

TRANSLATION

Content Statements:

- D1.2.5 Translation as the synthesis of polypeptides from mRNA
- D1.2.6 Roles of mRNA, ribosomes and tRNA in translation
- D1.2.7 Complementary base pairing between tRNA and mRNA
- D1.2.8 Features of the genetic code
- D1.2.9 Using the genetic code expressed as a table of mRNA codons
- D1.2.10 Stepwise movement of the ribosome along mRNA and linkage of amino acids by peptide bonds to the growing polypeptide chain
- D1.2.11 Mutations that change protein structure

TRANSLATION

Translation is the process of **protein synthesis**, in which genetic information encoded in mRNA is translated into a sequence of amino acids (polypeptide).

- **Messenger RNA (mRNA)** is transported to the ribosomes (in the cytosol)
- **Ribosomes** read the mRNA sequence in triplets of bases called codons
- **Codons** code for specific amino acids according to a genetic code
- **Amino acids** are brought to the ribosome by transfer RNA (tRNA)
- **Transfer RNA** binds to specific codons via complementary anticodons
- **Anticodons** cause tRNA molecules to line up according to codon order
- **Peptide bonds** form between amino acids (catalysed by the ribosome)
- **Polypeptides** are produced as the ribosome moves along the mRNA



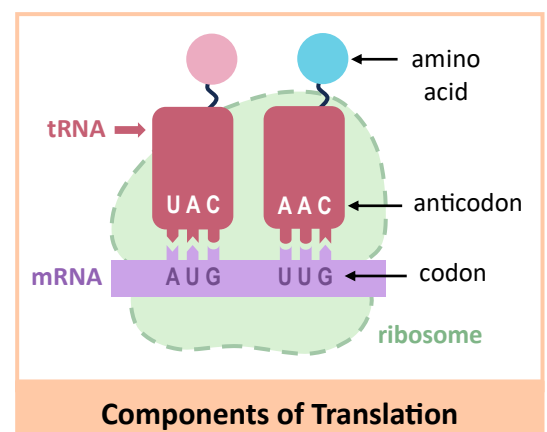
Hint: MR CAT APP

RIBOSOMES

The ribosome is made up of two distinct subunits – each composed of protein and ribosomal RNA (rRNA):

- The **small subunit** binds to the messenger RNA (mRNA), which is read in triplets of bases called codons
- The **large subunit** contains binding sites for two tRNA molecules, which each carry a specific amino acid

The role of the ribosome is to transfer the amino acid from one tRNA molecule to the next, sequentially growing a polypeptide chain as it moves along the mRNA. Once a given tRNA molecule has transferred its amino acid to a chain, it is released in order to collect another amino acid for future use. Ribosomes initiate translation when they reach a **start codon** (AUG) and terminate translation when they reach a **stop codon**. The start codon acts to establish the appropriate **reading frame** in which the triplets of mRNA bases are read (translated) by the particular ribosome. Multiple ribosomes can translate an mRNA sequence at once.

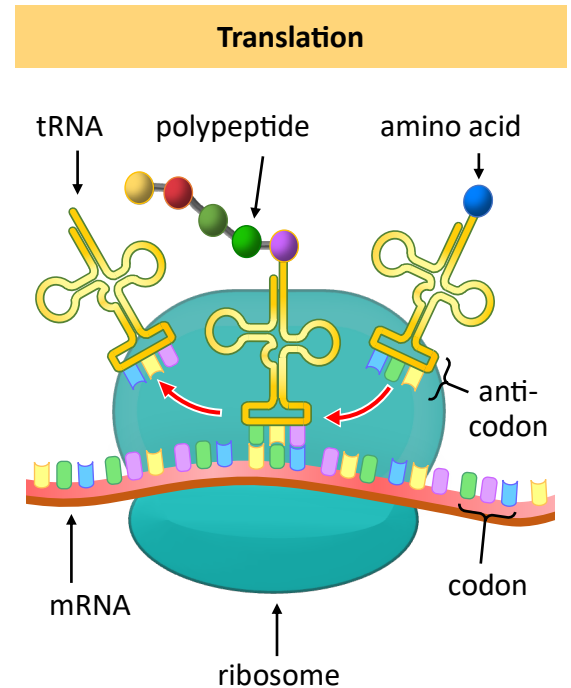


GENETIC CODE

The genetic code is the set of rules that identifies which amino acid corresponds to each mRNA codon. It is typically represented as a table. The genetic code possesses two key characteristics:

- **Universality:** Almost every living organism uses the same code (there are a few viral exceptions)
- **Degeneracy:** Some codons code for the same amino acid (there are 64 codons and only 20 amino acids)

The Genetic Code							
UUU	Phe	UCU	Ser	UAU	Tyr	UGU	Cys
UUC		UCC		UAC		UGC	
UUA	Leu	UCA	STOP	UAA	STOP	UGA	STOP
UUG		UCG		UAG		UGG	Trp
CUU	Leu	CCU	Pro	CAU	His	CGU	Arg
CUC		CCC		CAC		CGC	
CUA		CCA		CAA	Gln	CGA	
CUG		CCG		CAG		CGG	
AUU	Ile	ACU	Thr	AAU	Asn	AGU	Ser
AUC		ACC		AAC		AGC	
AUA		ACA		AAA	Lys	AGA	Arg
AUG	Met	ACG		AAG		AGG	
GUU	Val	GCU	Ala	GAU	Asp	GGU	Gly
GUC		GCC		GAC		GGC	
GUA		GCA		GAA	Glu	GGA	
GUG		GCG		GAG		GGG	



The codons are recognised by anticodons on specific tRNA molecules. The codons and the anticodons are complementary in base sequence, ensuring correct pairing. Guanine and cytosine undergo complementary pairing, while adenine partners with uracil. For instance, a codon with a sequence of AUG will correspond to anticodons with a sequence of UAC. Complementary pairing ensures sequences are correctly translated.

GENETIC DISEASES

As proteins are encoded by DNA sequences (genes), a change in nucleotide sequence can alter the protein structure. If a change in protein sequence leads to the abrogation of its function, a disease condition may arise. An example of a genetic disease caused by a mutation that changes protein structure is **sickle cell anaemia**. Sickle cell anaemia results from a mutation to the gene coding for haemoglobin. The mRNA sequence is changed from GAG → GUG, which in turn changes the amino acid sequence from glutamic acid to valine (Glu → Val). The haemoglobin now forms **insoluble fibrous strands** that cannot carry oxygen as effectively (resulting in anaemia). The fibrous strands also change the shape of the red blood cell to a **sickle shape**, which are destroyed more rapidly than normal cells, leading to a much lower red blood cell count.

