Chapter 3: DNA

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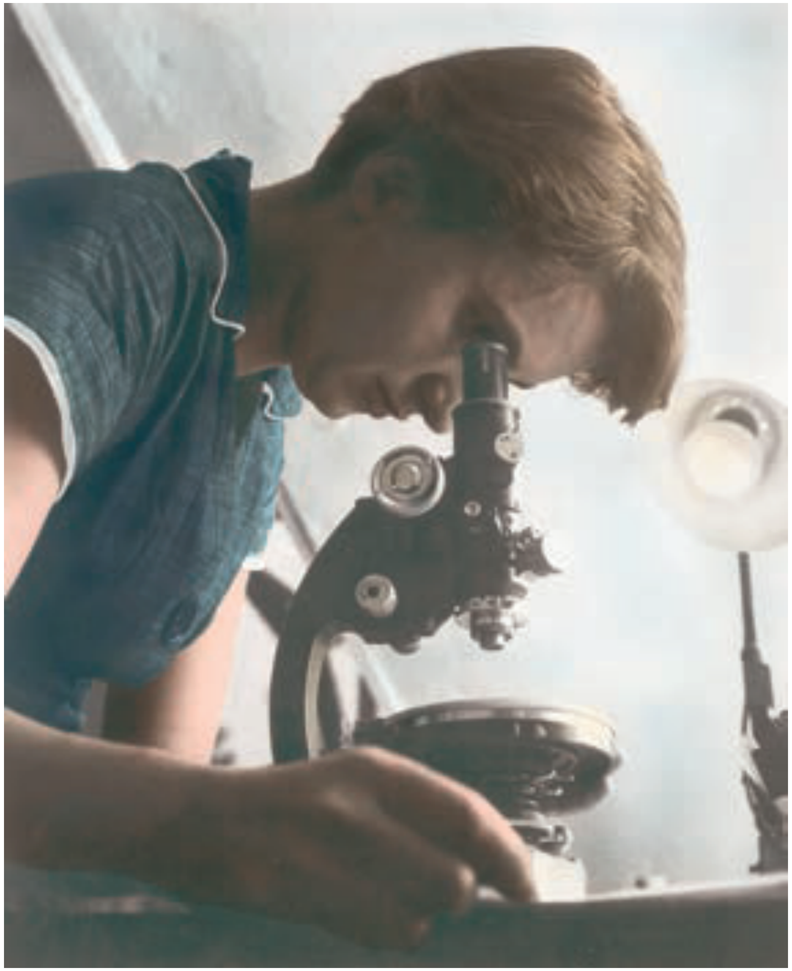
The discovery of DNA



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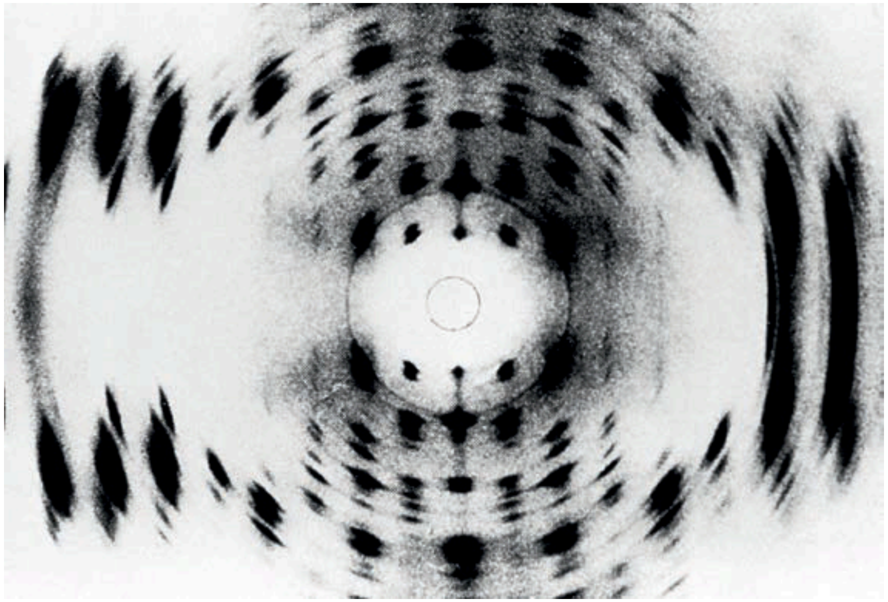
Rosalind Franklin took the first clear X-ray diffraction image of **DNA (deoxyribonucleic acid)** in 1952. Franklin's photograph helped confirm the spiral nature of DNA.



