Ministry of Public Health of Ukraine
Poltava State Medical University

DNA replication and RNA transcription. Biosynthesis of proteins in ribosomes.

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Lecture plan

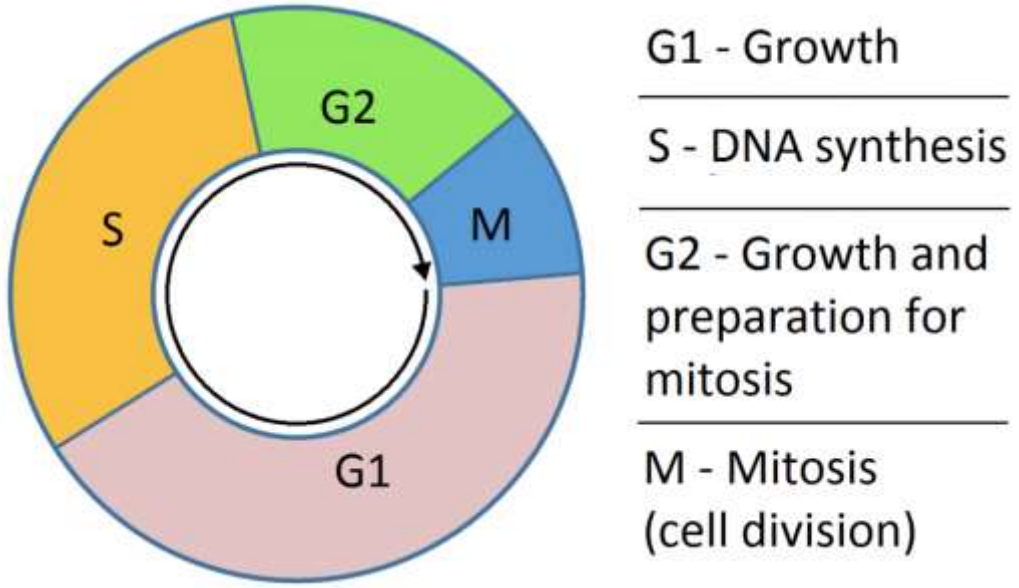
Stages and mechanisms of DNA replication.

Stages and mechanisms of RNA transcription.

Stages and mechanisms of translation.

Cell cycle

The cell cycle is a four-stage process in which the cell increases in size (gap 1, or G1, stage), copies its DNA (synthesis, or S, stage), prepares to divide (gap 2, or G2, stage), and divides (mitosis, or M, stage). The stages G1, S, and G2 make up interphase, which accounts for the span between cell divisions.



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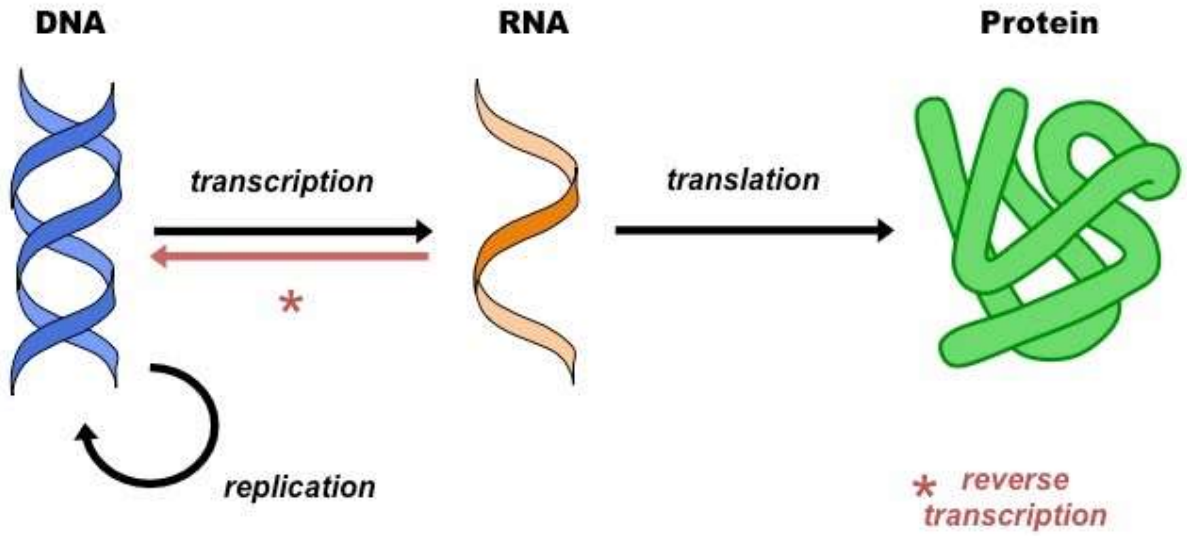
The central dogma of molecular biology



The central dogma of molecular biology explains the flow of genetic information within a cell

DNA codes for RNA via the process of transcription (occurs within the nucleus)

RNA codes for protein via the process of translation (occurs at the ribosomes)

This information flow was always considered to be uni-directional: DNA → RNA → Protein

In 1970 it was discovered that retroviruses could copy DNA from an RNA sequence

These viruses possess an enzyme (*reverse transcriptase*) that allows for reverse transcription to occur

Reverse transcription is now commonly used in scientific studies to establish gene expression profiles

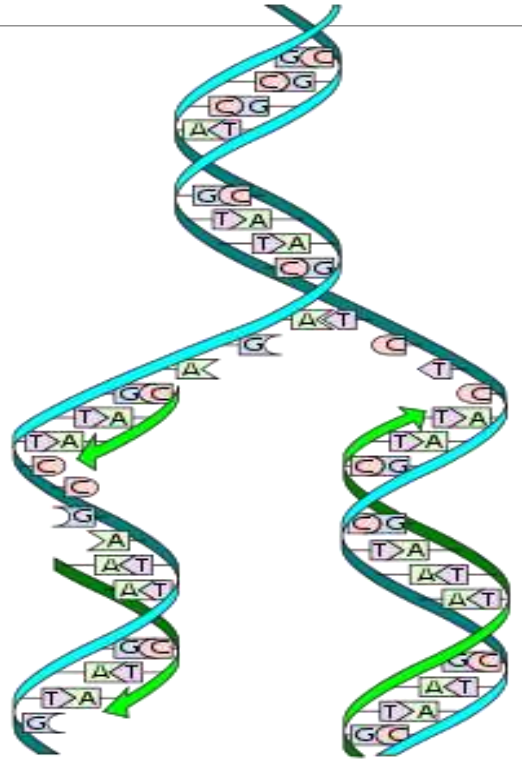
https://ib.bioninja.com.au/standard-level/topic-2-molecular-biology/27-dna-replication-transcri/central-dogma.html

DNA Replication.

DNA replication is the biological process of producing two identical replicas of DNA from one original DNA molecule.

DNA replication is a semiconservative process in which each parental strand serves as a template for the synthesis of a new complementary daughter strand. The central enzyme involved is DNA polymerase, which catalyzes the joining of deoxyribonucleoside 5’-triphosphates (dNTPs) to form the growing DNA chain.

There are three main steps of DNA replication: **initiation, elongation, and termination.**



