PROFESSOR: Hi. In this clip, we're going to go through problem two of the transcription and translation unit. We're also going to review all of the information you would need to fill out problem one, the table. If you haven't tried these problems yet on your own, please pause the video now and try them, and then come back and watch this explanation.

OK. So here we have, as in problem two, the double stranded DNA. Now, this is a piece of the eukaryotic genome, and so this DNA is in the nucleus of the cell. Now what we're going to do is we're going to go through transcription and translation with this gene.

So the first thing we need to do is we need to figure out where we want to start transcription and in what direction we want to go and what strand we want to use as our template. So in the problem, we're given our promoter region and we're given that our transcription starts right here at this arrow and moves in this direction.

So we know where we're starting and what direction we're moving in. All transcription will proceed reading a template in the three prime to five prime direction and will polymerize the RNA made in the five prime to three prime direction.

So what we need to do now is figure out what strand is going in the three prime to five prime direction and the direction that we're going to be transcribed. So that means that this strand, which is going from three prime over here down to five prime at the end, this is going to be our template strand. So our template strand is going to be at the bottom.

OK. So when our RNA polymerase starts, it's going to be reading this template strand and adding nucleic acid, adding nucleotide triphosphates, or NTPs, one by one together to make the RNA. Now it's going to add these together by adding a phosphodiester bond in between all of the monomers.

So we're going to start our transcription. And basically, what I need to do is just use

the complimentary base pair to my template strand. So I'm going to write it out here.

So I've done a lot of transcription here. Now where am I going to stop my transcription? I'm not going to stop just randomly in the middle of nowhere. What my RNA polymerase is going to do is it's going to stop when it gets to the end of this terminator sequence. So I'm going to keep transcribing until I get to the end of my terminator here.

OK. So this is my RNA strand. And as I said before, we're going to polymerize this mRNA in the five prime to three prime direction.

OK, we've got our mRNA. Since this is a eukaryotic cell and the mRNA right now is in the nucleus, what we need to do is transport it out of the nucleus and into the cytoplasm where it will be translated by a ribosome.

Now what the ribosome is going to do is it's going to take this mRNA, which is a message that encodes the sequence of amino acids that we need to put together to make the protein, and we're going to take this message and we're going to find a place to start translation. So what the ribosome is going to do is it's going to start at the five prime end of the template and read towards the three prime end of the template.

It's going to read until it gets to a start codon. The start codon is AUG. So this is where we're going to start, and AUG encodes methionine. We're then going to read in three base pair codons down from the five prime end of our template to the three prime end of our template.

And so we're going to keep going in this translation until we reach what's called a stop codon. Now there are three stop codons. Stop codons are UAA, UGA, and UAG. So if when my ribosome finds any of these three codons in frame, it's going to stop. So I get all the way down here before I hit a stop codon on this transcript.

So what my ribosome is going to be doing as it's reading these codons is it's going to insert amino acid by amino acid, pairing them together with a peptide bond. So we've got methionine bonded to histidine, tyrosine, leucine, and so on and so forth.

OK, so this is the protein chain that's encoded by this gene in the DNA. And in proteins, we always synthesize from the N terminus to the C terminus.

OK, so we've gone through both transcription and translation. Now what we want to do is we want to take into account what would happen if we had a mutation in our sequence. So in this case, in this problem, we're going to insert a base pair right here. So we're going to insert an extra T here and an extra A here.

Now, if this is happening in the DNA, when our DNA is transcribed to make our RNA, what's going to happen to the RNA? Well, we're going to also add the corresponding base into our RNA, so we're going to have an extra U here. So in addition to only adding one nucleotide in our RNA, this is also going to throw off our frame that we're reading when our ribosome is reading our RNA.

So instead of the frame that we had previously, we're now going to have a new frame. So it's going to start at the same start codon and then read this codon just as normal, but then this U will make UUA and then will read in codons of three from there.

So again, I need to translate until I hit a stop codon. And so the stop codon is going to be different in this case, because this stop codon is no longer in frame. I need to find an in frame stop codon. And the first stop codon that I hit is going to be this you UAG right here. And so our new protein sequence is now going to be N terminus, and then the beginning is going to be very similar, and then our amino acids are going to be completely different because we're reading this in a different frame.

OK, so we can see how this one mutation, addition of one base pair into our DNA, has caused us to create a completely different peptide. It's probably not going to perform the same function.

OK. So we've gone over transcription and translation. You should be able at this point to answer all of question two and you should also be able to fill in all of table one. Thank you for watching.