Molecular Biology
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Module - 07
Translation
Lecture-31 Translation in Eukaryotic System

Hello everyone, this is Dr. Vishal Trivedi from department of biosciences and bioengineering at IIT Guwahati and what we were discussing in the course molecular biology. We are discussing about the cell biology, we discuss about the cellular processes, we discuss about the different types of organelles and then we have also discuss about the biomolecules their function and then followed by we have also discuss about the genetic material. So, we discuss about genetic material in the prokaryotes, eukaryotes and how the genetic material is been packed into these two different types of organisms and subsequent to that we were also discussing about the central dogma of molecular biology. So, within the central dogma of molecular biology so far what we have discuss we have discuss about the replication, transcription and in this current module we are discussing about the translations. So, as we said that the central dogma of molecular biology is a very important phenomena in which the three different types of activities such as the production of origin or the synthesis of the new DNA from the pre-existing DNA is been done by a process known as replications whereas, the RNA is been produced from the DNA with a process known as transcription and in today's and in this current module we are discussing about the translation where the information what is given on the RNA is been used to synthesize the protein molecules.

If you recall in our previous lecture we have discuss about the prokaryotic replication. So, we have discuss about the different types of machinery what is required for prokaryotic applications so we discuss about the ribosomes tRNA messenger RNA and so on. And then we have also discuss about how the different types of events are happening such as initiation, elongation and terminations in the case of the prokaryotic system. In today's lecture we are going to discuss about the eukaryotic system.

So, before we get into the detail of what is the major difference of the translation in the prokaryotic versus eukaryotic we would like to you know give you a very small description about the machinery what is required for the translations and then we are actually going to tell you in detail about the different processes what is happening in the case of the eukaryotic translations. So, eukaryotic translation is a process or the translation is the process of messenger RNA coded protein synthesis this is a universal process that occurs both in the prokaryotes and the eukaryotes. Members of the prokaryotes or the eukaryotes use the information what is given in the messenger RNA

which comes from the DNA by transcription to synthesize the protein with the ribosome as a machinery. So, protein form a variety of critical functions such as enzymes, structural proteins or hormones and therefore, they are crucial for the biological component and that is why we said that the central dogma of molecular biology is very crucial because it explains how the different events are connected to each other and why they are so much crucial because once you have a requirement of a particular hormone you are actually going to activate the transcription of that particular gene and then you are actually going to activate the translational machinery. So, that the ribosomes will go and sit on that particular RNA and it will going to give you the proteins.

Protein biosynthesis has a key role in the disease as changes and occurs errors in this process through underlining DNA mutations or protein misfolding are often the underlining cause of the disease. And protein machinery is very crucial because it can give you a misfolded protein, it can give you a protein which may have mutations, it may give you the protein which may not be useful for or it may not be optimal for you know doing the its natural function and because of these things it may actually lead to the development of the disease. So, the process by which the sequence of nucleotide in a messenger RNA molecule direct the membrane incorporation of the amino acid into the protein is called as the translation. So, this is all we have already discussed but I thought when we were discussing about the eukaryotic translation we should also briefly discuss about these aspects as well so that it will refresh your memories so that it will be easy for you to follow the follow the content actually. Now, as far as the machinery is concerned the machinery required for translating the language of the messenger RNA into language of protein is composed of the four primary components so it requires the messenger RNA right so that is the component number one and that is the most crucial component.

Then you requires the tRNAs so you require the tRNA so that it can actually be able to read the anticodons with the help of the codon versus anticodon interrecon and the other side it also can supply the specific amino acids then it also requires the ribosomes and it also requires the different types of proteins and as well as the enzymes so that it can actually be able to perform the different types of activities such as aminoacyl tRNA oscillations and all that and peptidyltransferase. So enzymes are two there are two crucial enzymes you have you require the aminoacyl tRNA synthetase and you also require the peptidyltransferase as well as the protein is concerned you will also require different types of translational factors we have discussed many of these translational factors when we were talking about the prokaryotic translations. So let us start with the first component and the first component is the messenger RNA so messenger RNA is a single standard RNA molecule that is complementary to the one of the strand of a gene during the protein synthesis ribosomes moves along the messenger RNA read its waste sequences and uses the genetic code to translate the each codon into a corresponding

