

“In the Name of Allah, the Most Beneficent, the Most Merciful.”

ASSIGNMENT

SUBJECT : CELLULAR PERSPECTIVE

TOPIC: TRANSLATION AND POST TRANSLATIONAL MODIFICATIONS, DNA RESPONSIBLE FOR INHERITANCE

SUBMITTED TO: MA'AM MARIA AKHTAR

SUBMITTED BY: GROUP C

SEMESTER: 2nd (B)

DEPARTMENT: CHEMISTRY

THE ISLAMIA UNIVERSITY OF BAHAWALPUR

TRANSLATION:

Translation is a process by which the genetic code contained within an mRNA molecule is decoded to produce the specific sequence of amino acids in a polypeptide chain.

SITE OF TRANSLATION:

It occurs in the cytoplasm following Transcription

STATES OF TRANSLATION :

Translation has three stages

- Initiation
- Elongation
- Termination

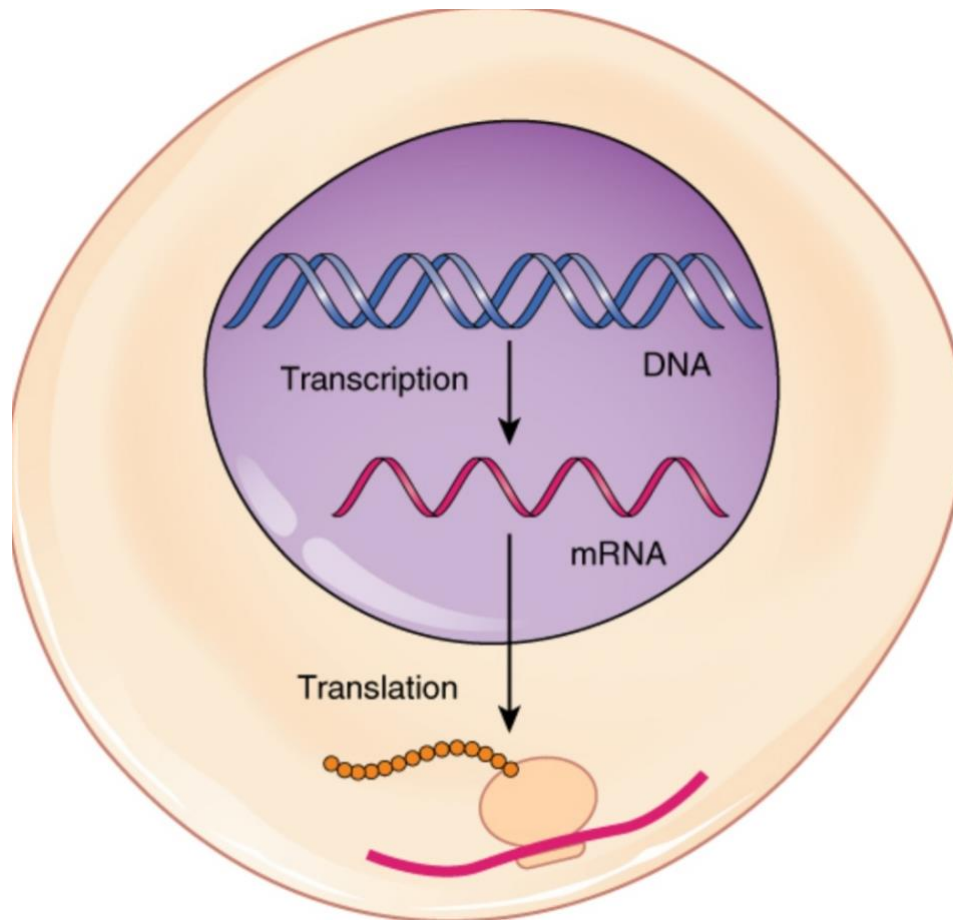


Fig: Summary of Transcription and translation.