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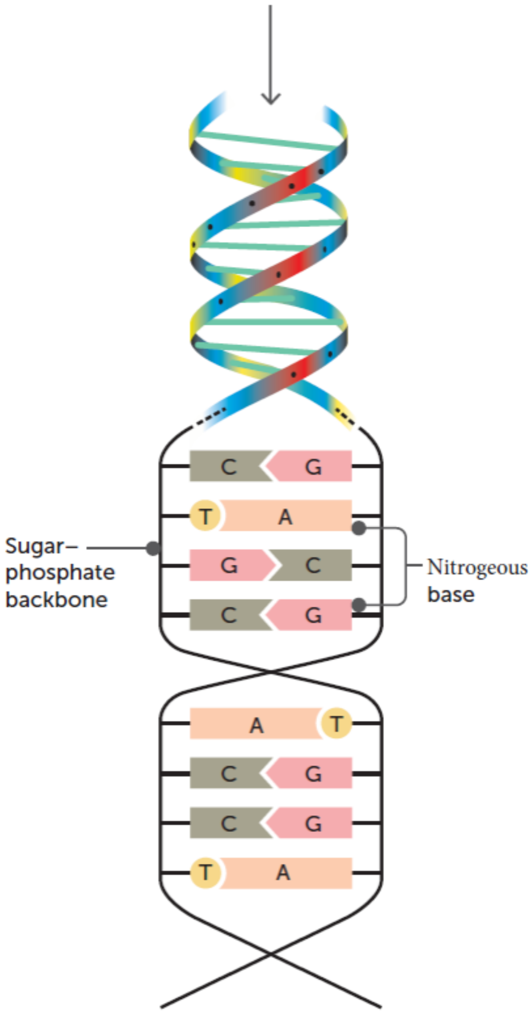
Complementary base pairs

Erwin Chargaff used a technique called chromatography to work out the ratios of the four types of **nitrogenous bases** in the nucleotide subunits: adenine (A), cytosine (C), guanine (G) and thymine (T).

He concluded that the amount of guanine was equal to the amount of cytosine, and the amount of adenine was equal to the amount of thymine.

Complementary pairing is the phenomenon whereby guanine always hydrogen bonds with cytosine, and adenine always hydrogen bonds with thymine. Guanine and cytosine share three hydrogen bonds, and adenine and thymine share two hydrogen bonds.



