

1 Translation

Codons are read as mRNA triplets, encoding all 20 amino acids, so there is a redundancy with multiple codons for most amino acids.

Reading frames define the amino acid sequence, which are in turn determined by the position of the starting codon AUG.

1.1 TmRNA and protein sequence

The 3' end has an acceptor arm, where it will stick to the acid. Anticodons will base-pair complementary and antiparallel to the codon.

There are modifications to traditional bases, such as D = dihydroeurydine.

1.2 Codon Redundancy

Some strategies of managing the redundancy for translation include the correspondence of more than 1 tRNA to many amino acids, with some tRNAs recognizing and base pairing with more than 1 codon. There are two sequential steps in ensuring fidelity: utilising aminoacyl-tRNA synthetases and base pairing. Hydrolytic editing, in turn, is conducted by aminoacyl-tRNA-synthetase.

Amino acid addition proceeds by condensation reactions.

1.3 Prokaryotic vs Eukaryotic Ribosomes

Both prokaryotic and eukaryotic ribosomes have large and small subunits.

Eukaryotic ribosomes are typically larger and more complex.

In eukaryotes, ribosomes are located on endoplasmic reticulum (which secretes proteins in some organelles) and in cytosol. In prokaryotes, ribosomes are only in cytosol.