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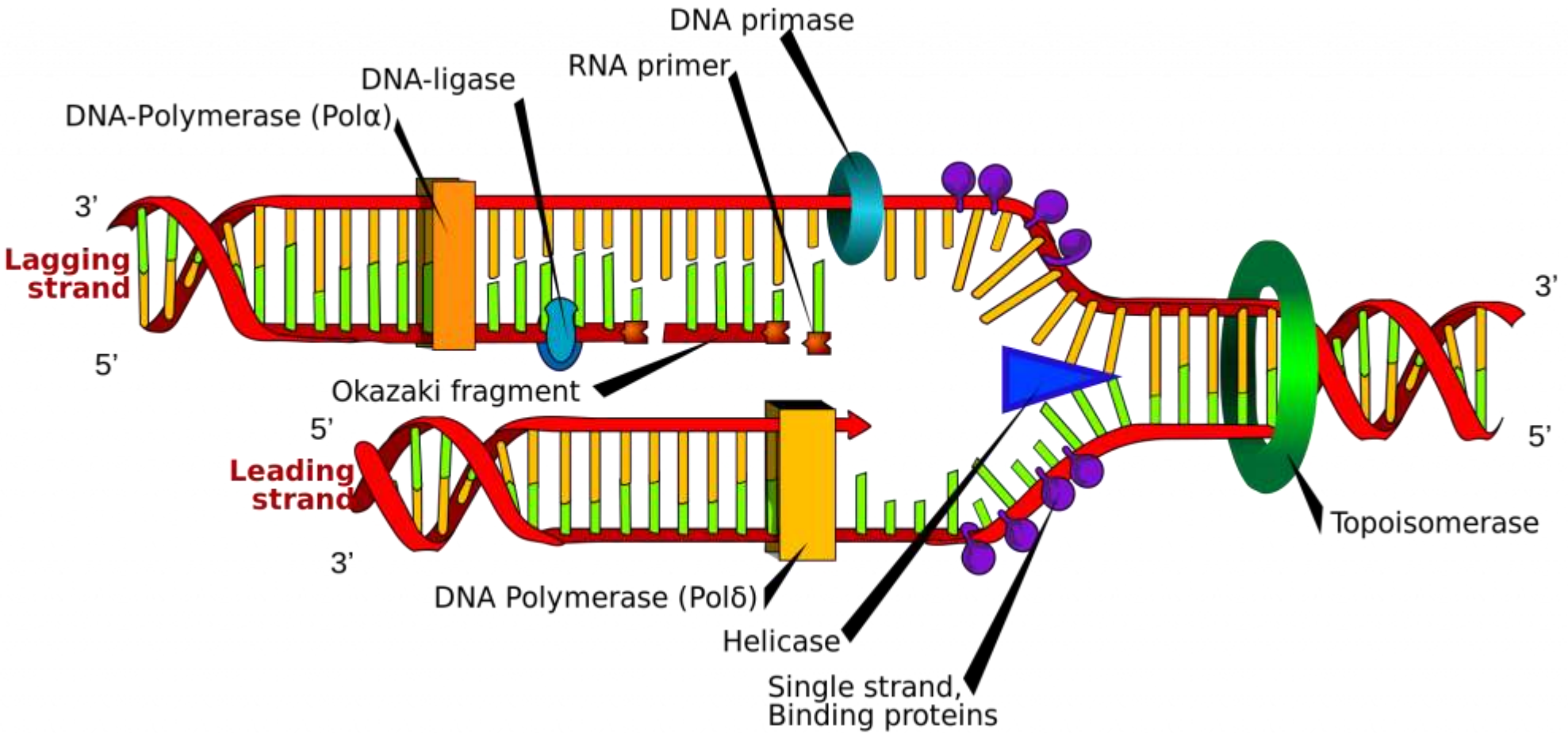


https://teachmephysiology.com/biochemistry/cell-growth-death/dna-replication/

Initiation of replication.

To start replication, free desrxribonucleotides are needed in the form of triphosphates.

Replication begins with the unwinding of the double strands of DNA and the formation of a replicative fork.

The following substances are used for initiation:

Topoisomerases (DNA topoisomerases) are enzymes that participate in the overwinding or underwinding of DNA.

Topoisomerases bind to DNA and cut phosphodiester bond of either one or both the DNA strands. the DNA to be untangled or unwound, and, at the end of these processes, the DNA backbone is resealed again.

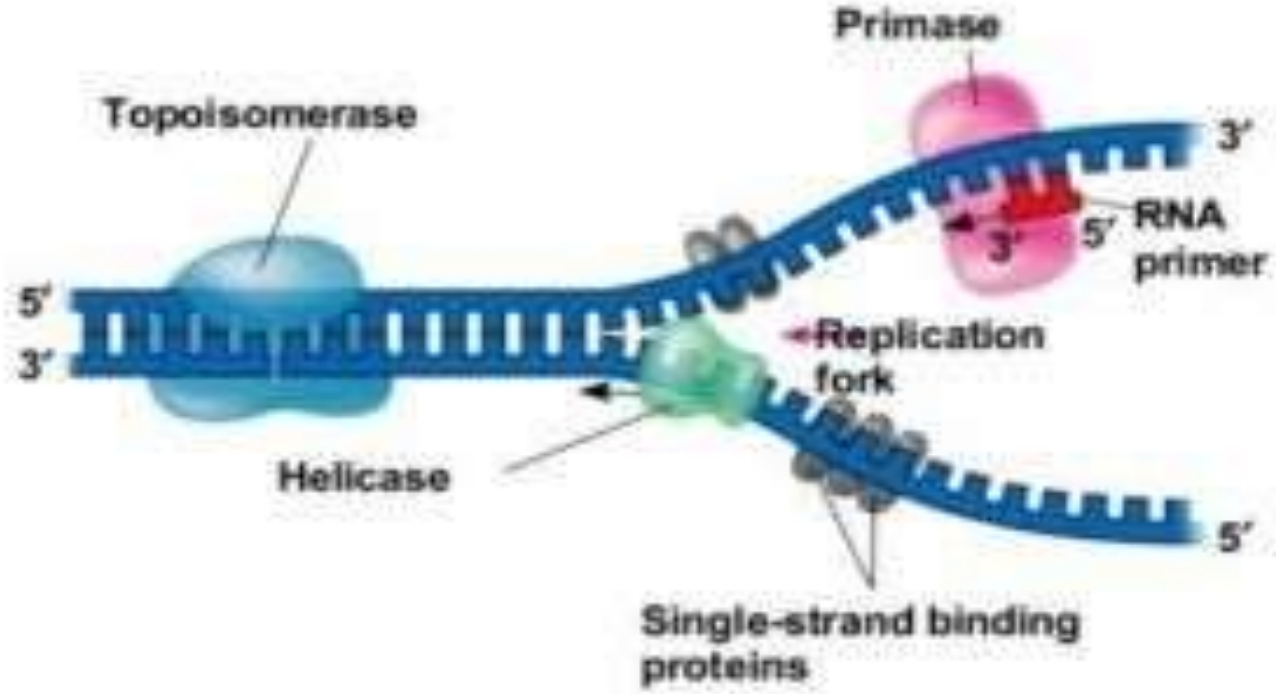
Helicase - enzyme, breaking the hydrogen bonds that hold the complementary bases of DNA together (A with T and C with G). The separation creates a 'Y' shape called a **replication fork** and the two single strands of DNA now act as templates for making new strands of DNA.

The Single-Stranded DNA Binding Protein (SSB Protein) binds to the now single-stranded DNA, preventing the separating strands from joining again.

The DNA primase (RNA polymerase**) -** enzyme synthesizes one primer per leading DNA strand to start replication and a lot of RNA lagging primers to synthesize lagging fragments to synthesize fragments Okazaki.

Primers are short strands of RNA. Primer RNA is RNA that initiates DNA synthesis, because no known DNA polymerase is able to initiate polynucleotide synthesis. DNA polymerases are specialized for elongating polynucleotide chains from their available 3′-hydroxyl termini. In contrast, RNA polymerases can elongate and initiate polynucleotides.

Initiation of replication.



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Elongation of replication.

Two DNA strands are antiparallel: one of the strands is oriented in the 3’ to 5’ direction (towards the replication fork), this is the leading strand. The other strand is oriented in the 5’ to 3’ direction (away from the replication fork), this is the lagging strand.

The most important enzyme of replication elongation - **DNA polymerase .** DNA polymerase, only functions in the 5′ to 3′ direction, this means that the daughter strands synthesize through different methods, one adding nucleotides one by one in the direction of the replication fork, the other able to add nucleotides only in chunks. The first strand, which replicates nucleotides one by one is the **leading strand**; the other strand, which replicates in fragments (Okazaki fragments), is the **lagging strand.**