amino acid so this is the eukaryotic messenger RNA where you are going to have the 5 prime UTR regions you are going to have the coding sequence and then you are also going to have the 3 prime UTR region and then you are going to have the poly A tail and that majority of the 5 prime UTR region or the 3 prime UTR region is actually the regulatory regions where the many of these regulatory proteins are going to bind and that is how they are actually going to regulate the translation within the coding sequence you are going to have the starting codon and you are also going to have the stop codon. So in the case of eukaryotic system you are going to have the start codon as AUG and which is actually going to code for methionine whereas there are 3 stop codons UA, UAG and UGA and these are the 3 stop codon which are also been the stop codon into the prokaryotic system. Then we have the tRNAs I am going to I am going through very fast with these content because the already we have discussed this is the you know the nucleotide sequence of the tRNA where you have this d arm right or then you are going to have the anticodon arm then you are going to have t psi c arm and this is actually going to be a cca end.

So this is going to be start from 5 prime end you are going to have d arm anticodon arm loop t psi c loops and the cca end and the cca end you know that it is actually going to bind the amino acid on one side whereas the anticodon loop is going to have the anticodon which is actually going to recognize the codon on to the on the messenger RNA and that is how it is actually going to serve the dual purposes. It is going to serve it is going to first identify the messenger RNA on one side and it is going to bring the corresponding amino acid from the 3 prime ends. So it the primary sequence primary structure of tRNA is a linear sequence of the nucleotides secondary structure is called as the clover leaf models and the tertiary structure is called as the 3D structure of tRNA or the L shape or the helix packing. So these are the some of the different names what we are using the tRNA is also called as transfer tRNA transfer RNA is a type of RNA molecule that help to decode a messenger RNA sequence into a protein and it is made up of a single standard poly nucleotide chain. It function at a specific site in the ribosome during translation which is a process that is inside the protein from a messenger RNA molecules.

Proteins are built up from the smaller units called as the amino acids which are specified by the 3 nucleotide messenger RNA sequence called as codon. All these we have already discussed when we were discussing in detail when we were discussing about the prokaryotic system. So each codon represent a particular amino acid and each codon is recognized by a specific tRNA. They are adapted between the codon and the amino acids each tRNA has its corresponding amino acid attached to its 3 prime end and the tRNA is named as sRNA or the soluble or the pneumatic RNA and the adapter RNA. tRNA the 10 to 15% of the total cellular RNA which actually includes the messenger

RNA or ribosomal RNA and the tRNA.

So out of these 3 RNA species total of the 10 to 15% is the tRNA species 74 to 95 nucleotides are present in the each tRNA molecules then it has the 3.8 sedimentation coefficient and the molecular weight of the tRNA is between the 25,000 to 30,000 Dalton. The structure of tRNA can be decomposed into the primary structures secondary structures and the tertiary structures. Secondary structure is also called as the cloverleaf model whereas the tertiary structure is called as L-shaped structure. In addition to the usual nucleotide bases it also tRNA contains a number of unusual bases such as ionosine, pseudo uracil and dihydro uridine and these are the amino acids modified nucleotides which are been by methylation.

So for example the ionosine is going to be produced from the adenine, pseudo uridine uracil is from produced from the uracil and pseudo uridine is produced from the uridine. The other unusual amino acid found is hypoxanthine, thymine and methyl guanine. So this is the structure of the tRNA this is the cloverleaf model of the tRNA where you have the 3 prime end which is also called as the CCA end then you all going to have T-SciC loop, D-loop, and decodone loop and all that. So 5 prime terminal is a phosphate group and then you are going to have the acceptor stem it is the 7 to 9 base pair stem by the base pairing of 5 prime nucleotide with the 3 prime nucleotide then you have a CCA tail it is a cytosol, cytosine amino acid sequence at the 3 prime end of the tRNA molecule the amino acid loaded onto tRNA by the amino acid tRNA synthesis to form the amino acid tRNA is covalently attached to the 3 prime hydroxyl group onto the T-R CCA tail. D-loop it is a 4 to 6 base pair stem ending the loop that often contains the dihydrouridine then you have anticodon loop it is a 5 base pair stem which loop contains the anticodon and anticodon is going to recognize the genetic code or the codon what is present onto the messenger RNA and then you have a tR it is a 4 to 5 base pair stem containing sequence of T-SciC where psi is the pseudouridine a modified uridine actually.