COMPONENTS OF TRANSLATION :

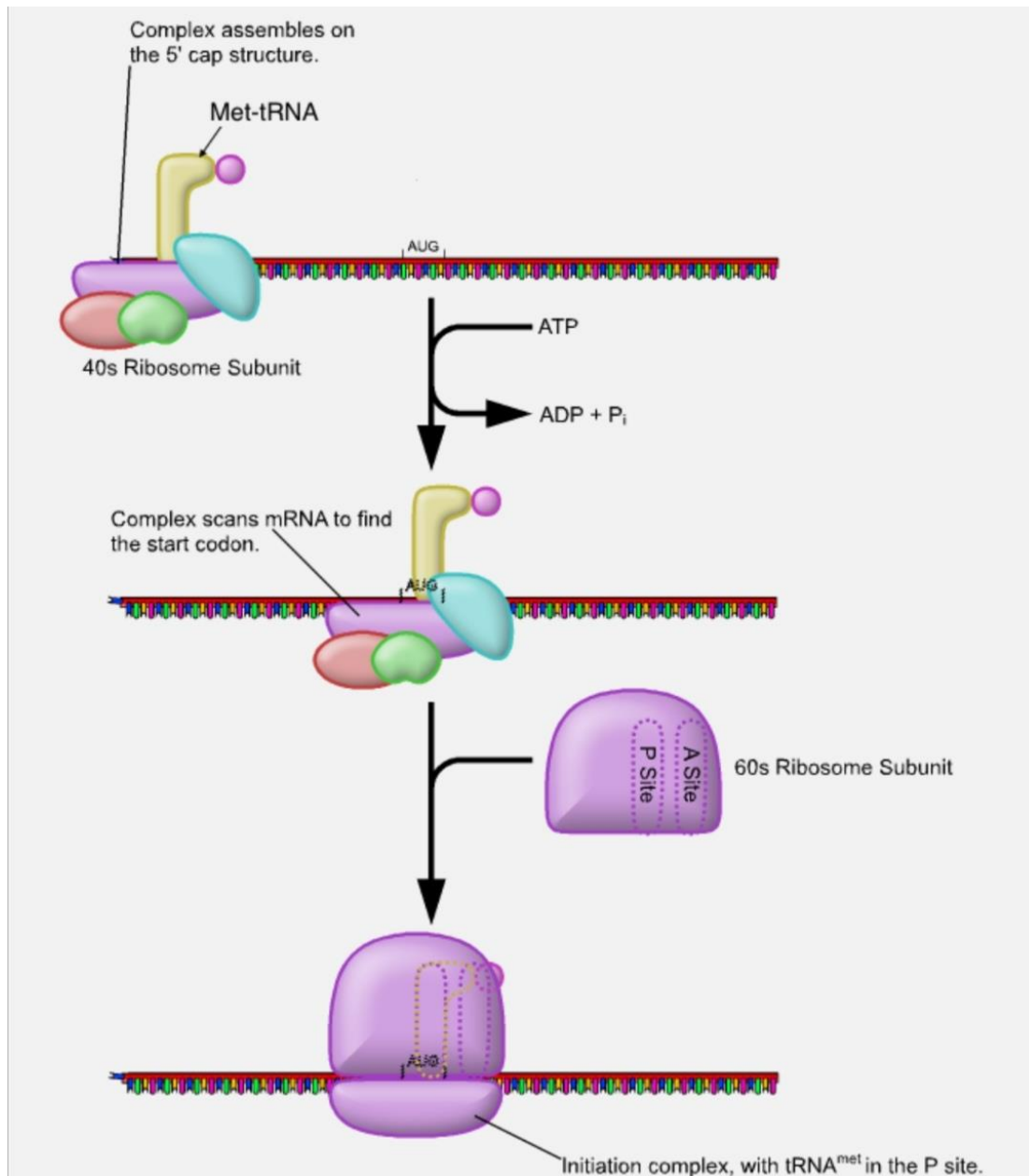
The key components required for translation are mRNA, ribosomes, tRNA and aminoacyl-tRNA synthetases. During translation mRNA nucleotide bases are read as three base codons, each of which codes for a particular amino acid.

Each tRNA molecule possesses an anticodon on the opposite end that is complementary to the mRNA codon. tRNA molecules are therefore responsible for bringing amino acids to the ribosome in the correct order ready for polypeptide assembly.