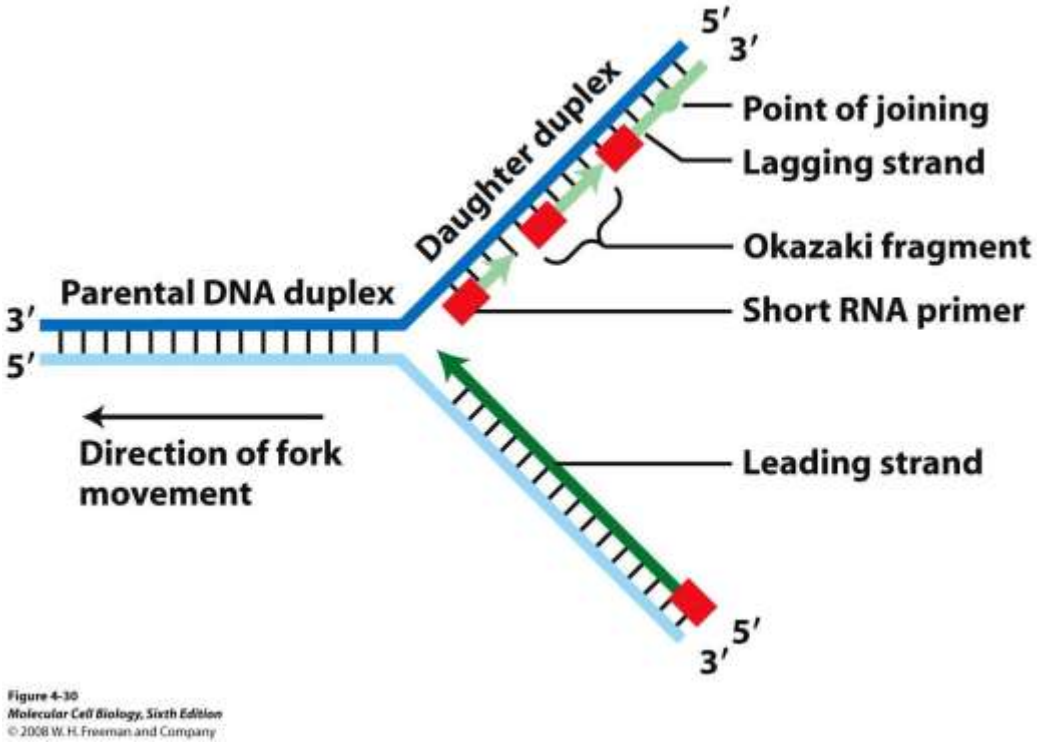

Figure 4-30
Molecular Cell Biology, Sixth Edition
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DNA polymerase

A **DNA polymerase** is a member of a family of enzymes that catalyze the synthesis of DNA molecules from nucleoside triphosphates. DNA polymerase catalyzes the formation of the phosphodiester bond which makes up the backbone of DNA molecules. plays a major role in replication and DNA repair mechanisms. **DNA polymerases** play a major role in **replication** and **DNA repair** mechanisms.

EUKARYOTIC DNA POLYMERASES

The eukaryotic cell contains five DNA polymerase **α, β, γ, δ**, and **ε**.

Polymerase **γ** is found in the cell mitochondria and it actively replicates the mitochondrial DNA, while polymerase **α, β, δ** are found in the cell nucleus hence are involved in the nuclear DNA replication.

Polymerase **α** and **δ** are majorly applied and active in diving cells hence involved in replication while polymerase **β** is active in both diving and nondividing cells hence it is involved in the repair of DNA damage.

PROCARYOTIC DNA POLYMERASES

The procariotic cell contains DNA polymerases: I, II, III, IV, V and Taq DNA polymerase. First the are the most important.

DNA Polymerase I

Its main function is excision repair of DNA strands from the 3′-5′ direction to the 5′-3 direction, as an exonuclease.It also helps with the maturation of Okazaki fragments.

DNA Polymerase II

Its major function is the 3′ – 5′ exonuclease activity and to also restart replication after replication stops due to DNA strand damages. The DNA polymerase II is found in the replication fork, to help in directing the activities of other polymerases.

DNA Polymerase III

This is the primary enzyme that is used in DNA replication. It is responsible for the synthesis of new strands by adding nucleotides to the 3′- OH group of the primer. It has a 3′-5′ exonuclease activity hence it can also proofread the errors that may arise during DNA strand replication.

Termination of replication.

In eukaryotic cells, replication stops when two replicative forks meet. Primers are removed. The resulting empty spaces are filled with deoxyribonucleotides. DNA polymerases are responsible for these reactions. Further, fragments of DNA strands are connected by DNA ligase

RNA transcription

Transcription is the first of several steps of DNA based gene expression in which a particular segment of DNA is copied into RNA (especially mRNA) by the enzyme RNA polymerase.

There are three main steps of transcripton: **initiation, elongation, and termination.**

RNA processing follows after transcription.

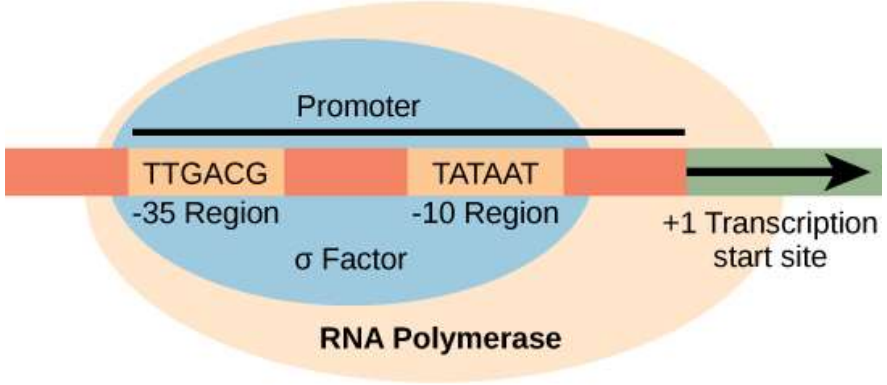
Initiation of transcription

Transcription begins with the binding of RNA polymerase, together with one or more general transcription factors, to a specific DNA sequence referred to as a "promoter" to form an RNA polymerase-promoter "closed complex". In the "closed complex" the promoter DNA is still fully double-stranded.

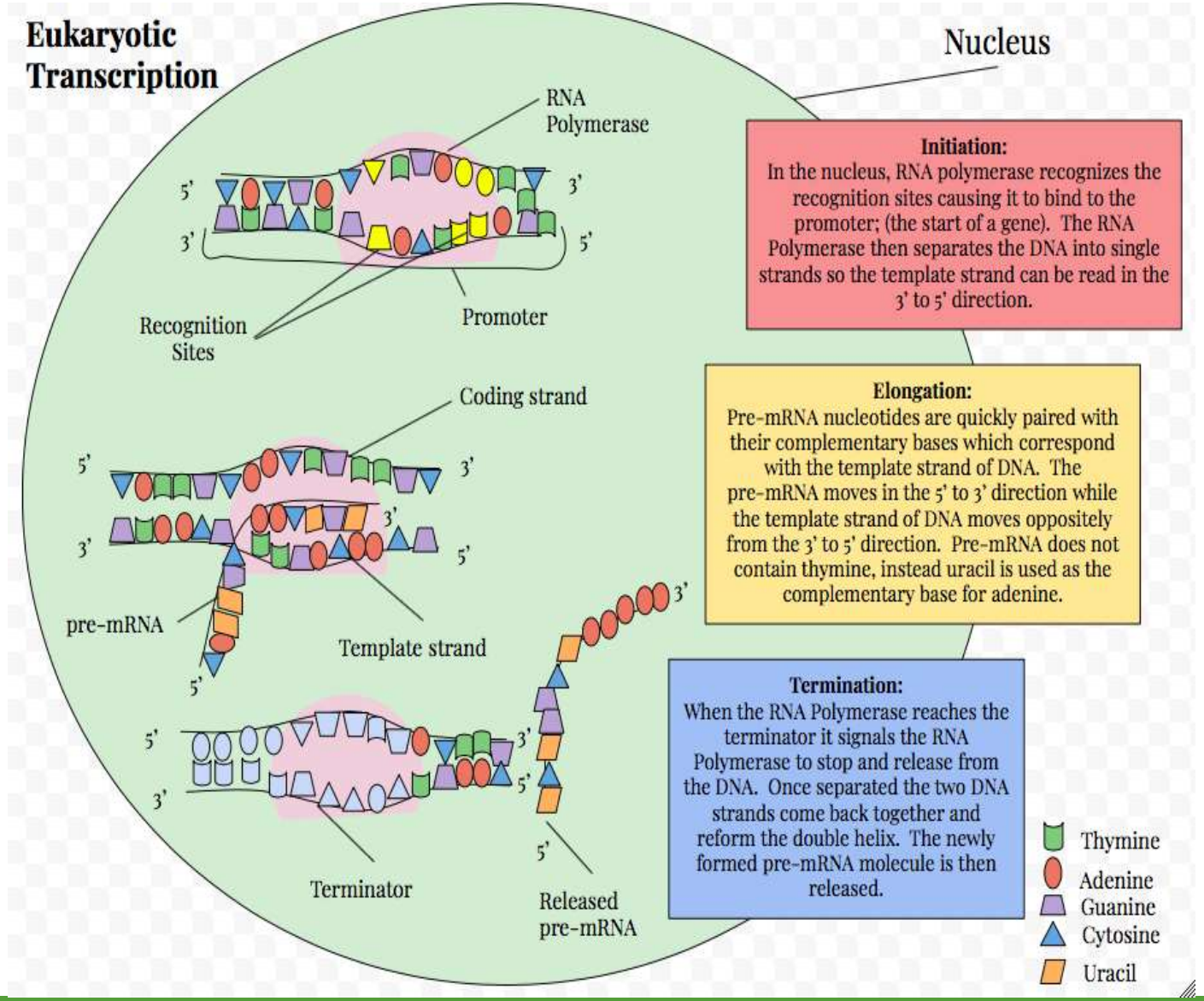
RNA polymerase, assisted by one or more general transcription factors, then unwinds approximately 14 base pairs of DNA to form an RNA polymerase-promoter "open complex". In the "open complex" the promoter DNA is partly unwound and single-stranded. The exposed, single-stranded DNA is referred to as the "transcription bubble."