Let us talk about then the ribosomes so ribosome is actually the real machinery of the protein synthesis which is different from the prokaryotic system versus eukaryotic system in the prokaryotic system you have the 70S ribosome whereas in the eukaryotic system you have a 80S ribosomes. So eukaryotic ribosomes are larger they are 80S ribosomes and a more complex than the prokaryotic ribosome which are 70S. Ribosome exists normally as a separate subunit that are composed of the proteins and the ribosomal RNA the subunits come together to form a ribosome when they bind to a messenger RNA near its 5 prime end on binding to the messenger RNA the ribosome read the nucleotide sequence from the 5 prime to 3 prime directions synthesizing the corresponding protein from the amino acid in a N terminal to C terminal directions. Ribosomes are located in the cytoplasm either freely floated or the associated with the

endoplasmic reticulum. They serve to synthesize the proteins the ribosomes are ribonucleoprotein particles to which the multiple ribosome proteins are bound the sequence and the structure or ribosomal components are conserved in all kingdom under underlining the common origin of the translational operators.

The ribosome provide the platform for proper assembly of the messenger RNA tRNA and the protein factors it consists of a small and the large subunits. So this is the structure of these large subunit and this is a structure of the small subunit and it has a three different types of binding site that has E site it has a P side and has a A side and the mammalian ribosome which is a 80S ribosome is consist of the two subunit this is a large subunit and this is a small subunit and a large subunit is composed of the different types of RNA species such as 28 ribosomal RNA 5.8 S ribosomal RNA and 5S ribosomal RNA and then it also contains the 49 different types of proteins. So all these 49 different types of proteins when they come together along with the 28 S ribosomal RNA 5.8 S ribosomal RNA and 5S ribosomal RNA that is actually going to give you large subunit which is going to have segmentation coefficient as 60S then you also have the small subunit which is a 40S subunits and that contains the 18 S ribosomal RNA and the 33 different types of proteins and when they come together they are actually going to make the ribonucleoproteins and they are actually going to make the small subunit which is going to be 40S and together they were actually going to when they will combine together they are actually going to give you the 80S complete ribosomal particle which is going to participate into the protein synthesis.

Now as far as the binding site is concerned the t are actually going to have the three binding sites for tRNAs they are going to have A site, P site and E site. A site is the site where the new amino acid or the new tRNA is actually going to enter the P site is the site where the peptide bond is going to be formed and the E site is the exit site from where the uncharged tRNA is actually going to get removed. So all three sites are formed by the ribosomal molecules into the ribosomes during the elongation the incoming RNA molecule binds to the A site the P site is where the tRNA linked to the growing polypeptide chain is bound and the E site is the bonding site for the undoded tRNA prior to its release from the ribosomes. Now as far as the translation in the eukaryotic is concerned they are actually going to have the three important events initiation, elongation and terminations. So initiation sets the stage for the polypeptide synthesis so it actually going to assemble all the protein components it is going to assemble the ribosomes it is going to have all those events so that the it is going to you know bring the raw material actually and then it is going to enter into the second phase which is the elongation.

So that causes the sequential addition of the amino acids to the polypeptide chain as

determined by the codons what are present on to the messenger RNA and then you are going to have the termination so this bring the polypeptide synthesis to a halt because once it reaches to a stop codon then it is actually going to terminate. So let us first start with the initiation so initiation if you recall we have discussed about the initiation in the pero-karyotic system. Now when we are going to discuss about the initiation into the eukaryotic system we just want to first understand what is the difference between the two different types of events before we get into the detail of the initiation into the eukaryotic system. There are significant differences between the initiation of the initiation stage of the prokaryotes and the eukaryotes. In eukaryotes there are only one start codon for the eukaryotes such as AUG and it is codes for the methionine it does not cone for the N-formyl methionine.

So eukaryotic cell need more initiation factor than the prokaryotic system. For example the eukaryotic cell requires the 12 different types of initiation factor whereas the prokaryotic system requires the lesser number of initiation factors. In prokaryotes the presence of association of messenger RNA with the small subunit is more complex than the prokaryotes. 40S subunit identify the 5 prime methylated cap of the messenger RNA and there is a scanning process involved whereas the initiation codon is recognized. This recognition is added by the ATP dependent helicases that hydrolyze the ATP.

This recognition of initiation codon is also been aided by the COSAC sequences and COSAC sequence are very much same as what we have seen in the role of the Scheinder-Ganno sequences into the prokaryotes. So let us discuss about the initiation. So the initiation of the translation in the eukaryotes involve the many initiation factors or the EFIs and it is divided into the four stage. In the stage 1 the ribosome is going to be dissociate. In the stage 2 the complex of 43 pre initiation complex is going to be formed and then this 43S initiation complex is going to be converted into the 40S initiation complex and then ultimately it is actually going to have the formation of 80S initiation complex.

