation sites.

So, it has two different types of activities for the nucleotide. Once it actually can recognize the nucleotides, that is how it can participate in the initiation sites, or it can also have the elongations. See the initiation site bind the first nucleotide within the open promoter complex as the plus one site. which is usually a purine-rich A or G sequence.

It means the first nucleotide can be ATP or GTP. The elongation scan site binds to the second incoming nucleotide base pairing at the plus 2 position. The two nucleotides are joined together, the first base is released from the initiation site, and the initiation is complete, which means the RNA polymerase has the two sites for the nucleotides. One is the initiation site, which is going to recognize the first nucleotides that are present at the plus 1 site, and that nucleotide could be either A or G, right? The second is the elongation site that is going to recognize the second incoming nucleotide. It binds to the first nucleotide, and then it will enter and start synthesizing the second nucleotide by utilizing the elongation sites; once it enters the elongation site, the initiation steps are over, and then it will enter the elongation phase. What will happen in the elongation phase is that chain elongation occurs in the 5' to 3' direction; RNA synthesis is carried out by the transcriptional bubble, which forms due to the transient separation of double-stranded DNA into a single-stranded DNA, and transcription takes place at the template strand.

So what you have is? See, this is the site where the DNA binds. So, this is the site where you have the promoters. So, initially, the sigma factor will come and start binding; then it is going to form the open complex. So, this is actually the open complex. Now, within the open complex, you have, "this is the template strand; this is the template strand.

" So, this black one is a template strand. And this blue one is the coding sequence, right? Or this is called the non-coding sequence, and what will happen is the RNA at site one, right? So, plus one site, you are going to have plus two sites, as plus one site RNA polymerase will go and sit, and then it will actually be looking for a nucleotide like A or G, and then it is going to start the transcription. As soon as it will start transcription, so it is actually going to keep utilizing this information. So, if you have the A, it is going to put the T into the template, right? So, if it is A, it is actually going, not T; it is going to synthesize the U and so on. So, if you have G, it is going to synthesize the C, and if you have a C, it is going to. So, it is going to read the incoming nucleotides utilizing the elongation site within the RNA polymerase, and that is why it is actually going to start synthesizing the RNA, and you will see the RNA coming out from this.

Transcriptional unit, and that is how this RNA is going to be utilized by the protein synthesis machine that we are going to discuss in our subsequent lecture, and that is how the protein synthesis machinery is going to bind this nascent RNA, and that is how it is actually going to participate in the protein synthesis. So, the chain elongation is going to occur in the 5' to 3' direction, right, and it is going to be unidirectional. So, RNA chain synthesis occurs basically in the 5 prime to 3 prime direction by adding the nucleotide at the 3 prime end. The 3' prime OH of the last nucleotide is combined with the incoming 5' prime nucleotide, and the alpha and beta phosphate groups are removed, leaving only the gamma phosphate to be used in the formation of phosphodiester bonds. Likewise, the other nucleotides added are complementary to the template strand, and thus the translocation of the RNA chain strands occurs.

In bacteria, the transcription rate is nearly 40 to 50 nucleotides per second at 37 degrees Celsius, which is nearly the same as the translation in prokaryotes, which means 50 amino acids per second. RNA polymerase binds to the promoter and creates a transcriptional bubble. See RNA polymerase moves along the DNA, and the RNA chains grow continuously. The length of the transcriptional bubble is approximately 12 to 14 base pairs. So this 12 to 14 base pair transcriptional bubble is going to be opened to allow the RNA polymerase to read the template strands, and then it is actually going to, based on the nucleotide present on the template strand, start putting the complementary strands into the RNA molecules.