RNA polymerase, assisted by one or more general transcription factors, then selects a transcription start site in the transcription bubble, binds to an initiating NTP and an extending NTP (or a short RNA primer and an extending NTP) complementary to the transcription start site sequence, and catalyzes bond formation to yield an initial RNA product.

The **promoter** is a sequence of DNA to which proteins bind that initiate transcription of a single RNA from the DNA downstream of it. Promoters are located near the transcription start sites of genes, upstream on the DNA (towards the 5' region of the sense strand). Promoters can be about 100–1000 base pairs long.



https://courses.lumenlearning.com/wm-biology1/chapter/prokaryotic-transcription/



https://en.wikipedia.org/wiki/Eukaryotic_transcription#/media/File:Eukaryotic_Transcription.png

RNA-polymerase

RNA polymerase (**RNAP** or **RNApol**, **DNA-directed RNA polymerase**), is an enzyme that synthesizes RNA from a DNA template.

Bacteria and archaea only have one RNA polymerase. Eukaryotes have multiple types of nuclear RNAP, each responsible for synthesis of a distinct subset of RNA:

RNA polymerase I synthesizes a pre-rRNA 45S (35S in yeast), which matures and will form the major RNA sections of the ribosome.

RNA polymerase II synthesizes precursors of mRNAs and most sRNA and microRNAs.

RNA polymerase III synthesizes tRNAs, rRNA 5S and other small RNAs found in the nucleus and cytosol.

RNA polymerase IV and V found in plants are less understood; they make siRNA. In addition to the ssRNAPs, chloroplasts also encode and use a bacteria-like RNAP.

RNA polymerase "core" from E. coli consists of five subunits: two alpha (α) subunits of 36 kDa, a beta (β) subunit of 150 kDa, a beta prime subunit (β′) of 155 kDa, and a small omega (ω) subunit. A sigma (σ) factor binds to the core, forming the holoenzyme. After transcription starts, the factor can unbind and let the core enzyme proceed with its work.[1] The core RNA polymerase complex forms a "crab claw" or "clamp-jaw" structure with an internal channel running along the full length.

Eukaryotic and archaeal RNA polymerases have a similar core structure and work in a similar manner, although they have many extra subunits.

All RNAPs contain metal cofactors, in particular zinc and magnesium cations which aid in the transcription process.

Elongation of transcription

The transcription elongation phase begins with the release of the σ subunit from the polymerase.

The dissociation of σ allows the core enzyme to proceed along the DNA template, synthesizing mRNA in the 5′ to 3′ direction at a rate of approximately 40 nucleotides per second. As elongation proceeds, the DNA is continuously unwound ahead of the core enzyme and rewound behind it .

The base pairing between DNA and RNA is not stable enough to maintain the stability of the mRNA synthesis components. Instead, the RNA polymerase acts as a stable linker between the DNA template and the nascent RNA strands to ensure that elongation is not interrupted prematurely.

Termination of transcription

Correct termination of transcription at specific sites is crucial as it serves to prevent the unwanted expression of genes that are downstream of a transcribed gene. Termination occurs through two processes:

intrinsic termination (also called Rho-independent termination), involves terminator sequences within the RNA that signal the RNA polymerase to stop. The terminator sequence is usually a **palindrome sequence** (reads the same forward as backward) that forms a stem-loop hairpin structure that leads to the dissociation of the RNA polymerase from the DNA template. One such common termination motif is the palindrome sequence 'GCCGCCG'. The RNA polymerase fails to proceed beyond this point and consequently, the nascent DNA-RNA hybrid dissociates. The RNA polymerase then proceeds to look for a new initiation-region from which to start the initiation process again.

factor-dependent termination, in which additional factors together with a sequence result in termination. Most factor-dependent termination is dependent on **Rho protein.** A hexamer of Rho proteins binds to a typically pyrimidine-rich, unstructured part of the message, called a rut (Rho utilization) site, and then moves along the RNA to reach the transcription machinery. Rho causes termination at specific sequences.

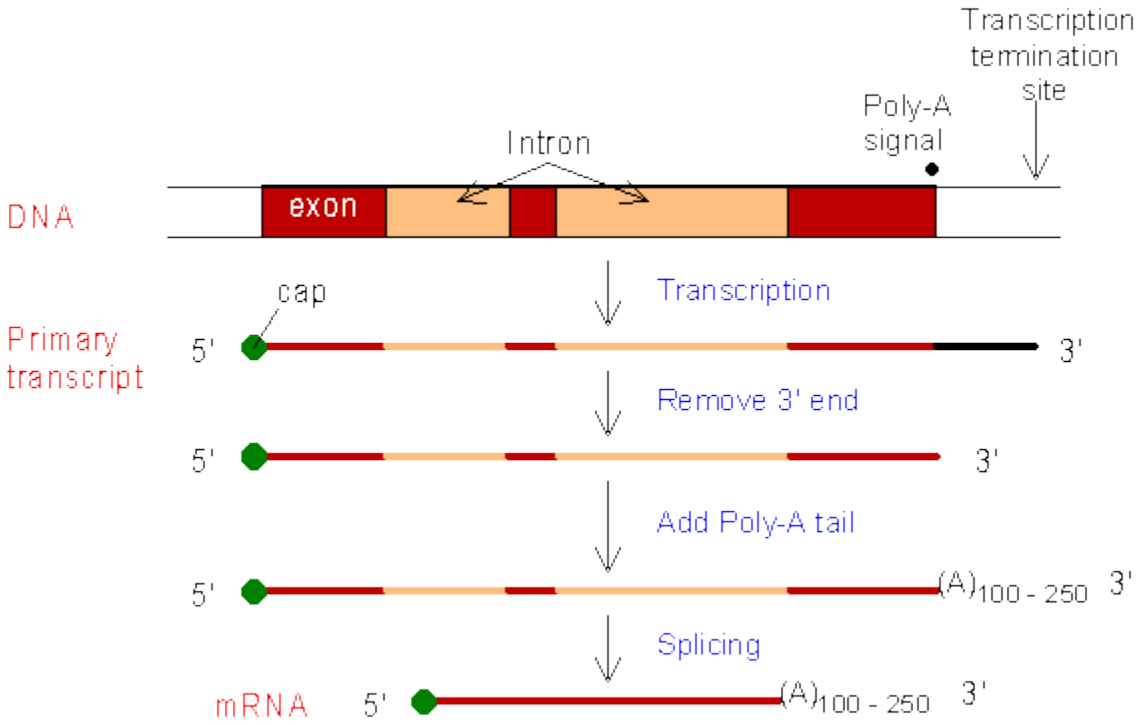
Processing of pre-mRNA

The initial product of transcription is **pre-mRNA** or **primary transcript.** After it has been processed and is ready to be exported from the nucleus, it is called the **mature mRNA** or **processed mRNA**.