Aminoacyl-tRNA synthetases :

Aminoacyl-tRNA synthetases are enzymes that link amino acids to their corresponding tRNA molecules. The resulting complex is charged and is referred to as an aminoacyl-tRNA.

INITIATION :



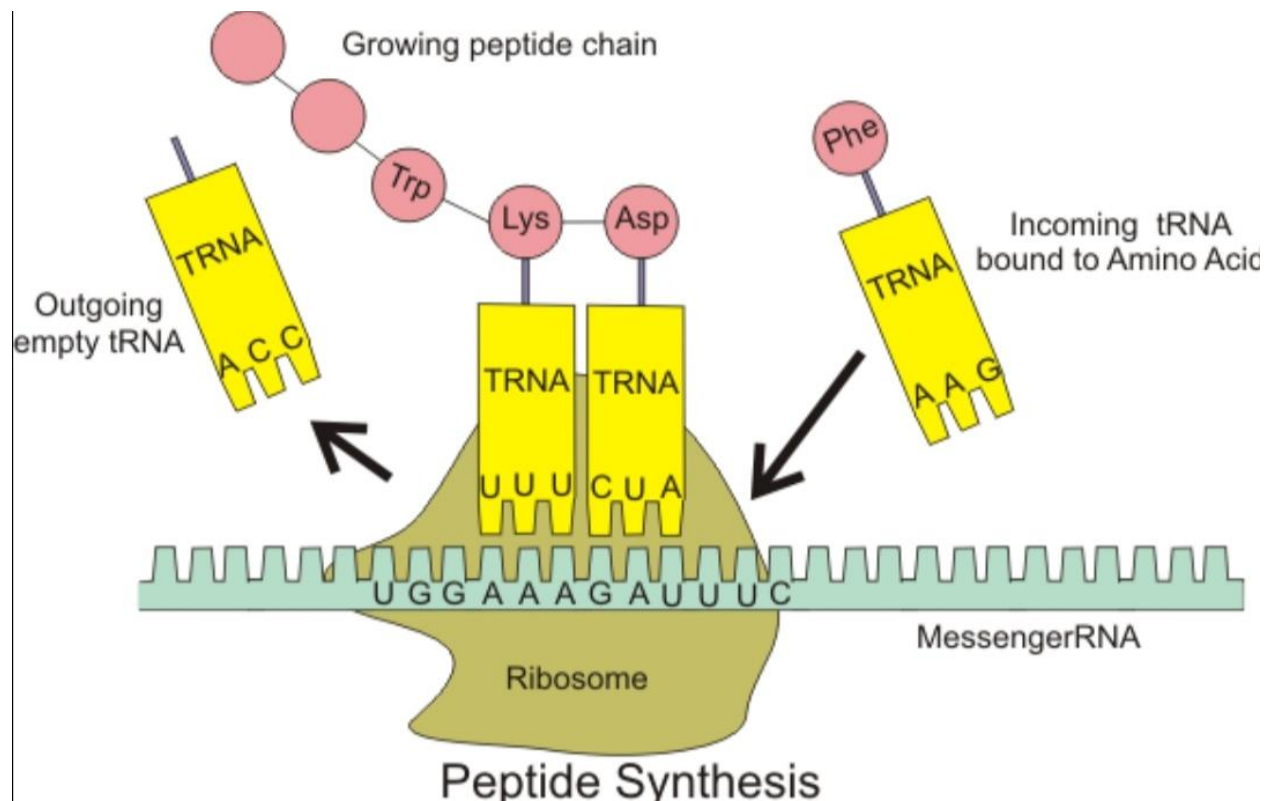
At the 5' cap of mRNA the small 40s subunit of the ribosome (with methionyl-tRNA) binds. For translation to start the start codon 5'AUG must be recognized. This is a codon specific to the amino acid methionine (anticodon on tRNA=5'CAU). The large 60s subunit of the ribosome then binds for elongation to occur.

The ribosome has two tRNA binding sites; the P site which holds the peptide chain and the A site which accepts the tRNA.