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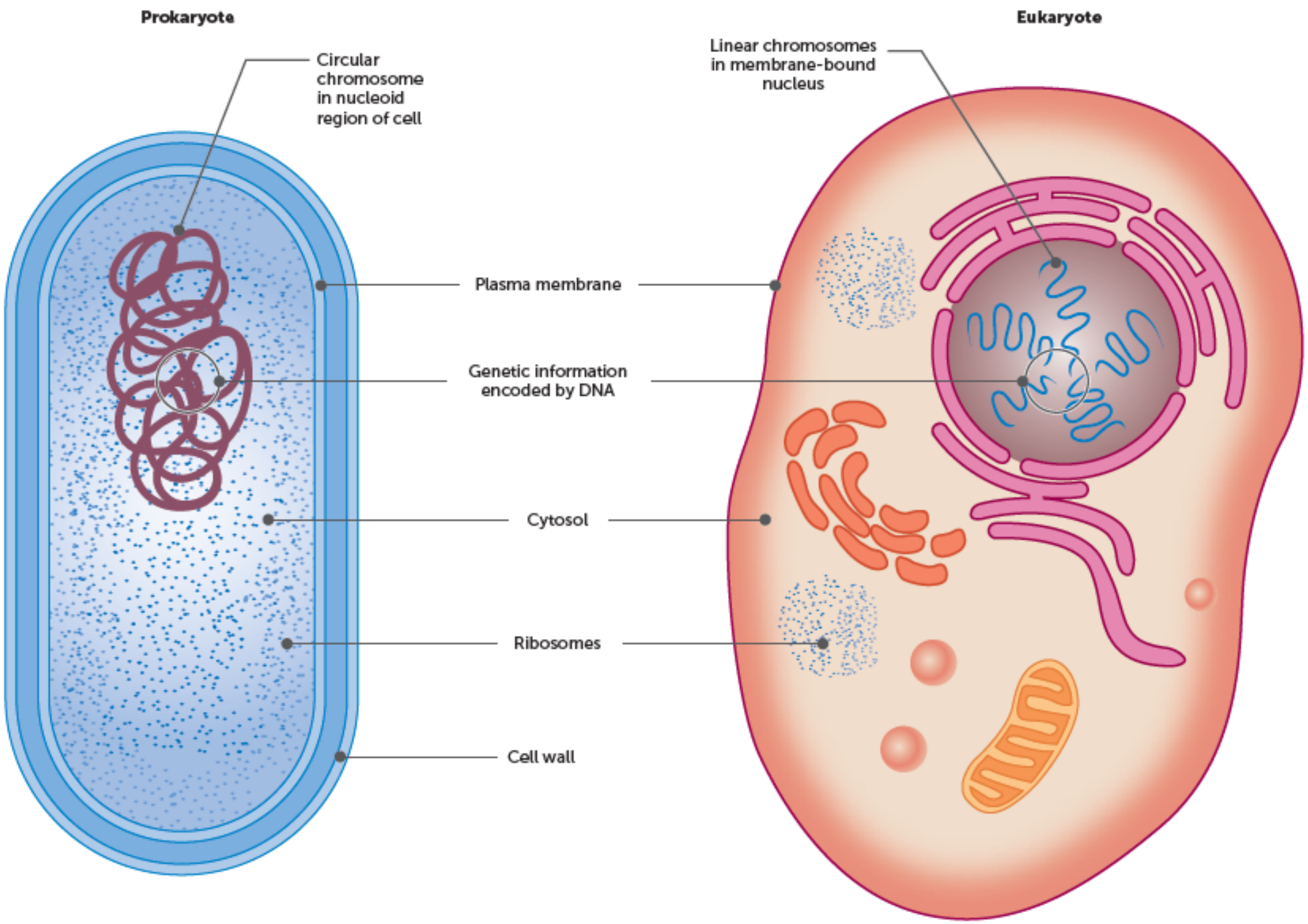
The discovery of DNA

Where is DNA found in prokaryotes and eukaryotes?

There are structural differences between prokaryotic cells and eukaryotic cells.



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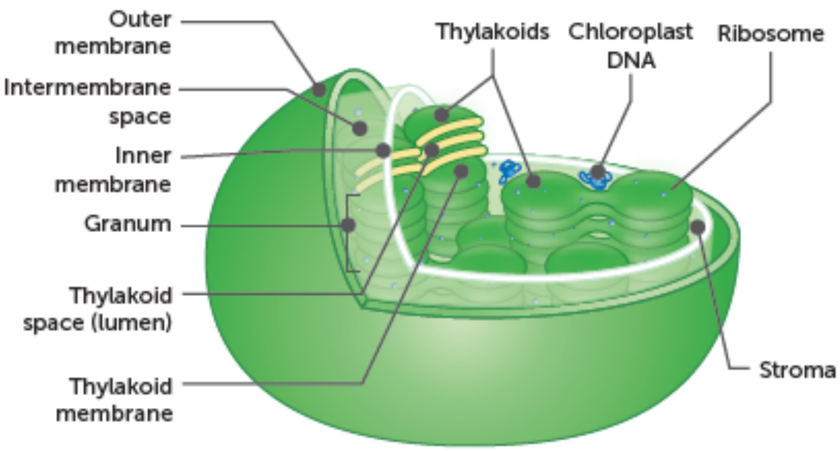
The discovery of DNA