Messenger RNAs are processed in eukaryotic cells, not in bacterial cells. **The three main processing steps are:**

1. **Capping** at the 5' end (a **7-methyl guanosine** is added at the 5' end of the mRNA). The cap protects the 5' end of the mRNA from degradation by nucleases and also helps to position the mRNA correctly on the ribosomes during protein synthesis.
2. **Addition of a polyA tail** at the 3' end (**PolyA Polymerase** adds a "tail" of about 200 adenylate nucleotides to the 3‘ end). PolyA tail plays a role in efficient translation of the mRNA, as well as in the stability of the mRNA.
3. **Splicing** - remove introns (non-coding regions) and join exons (non-coding regions). Introns are removed from the pre-mRNA by the activity of a complex called the **spliceosome**. The spliceosome is made up of **proteins** and **small RNAs** that are associated to form protein-RNA enzymes called small nuclear ribonucleoproteins or **snRNPs** (pronounced **SNURPS**). There are two main steps in splicing- In the ***first step***, the pre-mRNA is cut at the 5' splice site (the junction of the 5' exon and the intron). The 5' end of the intron then is joined to the branch point within the intron. This generates the lariat-shaped molecule characteristic of the splicing process. In the ***second step***, the 3' splice site is cut, and the two exons are joined together, and the intron is released. Alternative splicing allows the production of many different proteins using relatively few genes, since *a single RNA* with many exons can, by mixing and matching its exons during splicing, *create many different protein coding messages*. As we noted when discussing the human genome, each gene in our DNA gives rise, on average, to three different proteins.

Processing of pre-mRNA



https://www.web-books.com/MoBio/Free/Ch5A.htm

Processing of pre-rRNA and pre-tRNA

Processing of pre-rRNA

The newly transcribed pre-rRNA is a cluster of three rRNAs: 18S, 5.8S and 28S in mammals. They must be separated to become functional. Pre-rRNA is synthesized in the nucleolus. The U3 snRNA, other U-rich snRNAs, and their associated proteins in the nucleolus are involved in the cleavage of the pre-rRNA.

5S rRNA is synthesized in the nucleoplasm. It does not require any processing. After 5S rRNA is synthesized, it will enter the nulceolus to combine with 28S and 5.8S rRNAs, forming the large subunit of the ribosome.

Processing of pre-tRNA

Pre-tRNA requires extensive processing to become a functional tRNA. Four types of modifications are involved:

Removing an extra segment (~ 16 nucleotides) at the 5' end by RNase P.

Removing an intron (~ 14 nucleotides) in the anticodon loop by splicing.

Replacing two U residues at the 3'end by CCA, which is found in all mature tRNAs.

Modifying some residues to characteristic bases, e.g., inosine, dihydrouridine and pseudouridine.

Inhibitors of Replication and transcription

INHIBITORS OF DNA REPLICATION

Aphidicolin is a reversible inhibitor of eukaryotic nuclear DNA replication. It blocks the cell cycle at early S phase. It is a specific inhibitor of DNA polymeras **α** and **δ** in eukaryotic cells and in some viruses.

Quinolones are a key group of antibiotics that interfere with DNA synthesis by inhibiting topoisomerase, most frequently topoisomerase II (DNA gyrase), an enzyme involved in DNA replication. DNA gyrase relaxes supercoiled DNA molecules and initiates transient breakages and rejoins phosphodiester bonds in superhelical turns of closed-circular DNA. This allows the DNA strand to be replicated by DNA or RNA polymerases. The **fluoroquinolones**, second-generation quinolones that include **levofloxacin, norfloxacin**, and ciprofloxacin, are active against both Gram-negative and Gram-positive bacteria.

Topoisomerases are present in both prokaryotic and eukaryotic cells, but the quinolones are specific inhibitors of bacterial topoisomerase II. Inhibitors that are effective against mammalian topoisomerases, such as **irinotecan** and etoposide, are used as antineoplastic drugs to kill cancer cells.

INHIBITORS OF RNA TRANSCRIPTION

Rifampicin blocks initiation of RNA synthesis by specifically inhibiting bacterial RNA polymerase. It does not interact with mammalian RNA polymerases, making it specific for Gram-positive bacteria and some Gram-negative bacteria.

Some antibiotics that interfere with RNA synthesis by inhibiting RNA polymerase, such as **doxorubicin** and **actinomycin D (dactinomycin),** are not specific for bacteria and interfere with both bacterial and mammalian systems. These are most often used as antineoplastic and antitumor drugs, attacking rapidly growing malignant cells as well as normal cells. Because cancerous cells are growing at a faster rate than surrounding normal tissue, a higher percentage of malignant cells are attacked by cytotoxic drugs. However, antitumor drugs cannot differentiate between malignant cells and fast-dividing normal cells such as those of the intestinal epithelium or hair follicles.

https://www.sigmaaldrich.com/technical-documents/articles/biofiles/inhibition-of-nucleic.html#:~:text=Quinolones%20are%20a%20key%20group,enzyme%20involved%20in%20DNA%20replication.

Translation

Translation is the process in which ribosomes in the cytoplasm or endoplasmic reticulum synthesize proteins after the process of transcription of DNA to RNA in the cell's nucleus.

The process of translation, or protein synthesis, involves the decoding of an mRNA message into a polypeptide product. Amino acids are covalently strung together by interlinking peptide bonds. Each individual amino acid has an amino group (NH_2) and a carboxyl (COOH) group. Polypeptides are formed when the amino group of one amino acid forms an amide (i.e., peptide) bond with the carboxyl group of another amino acid.

Activation of amino acids takes place before translation.

There are three main steps of translation: **initiation, elongation, and termination.**

Posttranslation modification follows after translation.

The Protein Synthesis Machinery

Translation requires the input of an **mRNA template**, **ribosomes**, **tRNAs**, and various enzymatic factors.

Ribosomes

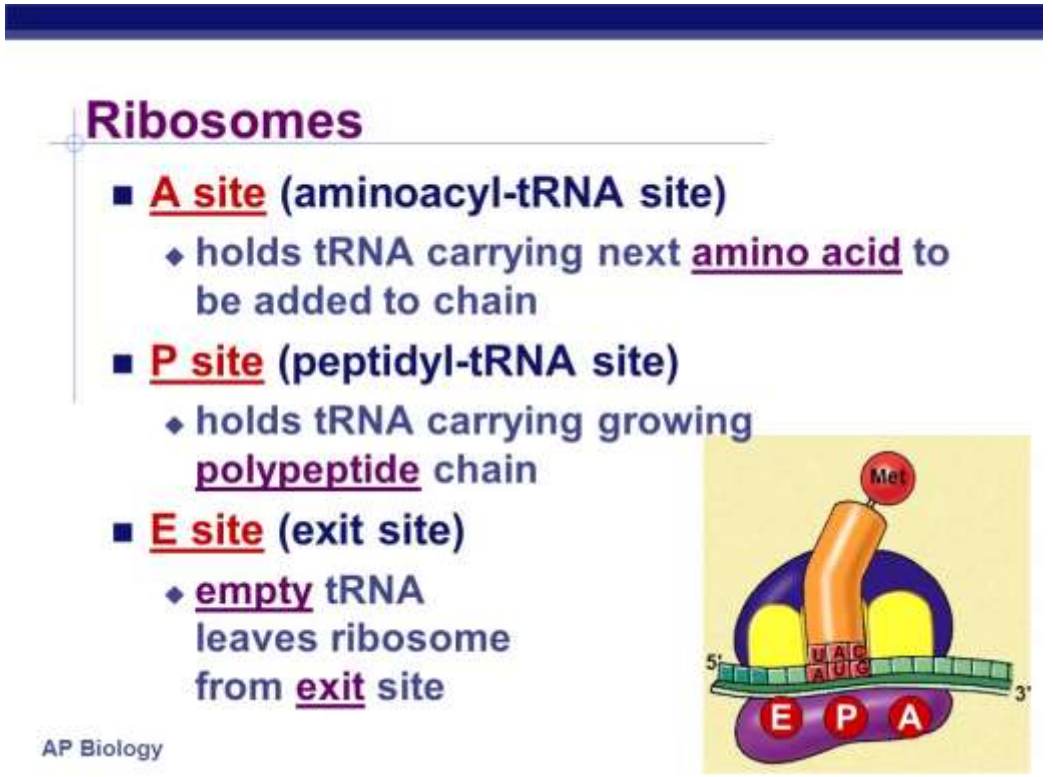
A ribosome is a complex macromolecule composed of structural and catalytic rRNAs, and many distinct polypeptides.

Ribosomes exist in the cytoplasm in prokaryotes and in the cytoplasm and rough endoplasmic reticulum in eukaryotes.

Ribosomes are made up of two subunits. In *E. coli*, the small subunit is described as 30S, and the large subunit is 50S, for a total of 70S.

Mammalian ribosomes have a small 40S subunit and a large 60S subunit, for a total of 80S.

The small subunit is responsible for binding the mRNA template, whereas the large subunit sequentially binds tRNAs.



tRNAs

The tRNAs are structural RNA molecules that were transcribed from genes by RNA polymerase III. Specific tRNAs bind to sequences on the mRNA template and add the corresponding amino acid to the polypeptide chain. Therefore, tRNAs are the molecules that actually "translate" the language of RNA into the language of proteins.