ELONGATION :

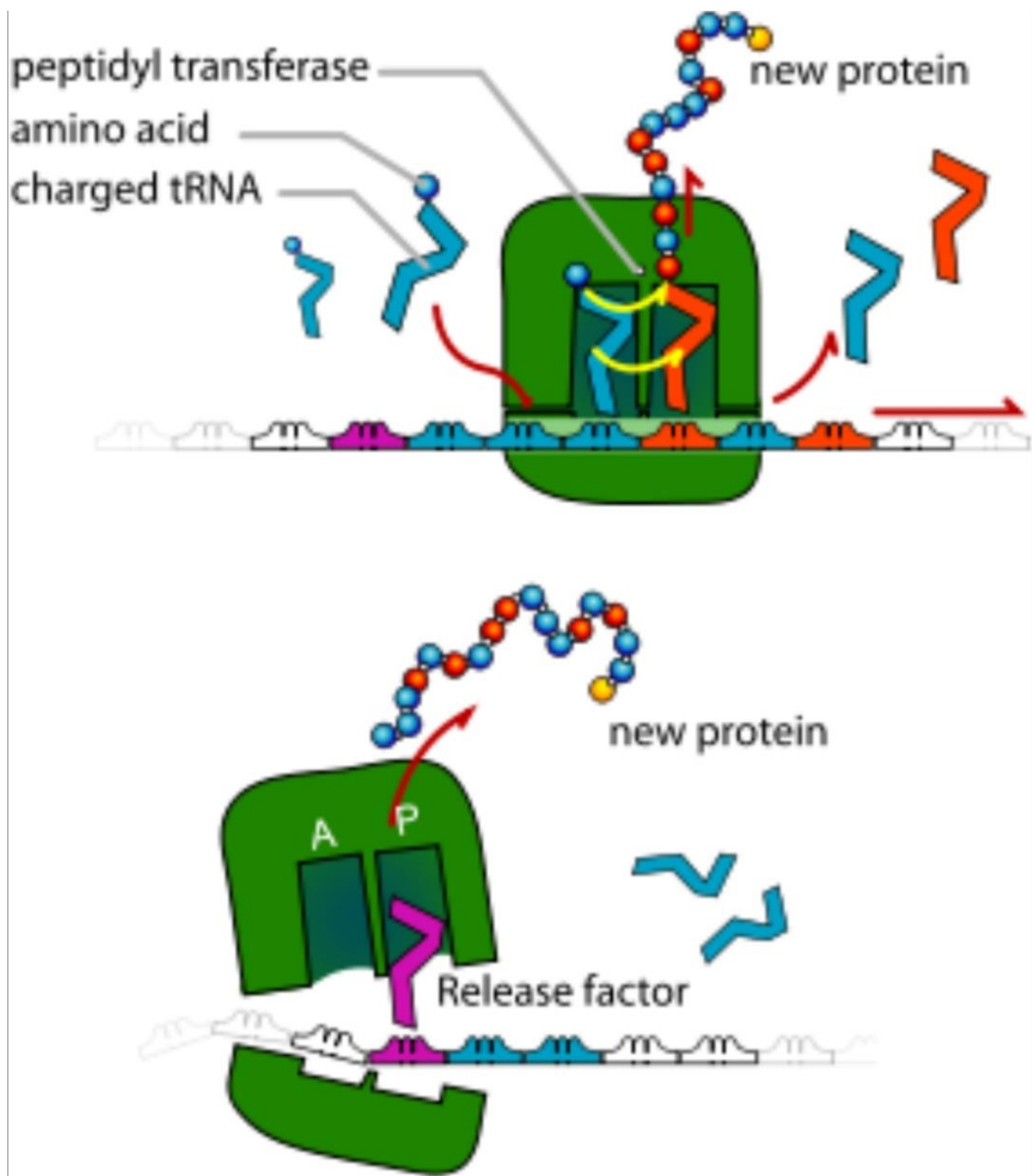
While Met-tRNA occupies the P site, another aminoacyl-tRNA with an anticodon complementary to the next codon comes to occupy the A site. This process requires GTP. The enzyme peptidyl-transferase forms a peptide bond between methionine and the next aminoacyl-tRNA.

The tRNA molecule in the P site becomes uncharged and leaves the ribosome. The ribosome then translocates along the mRNA molecule to the next codon. This opens up the A site for the next aminoacyl-tRNA. The polypeptide chain is built up in the direction from the N terminal to the C terminal.



