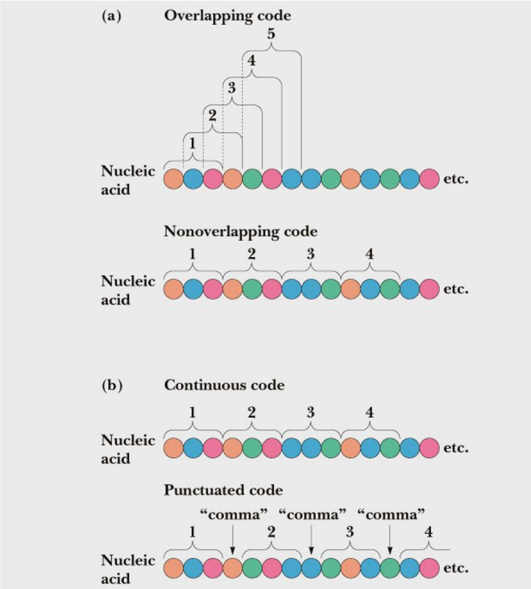
L.8 Genetic code (codon):

Refer to **the triplet sequence of mRNA that specifies certain amino acid. In other words;** translate of the four –character codes (A, U, G and C) into 20 amino acids of proteins.

It would see that there must be a code for each 20 amino acids found in proteins , but can 4 nucleotides provides enough combinations to code for 20 amino acids? If each code word (codon), were made up of 2 bases, such as AG, there could be only 16 codons ,not enough to code for 20 amino acids but if each codon were made up of 3 bases such as AGC, there would be 64 codons more than enough to code for 20 different amino acids .Therefore called triplet code 61 of 64 triplet code for amino acids. The triplet AUG has a many function .It's not only codes for amino acid methionine but also can provide a signal for the start of polypeptide chain .Three of other codons do not designate amino acids . There are the stop codons that instruct the ribosome to end the polypeptide . The triplet codon also characterized by:

1- **Unambiguous**: Each codon specifies a particular amino acid, the codon ACG codes for the amino acid threonine, and only threonine.
2- **None overlapping (**The triplet codons are adjacent), This means that successive triplets are read in order. Each nucleotide is part of only one triplet codon.
3- They are not separated by **punctuation** (comma-less) .

First Base	Second Base				Third Base
	U	C	A	G	
U	UUU phenylalanine	UCU serine	UAU tyrosine	UGU cysteine	U
	UUC phenylalanine	UCC serine	UAC tyrosine	UGC cysteine	C
	UUA leucine	UCA serine	UAA *stop*	UGA *stop*	A
	UUG leucine	UCG serine	UAG *stop*	UGG tryptophan	G

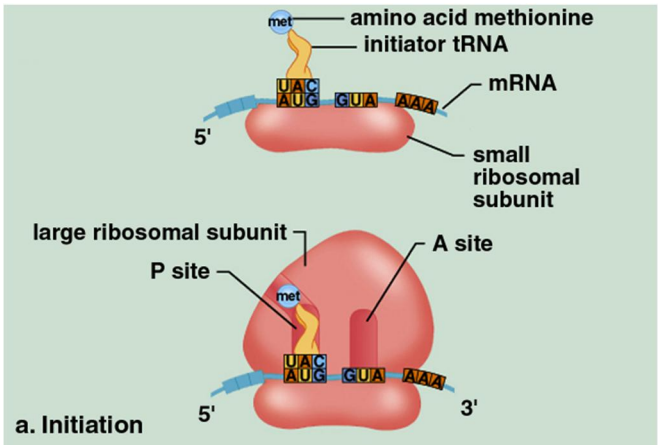


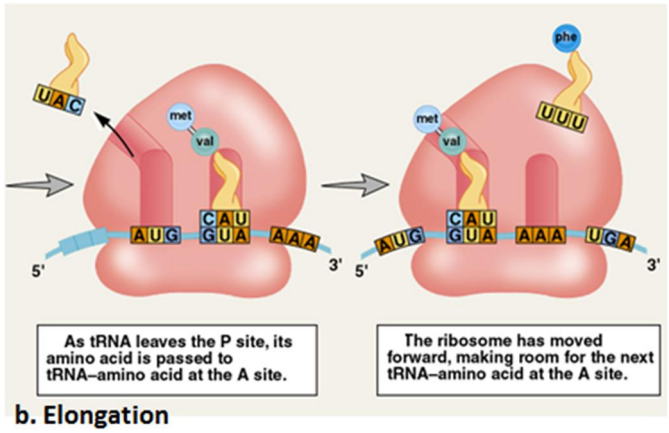
Protein synthesis:

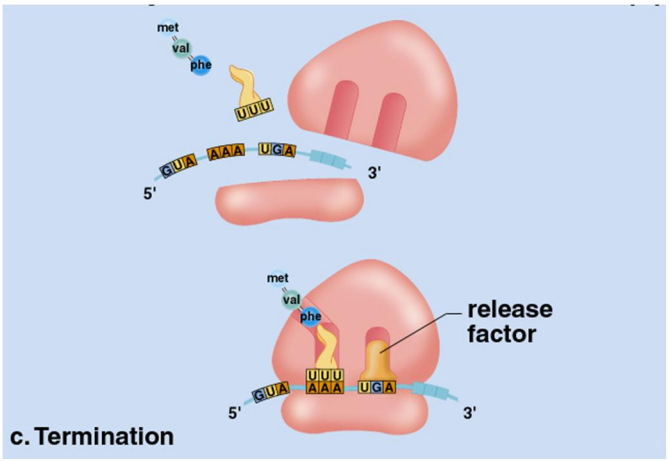
Messenger RNA leaves the nucleus and then moves into cytoplasm. The transfer of the information from m RNA to polypeptide called translation, the translation begins when a small subunit ribosome binds to an mRNA molecule near the AUG codon forming mRNA-ribosome complex (AUG indicates the beginning of gene called start codon which specifies for amino acid called methionine in the cytoplasm, its activated by amino acid-activating enzyme, then recognized and pick up by tRNA to form Met-tRNA) .Then a large ribosomal subunit joins to the small subunit. This process called **initiation of translation.**

Next, a second tRNA with its amino acid, bind to the second codon on the mRNA molecules at (A) site. This process is repeated over and over again as the ribosome moves along the mRNA chain, adding amino acid to the growing polypeptide chain at "p" site .The amino acids bind together by peptide bonds is catalyzed by an enzyme (peptidyl transferase) in the larger ribosomal subunit. This phase of translation called **chain elongation, chain** elongation continues until the ribosome encounters one of the three possible stop codons. The polypeptide chain is enzymatically cleaved from the last tRNA, and it leaves the ribosome, which dissociates into two subunits. This step called **chain termination .** Finally, certain proteins must be altered before they can function .For example, is initially translated as a polypeptide proinsuline, which is 80

amino acids long. Enzymes cut it to 51. Some proteins must have sugars attached for them to become functional, or must aggregate.



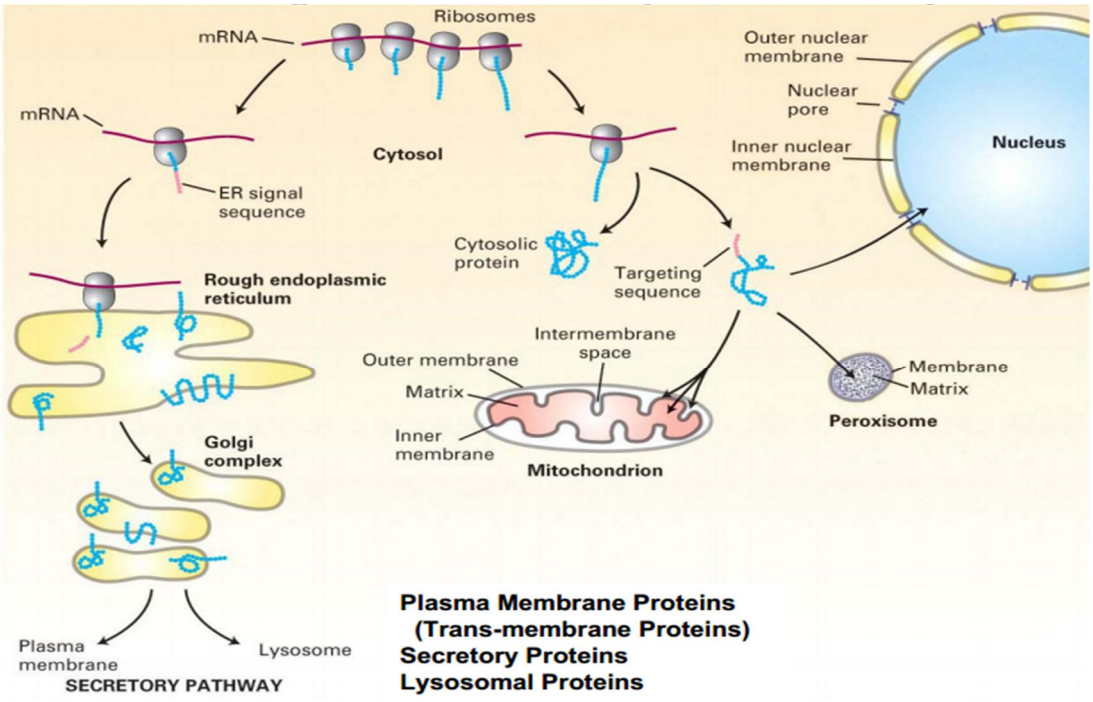




Synthesis of proteins on rough endoplasmic reticulum (RER):

This process began when mRNA leaves the nucleus and then moves into cytoplasm. mRNA associate with ribosome or form polysome (the individual

ribosomes are held together by a common strand of m RNA) attached to the membranes of the endoplasmic reticulum by assist of proteins called **ribophorins** .The first sequence of amino acids assembled from the code is called **signal sequence** and is able to penetrate the membrane of the E.R., and the ribosome continue reading of the mRNA to form secretory proteins then the secretory proteins injected into the lumen of RER ,the signal sequence is enzymatically cleaved from newly synthesized protein molecule .