This means the ribosome is going to be fully assembled onto the messenger RNA and then it will enter into the elongation phase and that is how it is actually going to start the initial elongations. So during this particular phase it requires the many type of accessory proteins and initiation factors for performing the different types of functions and as I said in the formation of these kind of pre initiation complexes. So it will require the different types of initiation factors. So some of the initiation factors are called as core initiation factors whereas the other factors are called as the accessory initiation factors. So these are the core initiation factors.

So you have the EF1 and EF2 and EF1A and that enhance the pre initiation complex

formation helps in ribosome scanning, assure the steadiness of the AUG selection, prevents the premature hydrolysis of the EF2. Then we have the elongation initiation factor 2 and that assists the binding of the methionine tRNA met to the 40S ribosome by forming a ternary complex of the initiation eukaryotic initiation factor 2 GTP and met tRNA. Then you have the eukaryotic initiation factor 2 and eukaryotic initiation factor 3. So the first initiation factor binding to the 40S subunit and promote the further steps having the you know the gonadine nucleotide exchange factor activity. So and then we have the eukaryotic initiation factor 4A that contains the 2 domains.

So it has the dead box ATPS domain and the ATP dependent RNA helicase activity. Then we have the initiation factor 4B that is the co-factor of the initiation factor 4A and it enhances the helicase activity of the initiation factor 4A. Then we have the initiation factor 4E and that binds to the 5 prime cap of the messenger RNA that is the M7 GPPPG cap right. Then we have the initiation factor 4F that recruits the 40S to the 5 prime and of the messenger RNA. Then we have the initiation factor 4G and that scaffolds for the initiation factor 4E, initiation factor 4A, initiation factor 3, initiation PAB, slip 1 and messenger RNA and also participate in enhancing the helicase activity of the initiation factor 4A.

Then we have the initiation factor 4H that enhances the helicase activity of the initiation factor 4A and then we also have the initiation factor 5A and 5 and 5B that having the JTPS activity that hydrolyzes and promote the dissociation of the various initiation factors from the 40S and also leads to the association of the 60S subunit to form the ATS ribosomes. And then we have the auxiliary initiation factors. So these are called as DHX29, DED1 initiation factor 6, P97 and PAB. So DHX29 is having the helicase activity which contains the DED box functioning in the initiation step and also requires for the ribosomal scanning onto the messenger RNA. Then we have the DED1 and it is a homologous of DHX29 found in the saccharomyces cerevisiae.

Then we have the initiation factor 6 that binds to the 60S subunit and prevents it binding with the 40S subunit. Then we have P97 that is homologous to the C terminals of the initiation factor 4A and considered as the translational repressor under the normal cellular conditions. Then we have PAB it binds to the poly A tail of the messenger RNA also with the initiation factor 4A and initiation factor of RF3A. It promotes the circularization of the messenger RNA and it stimulates to the 40S subunit recruitments. So the first step is the RB ribosomal dissociation.

So ATS ribosome dissociate to form the 40S and the 60S subunits. The two initiation factor namely the initiation factor 3 and initiation factor 1A binds to the newly formed 40S subunit thereby block its re-association with the 60S subunits. This means this

ribosome is going to be first the ribosome where the you know initially the ribosome would be involved into a protein synthesis and as soon as it will reach to the termination site then it will get dissociate you know dissociate and it is going to dissociate into the 40S and the 60S ribosomes. Once the 40S is been produced then it is actually going to be bind by the initiation factor 3 and initiation factor 1A and it is going to bind in such a way that it is going to block the association of these two because they will get recruited and they will be get associated but with the new messenger RNA and then only it is actually going to start the initiation of the new messenger RNA. So for initiating the new cycle it has to be dissociated from the older cycle.

So it is actually present on the some other messenger RNA and it reaches to the termination site. So at when it reaches to a termination site that the protein synthesis is going to stop but the ribosome has to be dissociated ribosome has to be broken apart so that you are going to have the 40S and the 60S subunits available and these 40S 60S subunit will assemble on to the new messenger RNA on which it is actually going to start the initiation and that is why this is actually the first step right and the second step is that the formation of 43 pre initiation complex. So a ternary complex containing the initiation tRNA that is the met tRNA and initiation factor 2 bounce to the GTP attached to the 40S subunit to form the 43 pre initiation complex. The presence of the initiation factor 3 and initiation factor 1A stabilizes this complex. So remember that these two factors are also important for you know blocking the attachment site so that it should not form the 80S ribosomes.