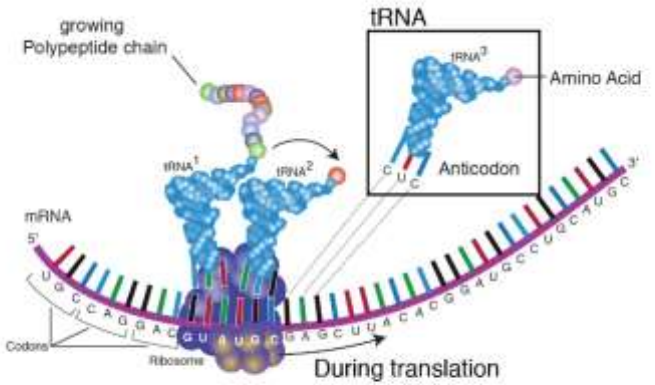
Mature tRNAs take on a three-dimensional structure through intramolecular hydrogen bonding to position the amino acid binding site at one end and the **anticodon** at the other end. The anticodon is a three-nucleotide sequence in a tRNA that interacts with an mRNA codon through complementary base pairing.

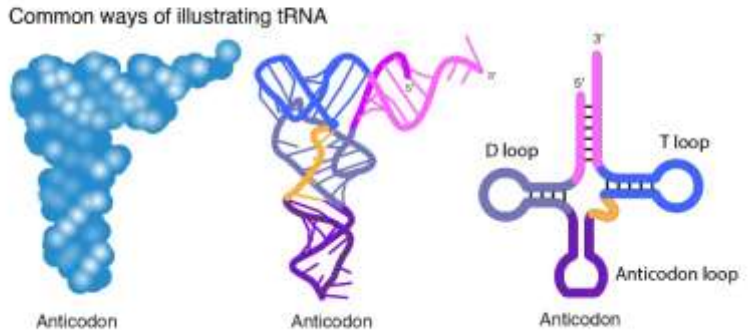
tRNAs need to interact with three factors:

They must be recognized by the correct aminoacyl synthetase.

They must be recognized by ribosomes.

They must bind to the correct sequence in mRNA.





https://www.genome.gov/genetics-glossary/Transfer-RNA

Genetic code

Properties of Genetic code

1. The genetic code is degenerate

Most amino acids have more than one codon, for example in the case of arginine, leucine, and serine amino acids each one of them has 6 different codons. In the case of leucine amino acid, these codons are CUA, CUC, CUG, CUU, UUA, and UUG. This helps in codes against the harmful effect of the mutation.

2. The genetic code is unambiguous

Each code has only one meaning - it codes only one amino acid. For example, AUG codes only one amino acid which is methionine. It can never code any other amino acid.

3. The genetic code has "start" and "stop" signals

There is only one start codon (AUG, initiation codon) which starts the translation process, but to stop this process three stop codons are present i.e.UAA, UGA and UAG.

4. A codon aways has an anticodon

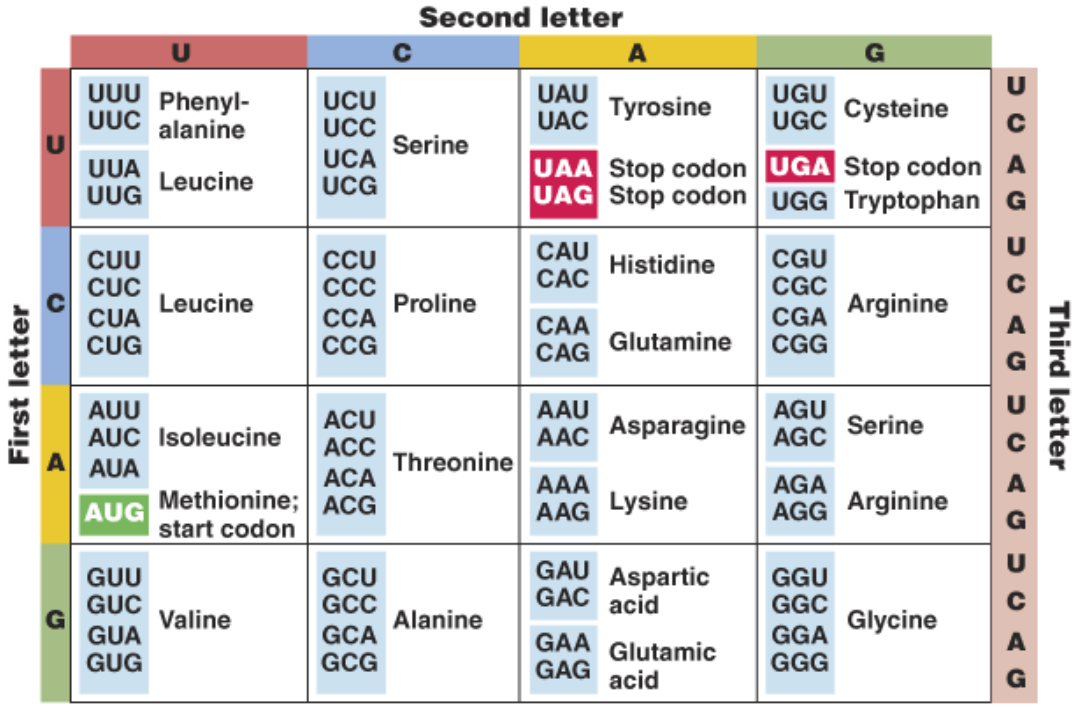
A specific tRNA molecule contains a set of three consecutive nucleotides that can base pair with the codon of mRNA. This set of nucleotide that can base pair with codon is called Anticodon. For example for codon of UGC on mRNA, tRNA will have anticodon ACG.

Type of codon which starts protein synthesis is called Initiation codon i.e. AUG.

Type of codon which terminates protein synthesis is called stop codon i.e. UAA, UGA, and UAG.

5. Genetic codes are universal except in rare cases

These will code same amino acids in all organisms, even it may be plant-animal of fungi, etc.



https://readbiology.com/genetic-code/

Activation of amino acids. Aminoacyl-tRNA synthetase

Aminoacyl-tRNA synthetase

An **aminoacyl-tRNA synthetase** (**aaRS** or **ARS**), also called tRNA-ligase, is an enzyme that attaches the appropriate amino acid onto its corresponding tRNA.

It does so by catalyzing the transesterification of a specific cognate amino acid or its precursor to one of all its compatible cognate tRNAs to form an aminoacyl-tRNA.

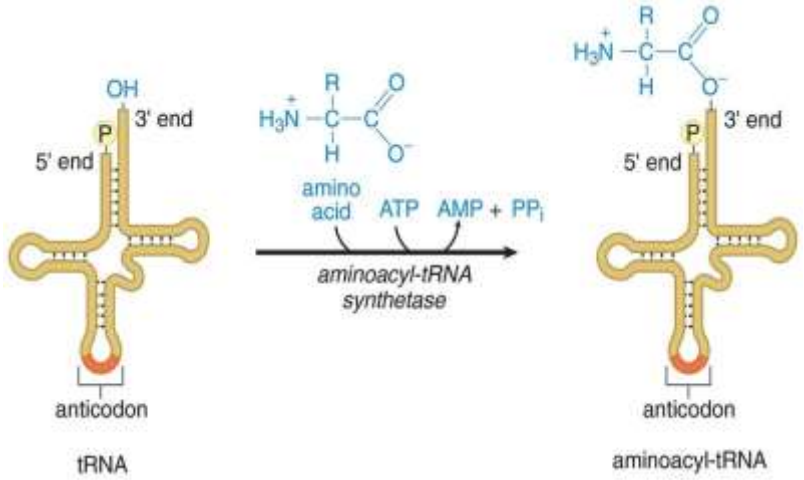
In humans, the 20 different types of aa-tRNA are made by the 20 different aminoacyl-tRNA synthetases, one for each amino acid of the genetic code.

Activation of amino acids

The mechanism can be summarized in the following reaction series:

Amino Acid + ATP → Aminoacyl-AMP + PP_i

Aminoacyl-AMP + tRNA → Aminoacyl-tRNA + AMP



https://www.toppr.com/ask/question/which-of-the-following-enzyme-is-used-for-the-activation-of-amino-acid-during-translation/

Stages of translation

Initiation:

-The small ribosomal subunit binds to the mRNA and moves along it in a 5' - 3' direction until it reaches a start codon (AUG).