TERMINATION :

One of the three stop codons enters the A site. No tRNA molecules bind to these codons so the peptide and tRNA in the P site become hydrolysed releasing the polypeptide into the cytoplasm



The small and large subunits of the ribosome **dissociate** ready for the next round of translation. Polypeptide enters the post translational modification.

POST TRANSLATIONAL MODIFICATIONS :

Post-translational modification (PTM) of proteins refers to the chemical changes that occur after a protein has been produced. It can impact the structure, electrophilicity and interactions of proteins.

TYPES OF POST TRANSLATIONAL MODIFICATIONS :

There are many types of protein modification, which are mostly catalyzed by enzymes that recognize specific target sequences in proteins. These modifications regulate protein folding by targeting specific subcellular compartments, interacting with ligands or other proteins, or by bringing about a change in their functional state including catalytic activity or signaling. The most common PTMs are:

Based on addition of chemical groups:

- Phosphorylation
- Acetylation
- Hydroxylation
- Methylation

Based on addition of complex groups:

- Glycosylation
- AMPylation
- Lipidation

Based on addition of polypeptides:

- Ubiquitination

Based on cleavage of proteins:

- Proteolysis

CHEMICAL GROUPS :

Phosphorylation:

Reversible phosphorylation of proteins involves addition of a phosphate group on serine, threonine, or tyrosine residues and is one of the important and extensively studied PTM in both prokaryotes and eukaryotes.

Several enzymes or signaling proteins are switched 'on' or 'off' by phosphorylation or dephosphorylation. Phosphorylation is performed by enzymes called 'kinases', while dephosphorylation is performed by 'phosphatases'.

Addition of a phosphate group can convert a previously uncharged pocket of protein into a negatively charged and hydrophilic protein thereby inducing conformational changes in the protein. Phosphorylation has implications in several cellular processes, including cell cycle, growth, apoptosis and signal transduction pathways

Acetylation:

Acetylation refers to addition of acetyl group in a protein. It is involved in several biological functions, including protein stability, location, synthesis; apoptosis; cancer; DNA stability. Acetylation and deacetylation of histone form a critical part of gene regulation.

Acetylation of histones reduces the positive charge on histone, reducing its interaction with the negatively charged phosphate groups of DNA, making it less tightly wound to DNA and accessible to gene transcription

Hydroxylation :

This process adds a hydroxyl group (-OH) to the proteins. It is catalyzed by enzymes termed as 'hydroxylases' and aids in converting hydrophobic or lipophilic compounds into hydrophilic compounds

Methylation :

Methylation refers to addition of a methyl group to lysine or arginine residue of a protein. Methylation is achieved by enzymes called methyltransferases. Methylation has been widely studied in histones wherein histone methylation can lead to gene activation or repression based on the residue that is **methyalted**.

COMPLEX GROUP:

Glycosylation:

Glycosylation involves addition of an oligosaccharide termed 'glycan' to either a nitrogen atom (N-linked glycosylation) or an oxygen atom (O-linked glycosylation). N-linked glycosylation occurs in the amide nitrogen of asparagine, while the O-linked glycosylation occurs on the oxygen atom of serine or threonine.

Carbohydrates present in the form of N-linked or O-linked oligosaccharides are present on the surface of cells and secrete proteins. They have critical roles in protein sorting, immune recognition, receptor binding, inflammation, and pathogenicity.

AMPylation:

AMPylation refers to reversible addition of AMP to a protein. It involves formation of a phosphodiester bond between the hydroxyl group of the protein and the phosphate group of AMP.

Lipidation:

The covalent binding of a lipid group to a protein is called lipidation. Lipidation can be further subdivided into prenylation, N-myristoylation, palmitoylation, and glycosylphosphatidylinositol (GPI)-anchor addition.