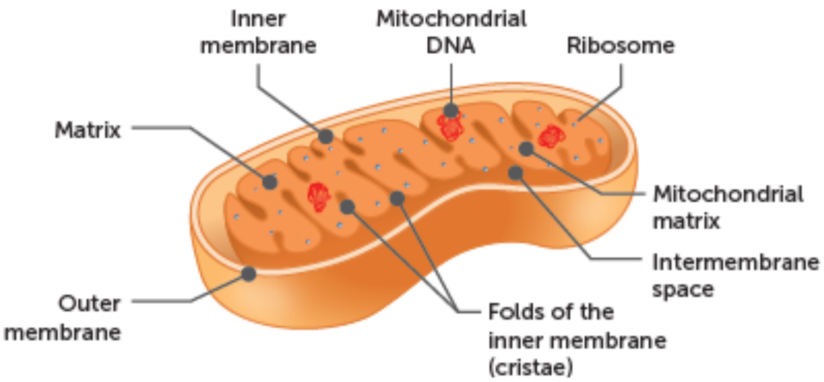
Eukaryotic cells: DNA occurs bound to proteins in chromosomes in the nucleus, which is enclosed in a nuclear membrane. DNA is also found in the mitochondria and chloroplasts of eukaryotic cells.

Prokaryotic cells: DNA occurs as unbound circular DNA in the nucleoid region of the cytosol. The nucleoid region is not bound by a nuclear membrane.

DNA is found in chloroplasts in eukaryotic plant and protista cells:



DNA is found in mitochondria in all eukaryotic cells:



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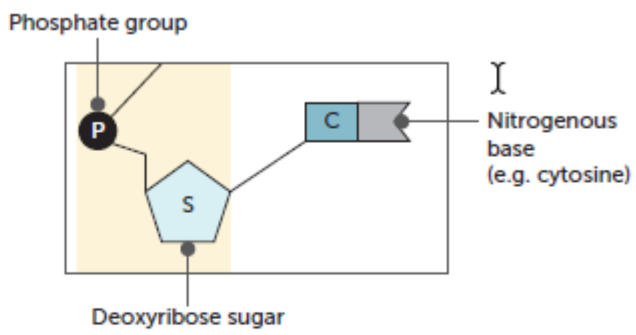
DNA structure – nucleotides

Nucleotides

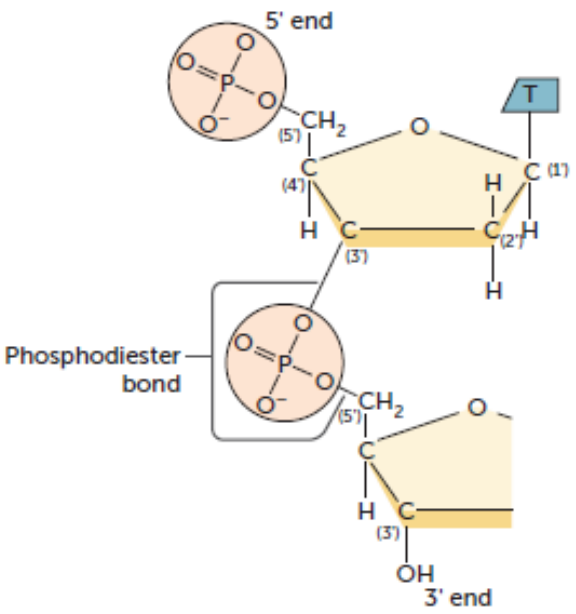
DNA is a nucleic acid made up of **nucleotides**. Each nucleotide consists of three parts: a five-carbon (pentose) sugar known as deoxyribose sugar, a phosphate group and a nitrogenous base (adenine, cytosine, guanine or thymine).

A nucleotide is the basic structural unit of DNA.



DNA structure – nucleotides

Nucleotides



Each phosphate group is attached to two sugar molecules by 'ester' bonds and is then called a phosphodiester bond.

The five molecule carbon atoms in each sugar molecule, which form a ring, are numbered 1' to 5'. One of the ester bonds is formed with the 3' carbon of one sugar ring and the other is formed with the 5' carbon of the next sugar ring.