Gene regulation:

The cells don't need the same enzymes and possibly other proteins all the time. For example in the mammalian cells lining the gut produce a lot of digestive enzymes while muscle cells need the contractile proteins actin and myosin. These enzymes or proteins controlled by genes, but they are expressed only in certain cells of the body , therefore, the eukaryotic cells also must have a way to regulate the action of genes. There are 6 primary levels for control of gene activity :

1- **Chromatin accessibility**. The structure of chromatin (DNA and its organizing proteins) can be regulated. More open or “relaxed” chromatin makes a gene more available for transcription.

2- **Transcriptional control:**

Most genes of plant and animals include noncoding regions called introns and coding region. The parts of a gene that are expressed called exons .Both exons and introns are transcribed from DNA into RNA. So the transcriptional control influence when and how a particular gene will be transcribed.

3- **Transcript processing control:**

Before the mRNA leaves the nucleus, the introns are removed, and the exons are joined to produce an mRNA molecule with a continuous coding sequence (just cap and tails considered parts of the first and last exons) .This process is called RNA splicing or modification. So the transcript processing controls either govern modification of the initial nucleus or not.

4- **Transport control:**

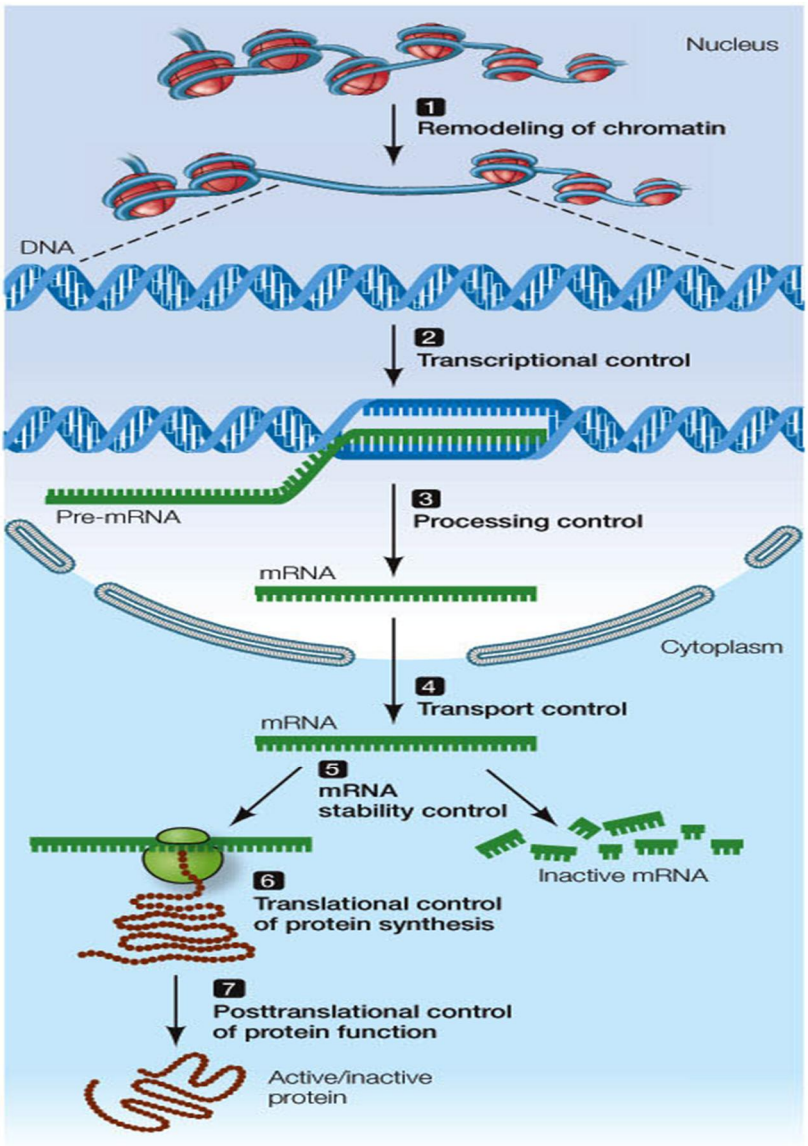
Determine which mature mRNA transcripts will be shipped out of the nucleus and into the cytoplasm.

5- **Translational controls:**

Govern which mRNA molecules that reach the cytoplasm will be translated into poly peptide chains at the ribosome.

6- **Post –translational controls:**

Govern how the polypeptide chains become modified into functional proteins. For example, some chains have specific sugar or phosphate groups attached to them; others are cleaved into smaller active fragments.



Genetic bases of cancer:

Cancer which divided uncontrolled can result from mutation in genes whose protein products regulate the cells cycle. A mutation can change a protoncogene (normal gene that promotes cell division) into an oncogene, which causes cells to divide excessively, and when tumor suppressor genes mutate also cause the same result. Tumor suppressor genes that normally act to inhibit cell division have provided insight into the regulation of the cell cycle.