It is critical in controlling the localization and activity of several proteins that have crucial functions in biological regulation and has functions in membrane association and apoptosis

POLYPEPTIDES:

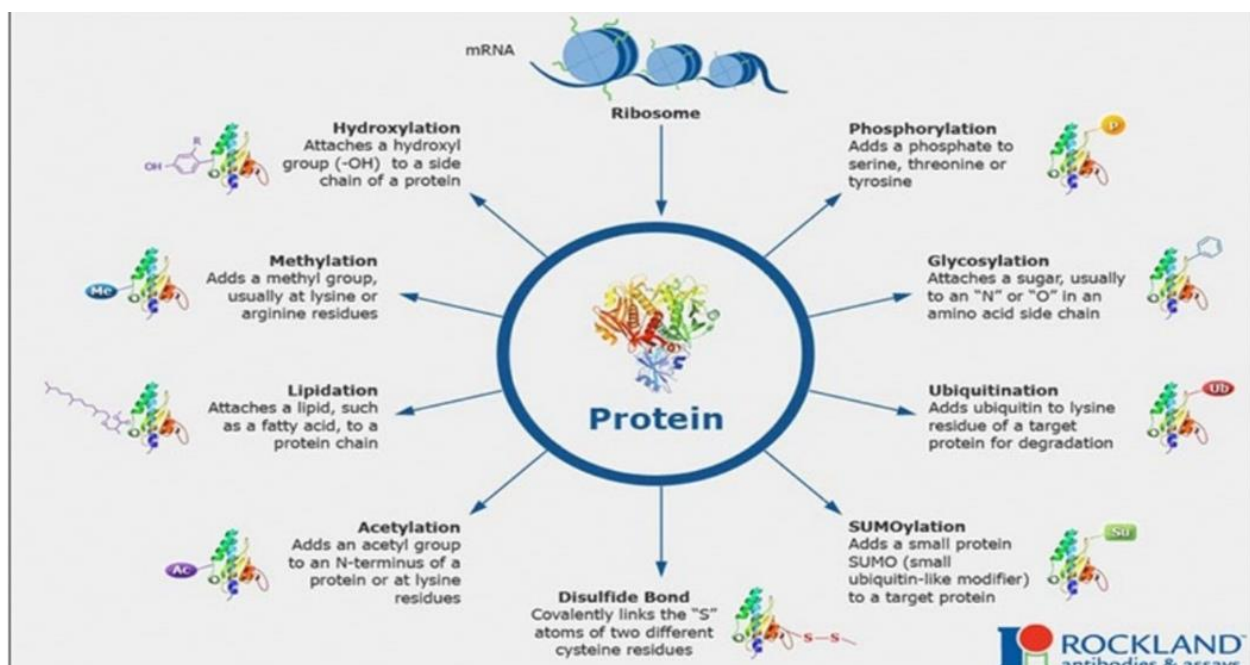
Ubiquitination :

Ubiquitination involves addition of a protein found ubiquitously, termed 'ubiquitin', to the lysine residue of a substrate. Either a single ubiquitin molecule (monoubiquitination) or a chain of several ubiquitin molecules may be attached (polyubiquitination).

PROTEIN CLEAVAGE :

Proteolysis:

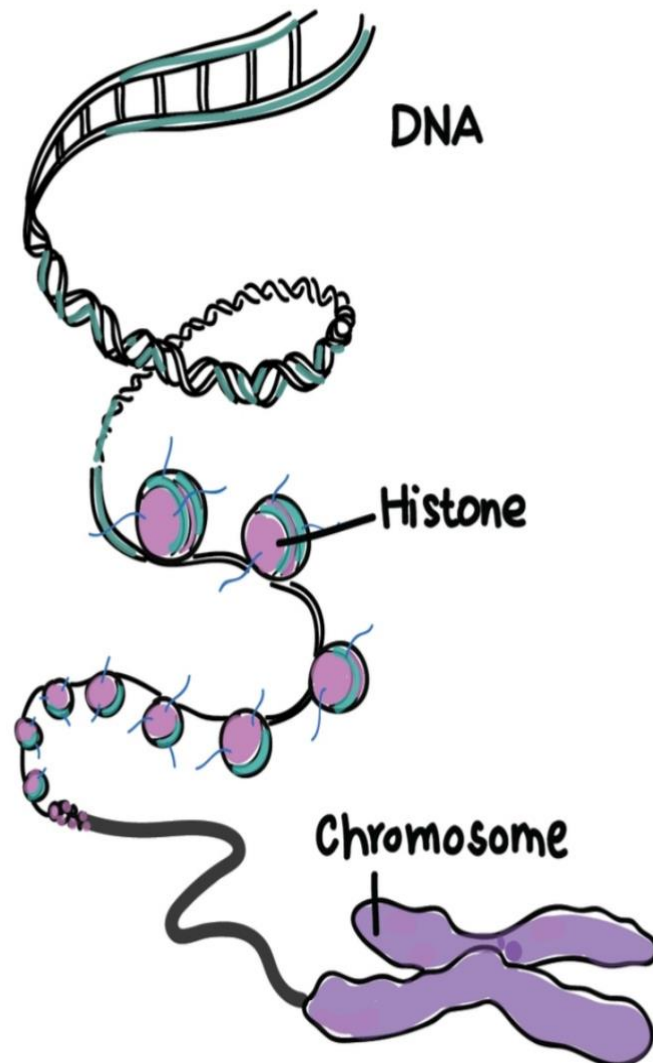
Proteolysis refers to breakdown of proteins into smaller polypeptides or amino acids. For example, removal of N-terminal methionine, a signal peptide, after translation leads to conversion of an inactive or non-functional protein to an active one.