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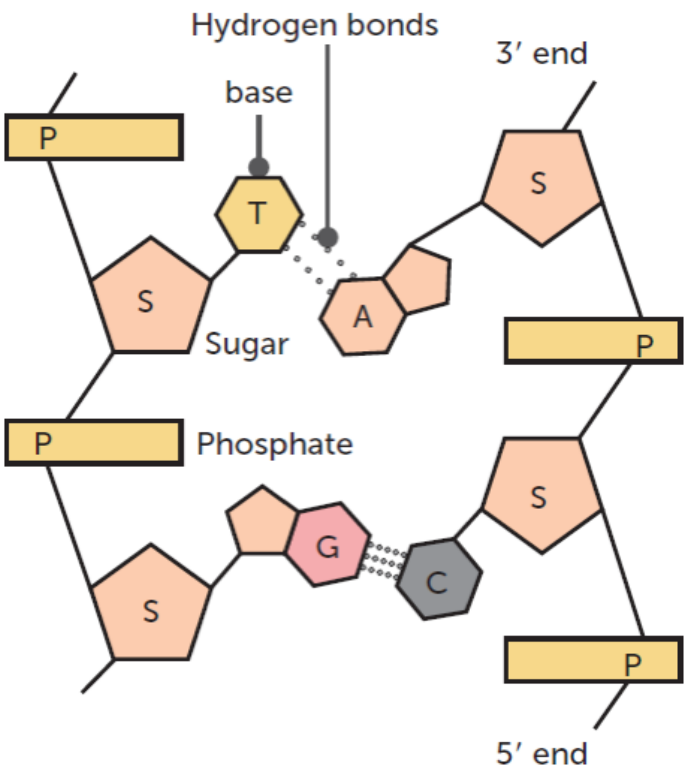
DNA structure – DNA molecule

DNA molecule

The shape of a DNA molecule is a double helix. The term ‘double’ means the molecule consists of two strands.

The strands are joined by weak hydrogen bonds between complementary pairs of nitrogenous bases.



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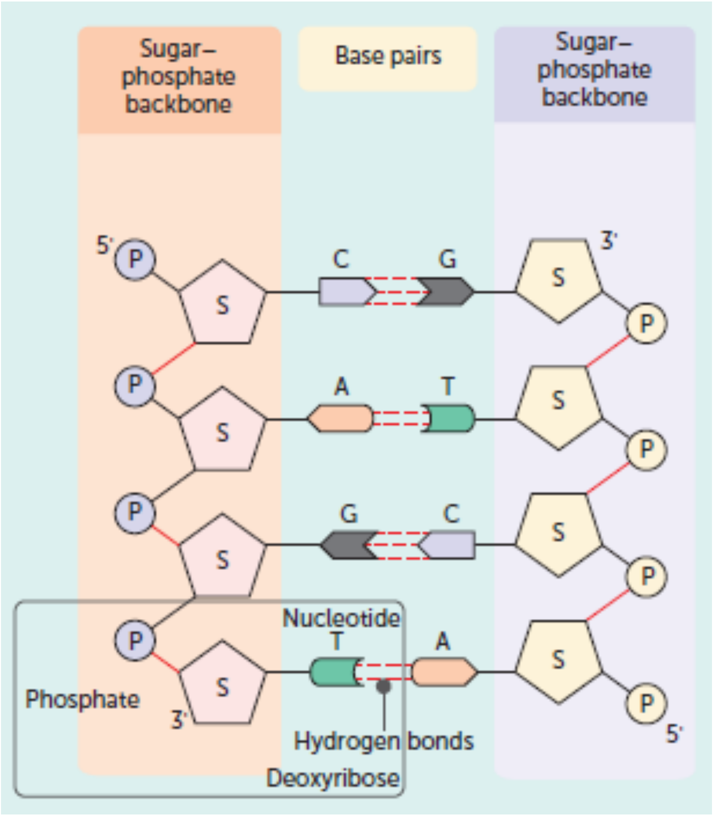
DNA structure – DNA molecule



The DNA structure includes a chain of alternating sugar molecules and phosphate groups: the sugar–phosphate backbone.