So, the 12 to 14 base pair length of the DNA-RNA hybrid is about 8 to 9 base pairs. So, within this 8 to 9 base pairs, DNA RNA hybrids are going to form. As the RNA polymerase moves, the duplex reforms again, right? So, as soon as the RNA polymerase moves on, the remaining DNA strand is actually going to coil back because there is a big difference between replication and transcription, right? You are supposed to remove the

helicases and topoisomerases, and then you also have to remove the single-stranded DNA binding protein so that you can unbind the DNA. Whereas in this case there is no such requirement that the RNA polymerase will be able to melt the DNA and will be able to start the transcription. So it is actually going to happen as soon as the RNA polymerase moves, there will be a factor responsible for the DNA to remain single-stranded.

So, it will again unwind, and the RNA hangs as free polynucleotide chains. Nucleotides are added covalently to the 3' end of the chain of the RNA. Beta and gamma phosphates are removed from the incoming nucleotide, and the adverse group is removed. And present at the end of the chain. So, as soon as the RNA polymerase is moving, it starts adding the nucleotides, and in this case, it is actually going to utilize the 3 prime end of the chain.

So, the 3' end of the chain is going to have the 5' end of the incoming nucleotide, and that is how it is going to synthesize, and that is how it is going to have the transcription in the direction of 5' to 3'. Now we are going to have the next stage; the next stage is the chain terminations. When the RNA polymerase stops adding nucleotides to the RNA chain, it releases a complete product, and the RNA gets free from the termination sequences. During termination, all the hydrogen bonds that hold the RNA-DNA hybrid together break down, and then the RNA chain is separated from the DNA, reforming the duplex. The site at which the enzyme stops adding nucleotides is known as the termination site, so when this bubble-like transcriptional bubble keeps moving and then reaches the transcriptional site or transcriptional termination site, it actually stops at that site.

There is no template strand, so the template strand does not provide any information for adding the nucleotides, and that is why the RNA polymerase stops adding the nucleotides. As soon as the RNA polymerase stops adding the nucleotides, the DNA-RNA hybrid is destabilized, and that is how it is removed, leading to the termination of transcription. In prokaryotes, we can have two different types of termination. One is called the intrinsic terminations, and the other one is called the row factor-dependent terminations.

So, let us look at the intrinsic terminations. In an intrinsic termination, in this mechanism of termination, the row factor is not required for the termination, and it depends on the RNA products. It required a GC-rich hairpin. So the hairpin structure is followed by the 7U structure. So what you see here is that this is the termination sequence where you have very high GC-rich content. So when you have a very high GC-rich content, first of all, this particular region is not going to be melted by the RNA polymerase.

And then it also has a hairpin-loop kind of structure. So you see, it's going to flip, right? And that's how it is actually going to form. So, the RNA-DNA hybrid requires the forces to hold the elongation factors and the elongation complex together; then the hybrid gets detached. It collapses the elongation complex, which causes the termination. In this type of termination, the dissociation of the polymerization occurs by destabilizing the attachment of the growing chain to the template. During this process, the hairpin structure is formed by transcription via complementary base pairing.

It includes palindromic sequences; this stem loop structure includes the GC-rich region by the U region. So, what you see here is that it has a GC-rich hairpin, and because of this, it is followed by 7 U residues on both sides, and that is how it is actually going to form the hairpin loop. So, what are the different steps in intrinsic terminations? So, here we have the two inverted GC-rich regions.

So, you have the two inverted repeats, like GCC and CGC. So, this is what you have. So, these are present in the DNA template which is transcribed. So, nearly six adenine residues follow the second inverted repeat. So, you have the 2 repeats; one is on this side, and the other one is on this side. So, as soon as this inverted repeat is being transcribed.

It is going to be followed by the 7 A residues. So, this is going to be 7 A residues that are going to be formed. And you know that the A is actually going to have the, when the A is present in the DNA, it is actually going to give you the U in the RNA molecule because that is complementary. So, it is going to give you the A and the U in the RNA molecule. So, it is actually going to form a much less stable DNA-RNA hybrid, and at the same time, inverted repeats are forming a hairpin-like structure. So, in the end, all these inverted repeats that are present here are actually going to form a hairpin-like structure.