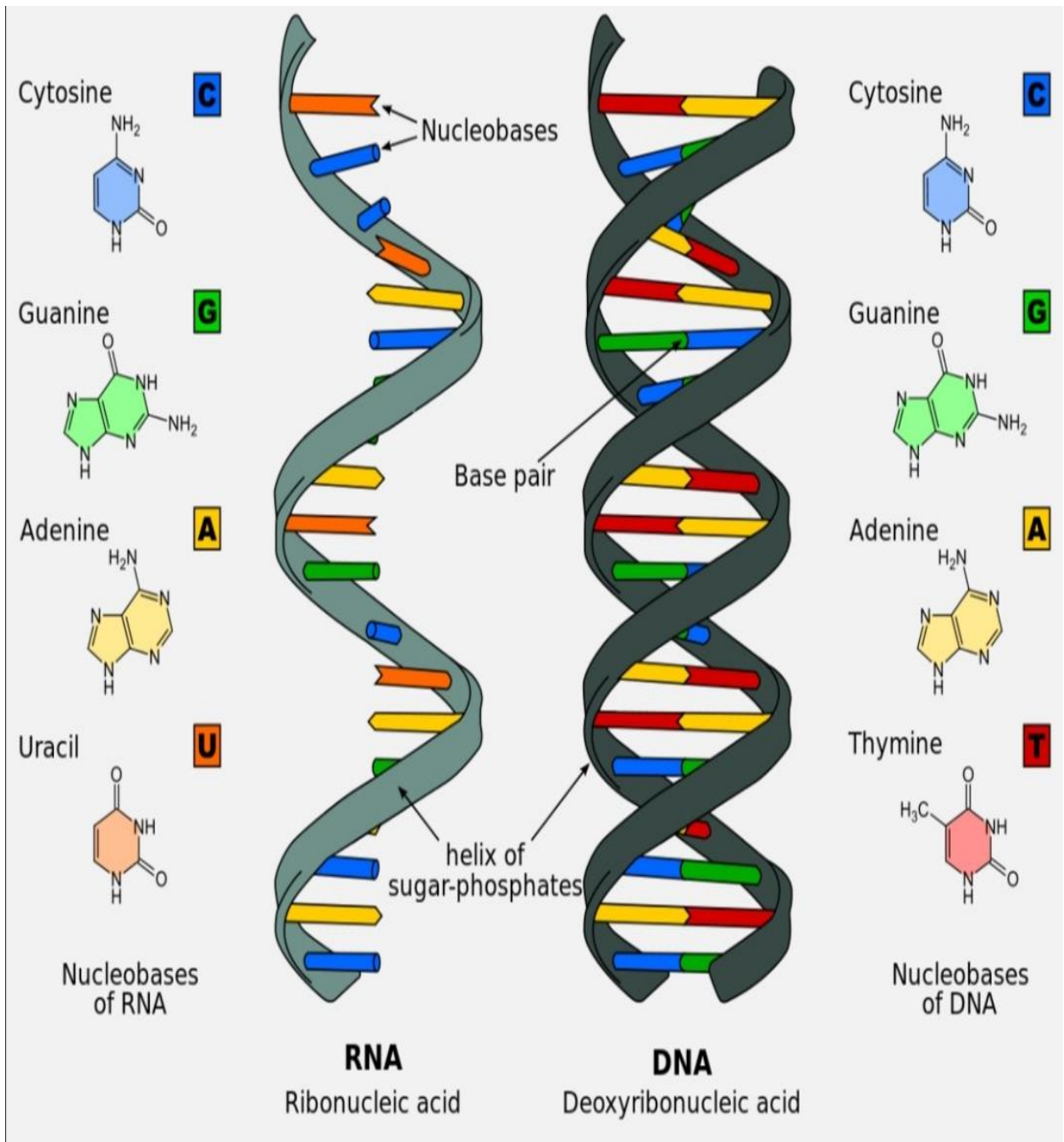


DNA RESPONSIBLE FOR INHERITANCE :

DNA (deoxyribonucleic acid) is a molecule vital to the survival of all organisms. It holds the instructions that are needed for normal cell function, growth, and reproduction. Our DNA dictates how we develop and function throughout our lives.

The structure of DNA was established by Watson and Crick in 1953. The basic structure is called a double helix. It consists of two strands, and each strand is made up of nucleotide . Each nucleotide is made of a nitrogenous base, a phosphate group, and a five-carbon sugar. Specific sequences of nucleotides make up genes, which contain instructions for cells. The amount of A bases in DNA equals the amount of T bases, and the amount of G bases equals the amount of C bases.