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DNA structure

DNA structure enables its function

Heritable

Genetic material can be passed to offspring

Used to compare

DNA very similar in different organisms and less similar in different species

Stores a code

The sequence of nucleotides contains a code in segments called genes

Replication

Complementary bases enable DNA molecule to be replicated

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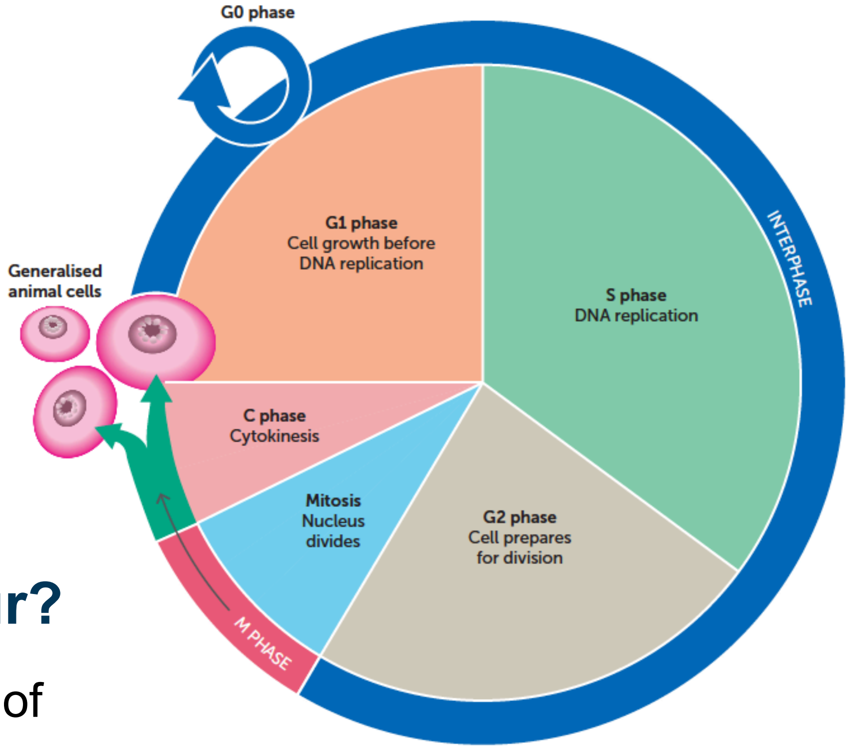
DNA replication

The purpose of DNA replication

The purpose of **DNA replication** is to duplicate the code it carries. The code can then be passed to daughter cells.

In eukaryotic cells, the chromosomes gain a sister chromatid and become double stranded.

DNA replication occurs in the preparation for all cell division, whether mitosis or meiosis



When does DNA replication occur?

DNA replication occurs during the S phase of interphase of the cell cycle.

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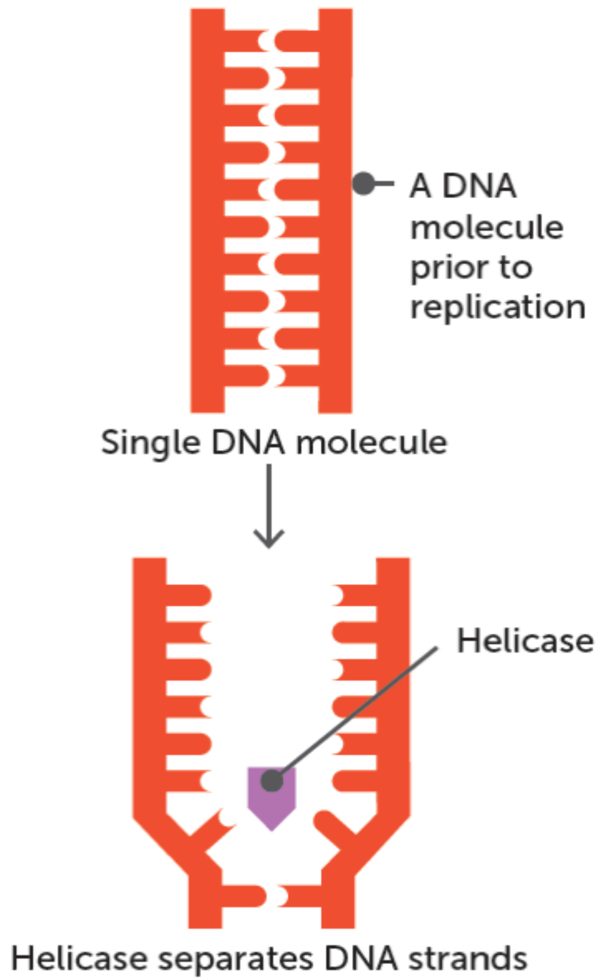
The process of DNA replication