-The tRNA molecule with the appropriate anticodon will align opposite the start codon according to complementary base pairing

- Each tRNA molecule carries a specific amino acid according to the genetic code (e.g. AUG = Methionine (Met))

- The large ribosomal subunit aligns itself to the tRNA molecule at its P-site and forms a complex with the small ribosomal subunit

Elongation:

- A second tRNA molecule pairs with the next codon in the ribosomal A-site

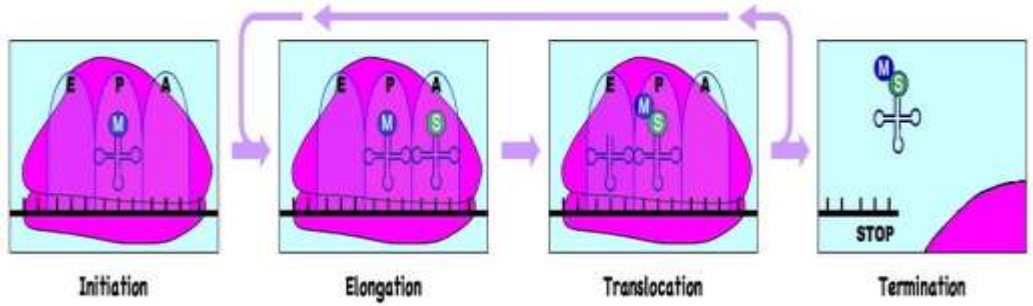
- The amino acid in the P-site is covalently attached via a peptide bond to the amino acid in the A-site.

- Translocation:

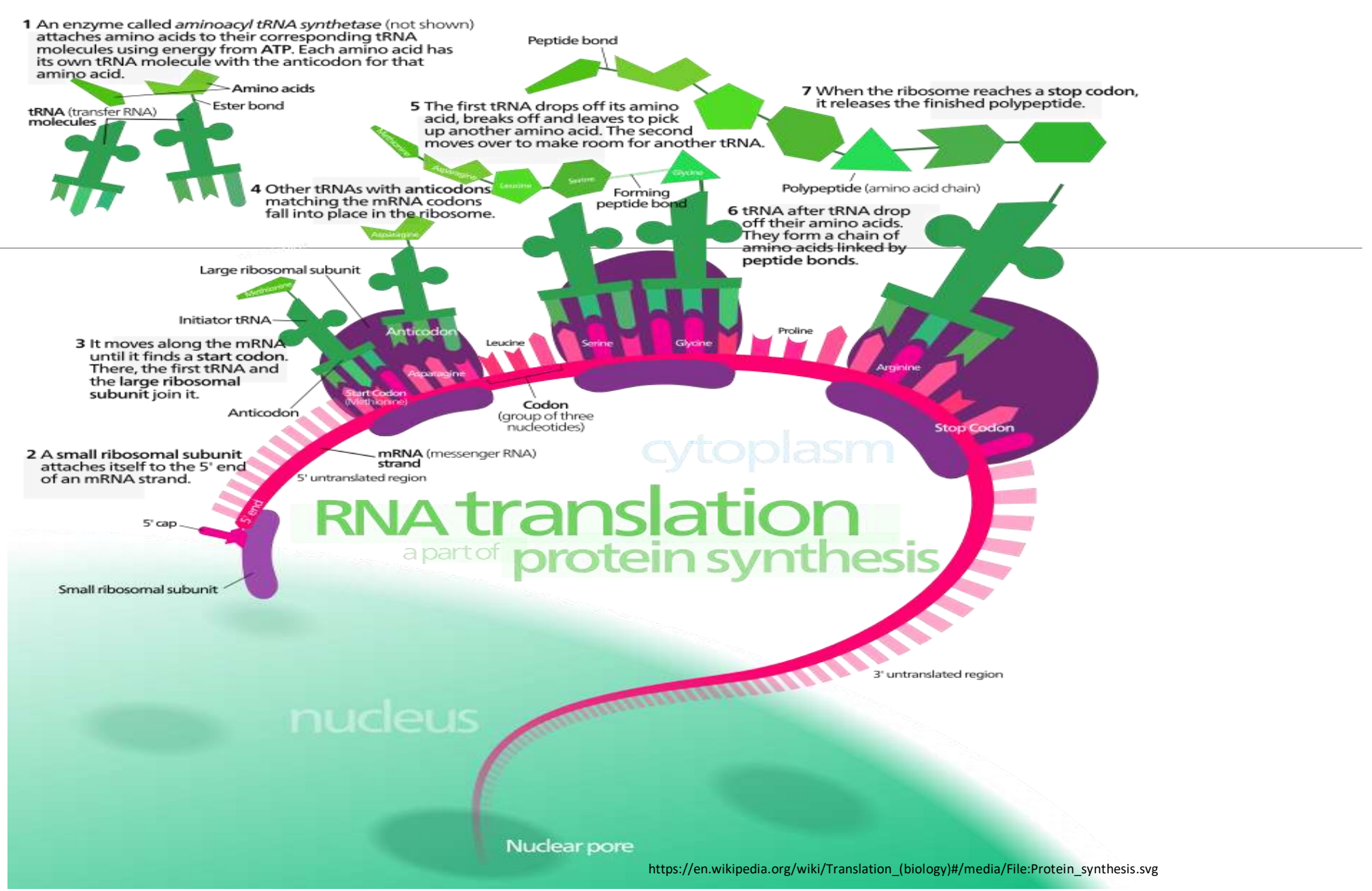
The ribosome moves along one codon position (in a 5' - 3' direction). The tRNA molecules that was in the P site is now in the E site and, having transferred it's amino acid, is released. The tRNA that was in the A site is now in the P site and has two amino acids ready to be transferred. A new tRNA molecule binds to the now empty A site and the elongation process is repeated

Termination:

- Elongation and translocation continue until the ribosome reaches a stop codon. These codons do not code for any amino acids and instead signal for translation to stop. The polypeptide is released and the ribosome disassembles back into subunits. The polypeptide may undergo post-translational modification prior to becoming a functional protein. Multiple ribosomes can translate a single mRNA sequence simultaneously (forming polysomes)



http://www.vce.bioninja.com.au/aos-3-heredity/molecular-genetics/translation.html



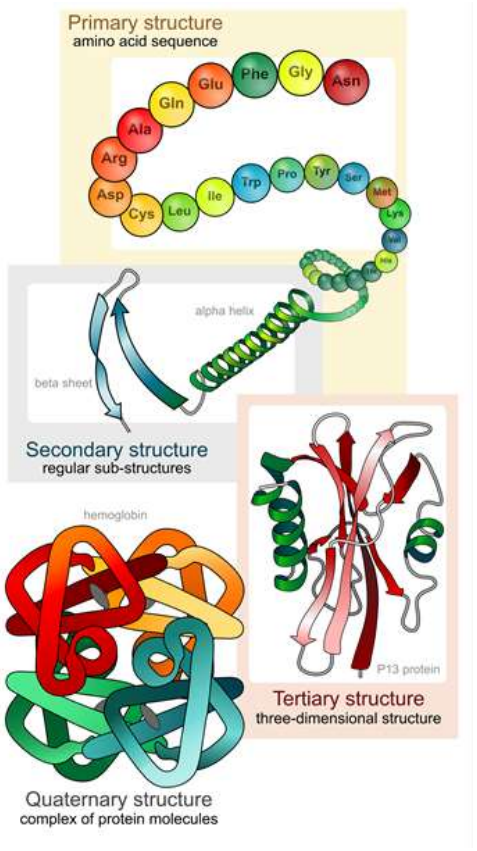
https://en.wikipedia.org/wiki/Translation_(biology)#/media/File:Protein_synthesis.svg

Protein folding

Protein folding is the physical process by which a protein chain acquires its native three-dimensional structure, a conformation that is usually biologically functional

It is the physical process by which a polypeptide folds into its characteristic and functional three-dimensional structure from a random coil. Each protein exists as an unfolded polypeptide or random coil when translated from a sequence of mRNA to a linear chain of amino acids. This polypeptide lacks any stable (long-lasting) three-dimensional structure. As the polypeptide chain is being synthesized by a ribosome, the linear chain begins to fold into its three-dimensional structure.