Then we have the formation of the 48 initiation complex. So the binding of messenger RNA to the 48 3 S initiation complex results in the formation of 48 initiation complex to the intermediate 43 S initiation complex. So initiation factor 4F complex is formed by the association of the initiation factor 4G initiation factor 4A and initiation factor 4E. The initiation factor 4F referred to as a cap binding protein binds to the cap of the messenger RNA and then the initiation factor 4A and the 4B binds to the messenger RNA and reduces its complex structure. This messenger RNA in then transferred to the 43 S complex for the appropriate association of the 43 pre initiation complex with the messenger RNA energy has to be supplied by the ATP.

The ribosomal initiation complex is scanned messenger RNA for the identification of the appropriate initiation complex that is the 5 prime AUG and then it is actually going to initiate the formation of the 80S ribosomes. So the next step is the formation of the 80S initiation complex. So 48 initiation complex binds to the 46 60 S ribosomal step unit to form the 80 S initiation complex. The binding involves the hydrolysis of GDP this is bound to the initiation factor 2 and this step is facilitated by the involvement of the initiation factor 5. As the 80 S complex is formed the initiation factor bound to the 40 S

initiation complex are released and the recycle.

So these are all the events what is being shown here that you are going to have the dissociation of the ribosomes. So in the first step you are going to have the dissociation of the ribosomes. So 40S and 60S which are present on to the previous some other messenger RNA where they have actually completed protein synthesis this is actually going to assemble going to dissociated and the 60 S is going to be get separated and the 40 S is going to get separated. So as soon as the 40 S is going to form it is actually going to bind the initiation factor 1 and initiation by 1A and the initiation factor 3 and then it is actually going to bind all these you know metionine metatRNA and mettRNA initiation factor 2 GDP and all that and that's how it is actually going to form the 43 initiation complex.

So that is going to be the second step. And once the 43 initiation complex is formed then it is actually going to bind the initiation factor 4E, 4G, 4A and 4B and after that it is actually going to be good enough to recruit the messenger RNA and once the messenger RNA is been recruited then the 43 messenger RNA complex is going to form on to the messenger RNA and then it is going to start scanning with the help of the ADP hydrolysis to know where the starting codon is right and then it is actually going to form the 49 S pre initiation complex and once it find the pre initiation complex 49 initiation complex and it found that there is a AUG right then it actually going to recruit the 60S ribosomes and 60S also going to assemble and that's how it is actually going to form the 80S initiation complex on to the initiation codons. Now it enters into the elongation phase. So ribosomes elongates the polypeptide chain by sequential addition of the amino acids. The amino acid sequence is determined by the order of codon into the specific messenger RNA elongation which is a cyclic process involve the certain elongation factor or EFs. Elongation can be divided into 3 steps binding of the aminoacyl tRNA into the A site peptide bond formation and the translocations.

This we have very detail in this we have discussed when we were talking about the prokaryotic system how the incoming aminoacyl tRNA is going to bind into the A site and then the existing peptide bond is actually going to form existing peptide chain is actually going to form the peptide bond and then it is actually going to be translocated on to the A site and then there will be a translocation so that newly formed peptide bond containing the peptide chain will get translocated and will bind the P site and then the tRNA what is present on to the P site will not have the any amino acid so it is going to be present on to the E site and from there it is actually going to get removed from the ribosomes. So this we are not going to discuss in detail. So the ATS initiation complex contain the met tRNA in the P site and the A site is free. Another aminoacyl tRNA is located into the A site this require the proper codon recognition on the messenger RNA

and involvement of the elongation factor 1A and the supply of energy by the GTP. The aminoacyl tRNA is placed in the A site elongation factor 1A and the GDP are recycled to bring another aminoacyl tRNA.

Then there will be a peptide bond formation so this is what it is actually going to happen. So initial the first codon is actually going to be present on the P site and then subsequent codon will come on to the A site and that is how it is actually going to be start doing the synthesis. So by sequential addition of the you know tRNA which actually contains the amino acids it is actually going to be participate into these peptide synthesis. So the enzyme peptidyltransferase catalyze the formation of the peptide bond the activity of this enzyme lies on to the 20S ribosomal RNA of 60S ribosomal subunits. It is therefore the rRNA not the protein referred to as ribosome that catalyze the peptide bond formation.