Step 1
DNA helicase (enzyme) unwinds and separates the double strand by breaking the weak hydrogen bonds. Each half of the parent molecule is used as a template.



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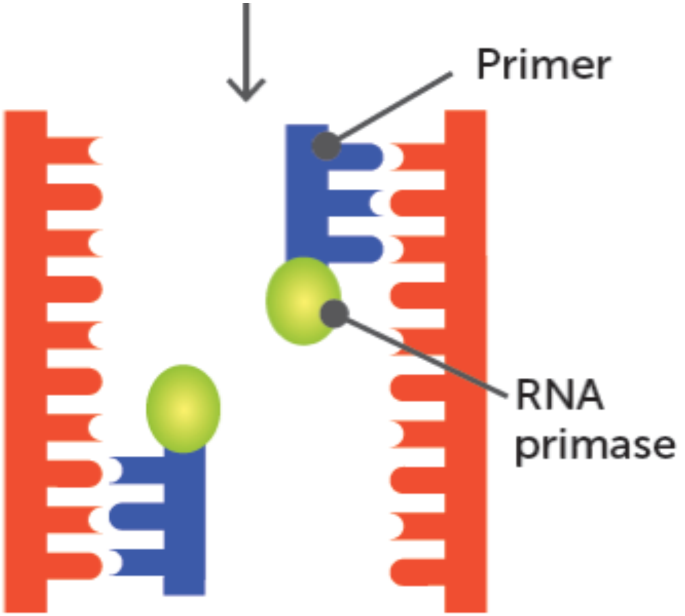
DNA replication – process

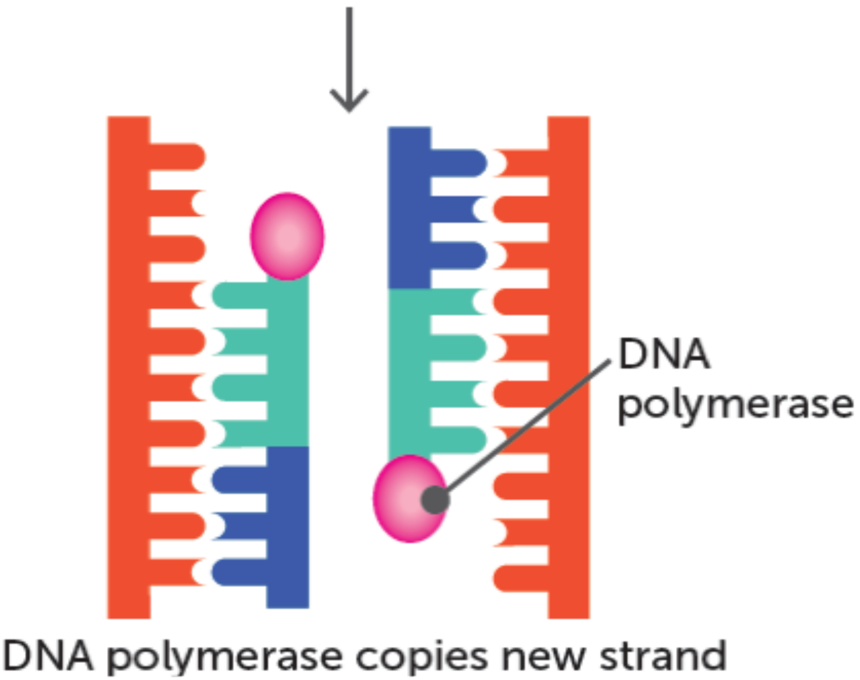
Step 2
The enzyme primase attaches a short sequence of RNA, known as a primer, to show DNA polymerase where to start adding nucleotides.