Folding of many proteins begins even during translation of the polypeptide chain. Amino acids interact with each other to produce a well-defined three-dimensional structure, the folded protein, known as the native state. The resulting three-dimensional structure is determined by the amino acid sequence or primary structure



https://www.news-medical.net/life-sciences/Protein-Folding.aspx

Diseases related to incorrect protein folding

Misfolded proteins denature easily and lose their structure and function. Incorrect protein folding can lead to many human diseases.

Alzheimer's disease is an example of a neurodegenerative condition caused by protein misfolding. This disease is characterized by dense plaques in the brain caused by misfolding of the secondary β-sheets of the fibrillar β-amyloid proteins present in brain matter.

Huntington's disease and Parkinson's disease are other examples of neurodegenerative diseases associated with protein misfolding.

Cystic fibrosis (CF) is a fatal disease caused by misfolding of the cystic fibrosis transmembrane conductance regulator (CFTR) protein. In most cases of CF, the phenylalanine at position 508 of the CFTR is deleted, causing misfolding of the regulator protein.

Several allergies have also been shown to be caused by incorrect protein folding.

Posttranslational modification (PTM) of proteins

Posttranslational modification (PTM) of proteins, being one of the later stages in protein biosynthesis, refers to the reversible or irreversible chemical changes proteins may undergo after translation.

Post-translational modifications can occur on the amino acid side chains or at the protein's C- or N- termini.

They can extend the chemical repertoire of the 20 standard amino acids by modifying an existing functional group or introducing a new one such as phosphate. Phosphorylation is a very common mechanism for regulating the activity of enzymes and is the most common post-translational modification.

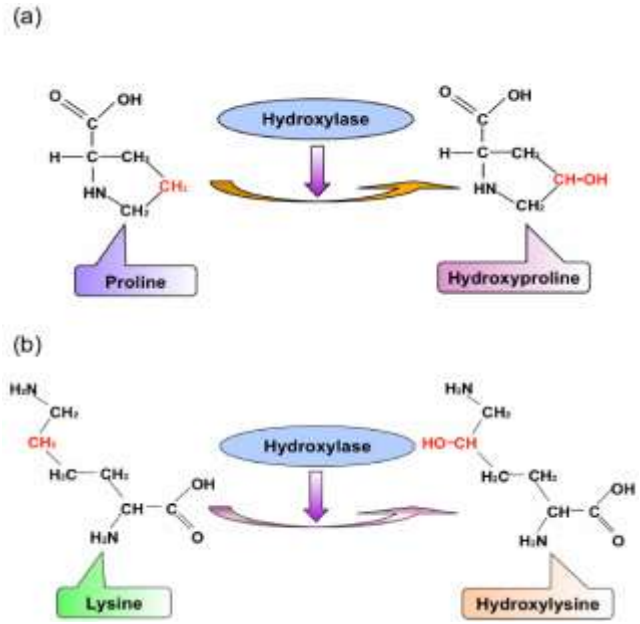
Many eukaryotic and prokaryotic proteins also have carbohydrate molecules attached to them in a process called glycosylation, which can promote protein folding and improve stability as well as serving regulatory functions.

Attachment of lipid molecules, known as lipidation, often targets a protein or part of a protein attached to the cell membrane.

Other forms of post-translational modification consist of cleaving peptide bonds, as in processing a propeptide to a mature form or removing the initiator methionine residue.

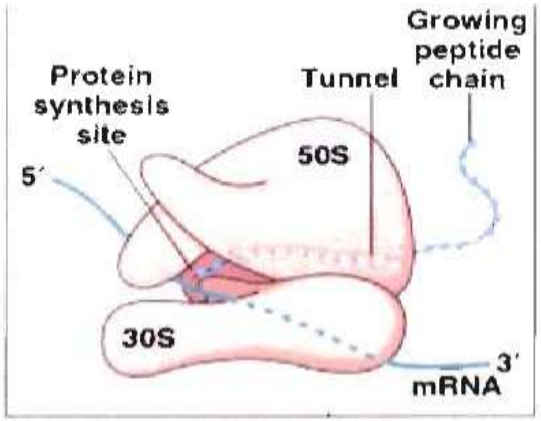
The formation of disulfide bonds from cysteine residues may also be referred to as a post-translational modification. For instance, the peptide hormone insulin is cut twice after disulfide bonds are formed, and a propeptide is removed from the middle of the chain; the resulting protein consists of two polypeptide chains connected by disulfide bonds.

The example of the amino acid modification (hydroxylation of proline and lysine in a collagen molecule)

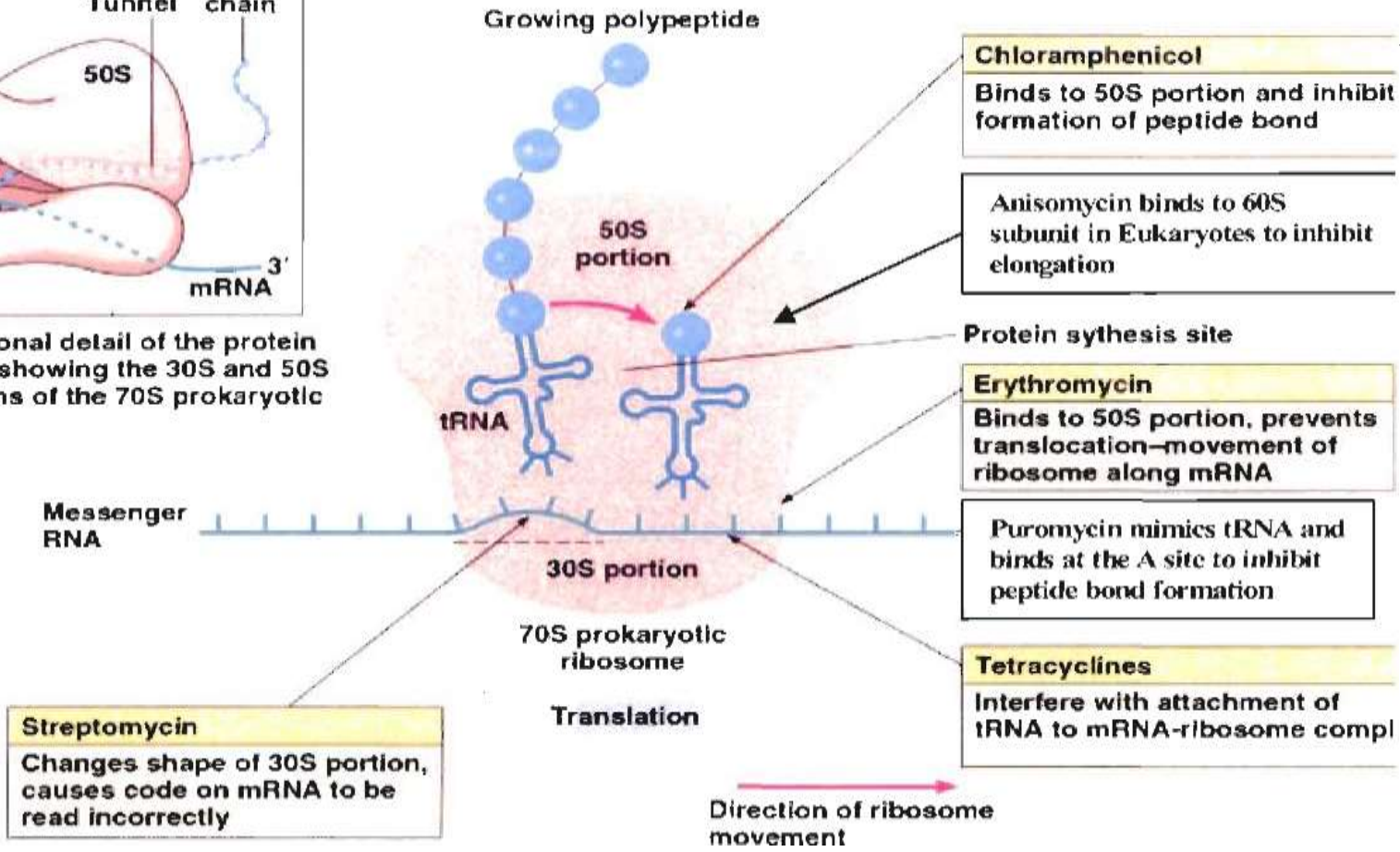


https://www.researchgate.net/figure/Schematic-drawing-to-show-protein-hydroxylation-occurring-at-a-proline-and-b_fig1_262608070

Protein synthesis inhibitors (procariotic cells)



(a) Three-dimensional detail of the protein synthesis site showing the 30S and 50S subunit portions of the 70S prokaryotic ribosome.



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