Next result of the peptide bond formation is the attachment of growing chain to the tRNA in the A site. So in this you know cartoon what you see here is that this is actually A site and this is actually the P site. So what you see here is that the codon is entering into the A site right it is sitting and then the peptide which is growing chain is actually been transferred on to this and then it moves on to the P site and from P site whatever is left over that will enter into the E site and it is actually going to exist. So this will continue as long as you have messenger RNA when it reaches to a place where you are actually going to have the stop codon then it will actually going to stop the synthesis of the peptide chains. So then you are going to have the translocation so ribosome move to the next codon of the messenger RNA this process involves the moment of the growing peptide chain from the A site to P site translocation require the elongation factor 2 and the GTP the GTP get hydrolyzed and supply energy to move on to the messenger RNA and the elongation factor 2 and GTP complex recycled for the translocation.

About 6 amino acid per second are incorporated in the course of elongation in the translation in the eukaryote. So this is actually the synthesis rate right where you have the 6 amino acid which are going to be synthesized in per second. So if I tell you the length of a protein they can actually be able to calculate how long it will take for a protein to synthesize remember that it does not include the transcription actually. So it is actually should be you know first the RNA is going to be transcribed and then after that it is actually going to be the this speed. So this is actually the diagram which actually shows how the elongation is going to happen in the eukaryotic system.

And then we have a termination so termination of eukaryote is almost similar with the prokaryotes which depends upon the eukaryotic release factors. So eukaryotic release factor or the RF 1 recognizes all three termination codons that is UA, UAG and UGA

and with the help of the RF 3 it terminate the translations. So upon termination the ribosome is disassembled and the complete polypeptide is released. The class 1 factor that is the RF 1 is responsible for the high fidelity stop codon recognition and the peptidality RNA hydrolysis. The class 2 factor that is the RF 3 is translational GTPase that is more closely related to the EFTU than EFG and RF 3 accelerate the peptide released and increase terminal efficiency at stop codon in a manner that depends upon the GTP hydrolysis.

So this is what exactly happened and it termination is exactly happened in the same way as we have discussed about the prokaryotic system. So these are the some of the steps what happened in the termination steps in the eukaryotic system. So one of the stop codon or terminal signal that is the UA, UGA and terminate the growing polypeptide chain and when the ribosome encounter the stop codon there is a no tRNA available to bind to the A side of the ribosome instead a release factor binds to it. Once you have the RF 1 recognizes all three stop codon and RF 3 stimulates the termination events. Once the release factor binds the ribosomal unit rival to the unit fall apart releasing the large and the small subunit the tRNA carrying the polypeptide is also released being upon the polypeptide product and the ribosome recycle occur at the end only in the eukaryotes.

So this is the ribosome recycling and or will say ribosome dissociation and then reassociation on to the next messenger RNA. So after the release of polypeptide and the release factor the ribosome is still bound to messenger RNA and it is left with the 2 deacylated tRNA. To participate in the new round of polypeptide synthesis these messenger RNA and tRNA must be released and the ribosome must be dissociated into the small subunit and to the large subunit that is what we have already discussed how the ribosome is getting dissociated with the help of the initiate so many eukaryotic initiation factors. Collectively these events are termed as ribosomes recycling so what happen is that when you are going to start with a start codon it is going to start then you are going to enter into the elongation phase and when it enter into the stop codon after the stop codon the ribosome is getting dissociated so it is going to it is going to dissociate the small subunit and the large subunit and then these small and large subunit are actually going to assemble onto the new messenger RNA. And once they are get dissociated this messenger RNA is also free for starting the new cycle of protein synthesis and that is how it is good for conserving the energy in terms of not synthesizing the same messenger RNA again and again that you can be able to reuse the same messenger RNA again for the synthesis of this particular protein and on the other hand you do not have to synthesize the ribosome also.

You can actually disassemble and then reassemble that onto the new messenger RNA on or onto this particular messenger RNA whatever the case these ribosomes are free for

starting the new protein synthesis cycle. So this is all about the central dogma of molecular biology where we have discussed about the translation into the eukaryotic system we have discussed about the translation in the prokaryotic system and what we have also discussed that how the eukaryotic system is different from the prokaryotic system and you might have seen that the eukaryotic system is much more complex much required many more elongation factors many more initiation factors and so on. So with this brief discussion about the translation I would like to conclude our lecture here in our subsequent lecture we are going to discuss about the post translational modifications. Thank you.