STEPS IN PROTEIN TRANSLATION

The process of translation is divided into three separate steps:

initiation, elongation, and termination.

The polypeptide chains produced may be modified by posttranslational modification.

-Initiation

In eukaryotes, the initiating AUG is recognized by a special initiator tRNA. Recognition is facilitated by eukaryotic initiating factors (eIFs).

The amino acid–charged initiator tRNA enters the ribosomal P site, and GTP is hydrolyzed to GDP.

Elongation

Elongation of the polypeptide chain involves the addition of amino acids to the growing chain. During elongation, the ribosome moves from the 5′ end to the 3′ end of the mRNA that is being translated.

After the peptide bond has been formed, the ribosome advances three nucleotides toward the 3′ end of the mRNA.

This process is known as translocation and requires the participation of eukaryotic elongation factor (eEF-2) and GTP hydrolysis. This causes movement of the uncharged tRNA into the ribosomal E site (before being released) and movement of the peptidyl-tRNA into the P site

Termination

Termination occurs when one of the three termination codons moves

into the A site. Eukaryotes release factor (eRF) recognizes all three termination codons.

Polysomes

Because of the length of most mRNAs, more than one ribosome at a time can generally translate a message. Such a complex of one mRNA and a number of ribosomes is called a polysome or polyribosome.

Mutations

Transversions are interchanges of purine for pyrim A mutation is the permanent alteration of the nucleotide sequence of the genome of an organism. When this alteration involve one nucleotide, it is called point mutation: A point mutation that changes a purine nucleotide to another purine (A ↔ G) or a pyrimidine nucleotide to another pyrimidine (C ↔ T) is called transition.

idine bases, which therefore involve exchange of one-ring and two-ring structures.

1. **Silent mutation**: The codon containing the changed bases may code for the same amino acid. For example, if the serine codon UCA is given a different third base "U" to become UCU, it still codes for serine. This is termed a "silent" mutation.

2 **. Missense mutation**: The codon containing the changed bases may code for a different amino acid. For example, if the serine codon UCA is given a different first base “C” to become CCA, it will code for a different amino acid, in this case, proline.

3- **Nonsense mutation**: The codon containing the changed bases may become a termination codon. For example, if the serine codon UCA is given a different second base “A” to become UAA, the new codon causes termination of translation at that point and the production of a shortened (truncated) protein.