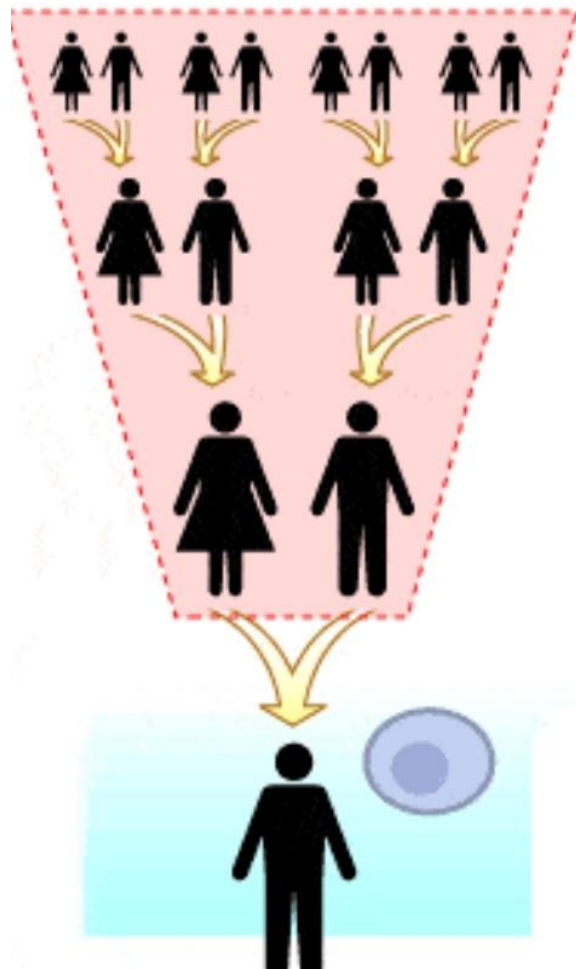


DNA contains a ton of information and is actually very long. If you took all the DNA out of one of your cells and stretched it out, it would be about six feet long. This is why DNA condenses into chromosomes to fit inside the cell.

DNA is the genetic information used to make proteins, and it contains the hereditary traits of organisms. There are two types of DNA: mitochondrial DNA, which you can only get from your mother, and nuclear DNA, which is a combination of both your ancestors' DNA.

You are who you are because of your DNA; the smallest change to it would make you a completely different person. DNA is what makes your dog a dog and not a wolf.

Nuclear DNA is inherited from all ancestors.



Mitochondrial DNA is inherited from a single lineage