So, one repeat you have on this side, the other repeat you have on this side, and that is why when they come together, they will be formed into the RNA; they will actually form a hairpin-like structure like this, and this hairpin-like structure is going to be attached. They are going to be connected to the DNA by the U U U-like sequences, and then these U U U-like sequences or the DNA-RNA hybrids, because of the interaction between the A and U, are going to be weak. Since it is going to be weak, it is actually going to detach from the template. So, due to the formation of the stem-loop structure, the AU bond is broken down, leading to termination and the RNA molecule being operated on.

So, that is why this is going to happen. Once the RNA polymerase reaches the termination site, you will have this GC clamp at the termination site. And this clamp is followed by the A7A nucleotides, and this J1GC clamp is actually going to form a hairpin-like structure, and once the hairpin-like structure is formed, it is actually going to

stop the growth of the RNA polymerase, and that is how it is actually going to hold here. Since it cannot remain on the template for a longer period of time because the stability of the A to U interaction is very low, the RNA polymerase along with the synthesized RNA is going to be removed from the templates. Now, the second mechanism is the row dependent mechanism.

So, the row-dependent mechanism depends on a protein called the row protein. So, this type of termination requires the row proteins, and row is an ATP-dependent helicase that disrupts the RNA-DNA hybrid. It is an essential protein which causes the transcriptional terminations and Rho protein is a hexamer. So, Rho protein is actually a hexamer and that actually binds to the RNA. So, in an ATP dependent helicase and its subunit contain the RNA binding and the ATP hydrolysis domain.

So, in the Rho protein, you have the two activities. nucleotide binding activity or the RNA binding activity and then you also has the ATP hydrolysis activity. So, you utilize the ATP hydrolysis and then you actually binds the RNA. So, these row protein firstly bind to the sequence which is present in the upstream of the termination sites. These sites are called as the rut sites and these sites are rich in the C residues.

So, the row factor followed to the RNA polymerase until it does not catch the RNA polymerases. So, Rho follow the RNA polymerase by its helicase activity which is driven by the ATP hydrolysis. When the RNA polymerase reached at the termination site, the Rho protein freezes the structure of the polymerase. And, when the rho factors collapse with the enzyme which causes the termination and the new RNA protein chain can released. So, this is what exactly happened right.

So, this is the RNA chain the rho protein will go and bind to the this growing chain. And then it will keep reaching or keep progressing or keep moving towards the transcription bubble. But what is happening is that when it reaches to the termination site, at the termination site the RNA polymerase speed is going to be reduced because the transcription site is going to be rich of RNA. gc sequences right and because of that it is difficult for the RNA polymerase to go there and once the RNA polymerase cannot move a very long time then the rho factor is going to come and it is actually going to utilize its helicase activity to break the interaction between RNA and DNA hybrid and because of that the whole complex the RNA polymerase, the RNA is going to jump into the cytosol and that is why it is actually going to cause the terminations. Now, let us talk about the transcription in the eukaryotes right. So, transcription in eukaryote is different from the prokaryote because the transcription I think we have already discussed about the different types of transcription references between the prokaryotic and the eukaryotic transcriptions.

So transcription, eukaryotic transcription is different from the prokaryotic transcriptions because eukaryotic transcription requires the transcriptional binding factors and enhancer along with the RNA polymerase and transcriptional factors are a protein which are essential for the transcription but these are not the part of RNA polymerase or the DNA templates. So this is all about the transcription in the prokaryotes and in our subsequent lecture we are going to discuss more about the transcription in eukaryotes and then we are also going to discuss about the post transcriptional modifications. So, what we have discussed, we have discussed about the transcription in prokaryotes. We have also discussed about the differences of the transcription between the eukaryotic as well as the prokaryotic organisms.

So, with this, I would like to conclude my lecture here. In our subsequent lecture, we are going to discuss about the transcription in eukaryotes and then we are also going to discuss about the post transcriptional modifications. Thank you.