RNA primase adds RNA primers

DNA replication – process

Step 3
Complementary nucleotides are added by the enzyme DNA polymerase. Synthesis of the new daughter strand is in a 5’ to 3’ direction. Adenine pairs with thymine, and cytosine pairs with guanine.



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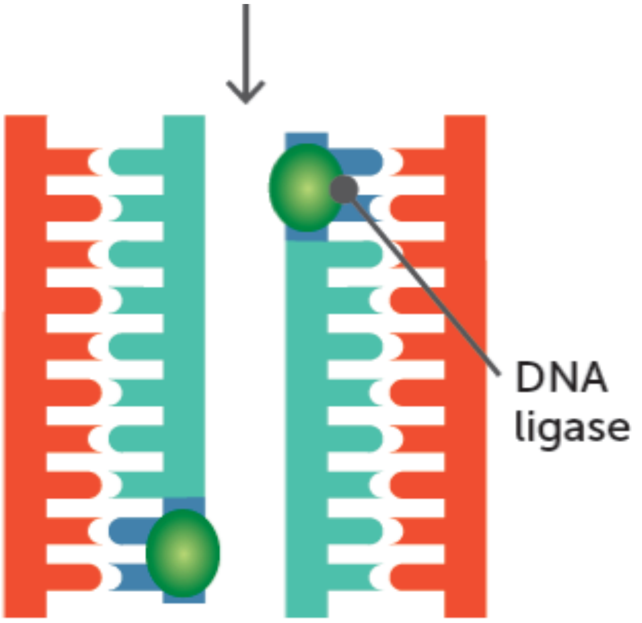
DNA replication – process

Step 4

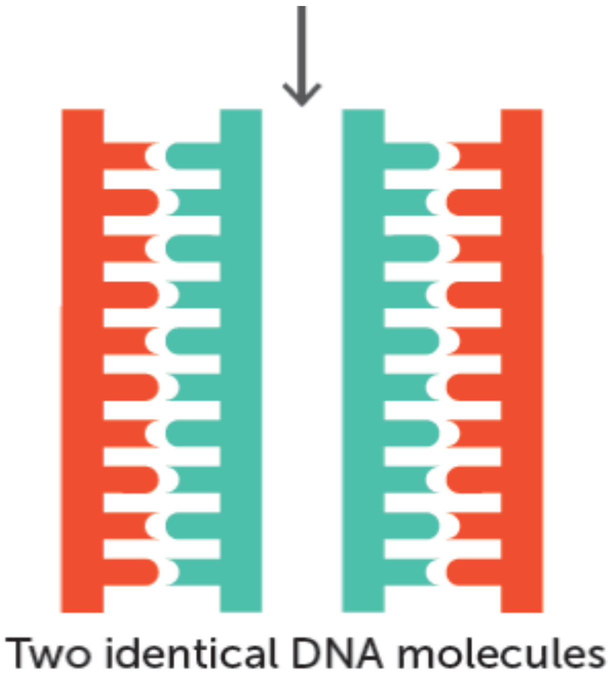
The result is the production of two identical DNA molecules that are each made of one parent strand and one new daughter strand. Therefore, the process is described as **semi-conservative**.



Enzymes remove and replace primers

DNA replication – process

Step 5
In eukaryotic organisms, two sister chromatids are now ready for cell division. In prokaryotes, two circular chromosomes are now ready for binary fission.



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DNA replication – process

Synthesis along continuous and discontinuous strands

Synthesis is continuous along the **leading strand**.

Synthesis is discontinuous along the **lagging strand**.

Primers are attached at short intervals, starting from the replication fork.

DNA polymerase synthesises short strands of new DNA called Okazaki fragments.

DNA polymerase moves in opposite directions on the two anti-parallel parent strands.

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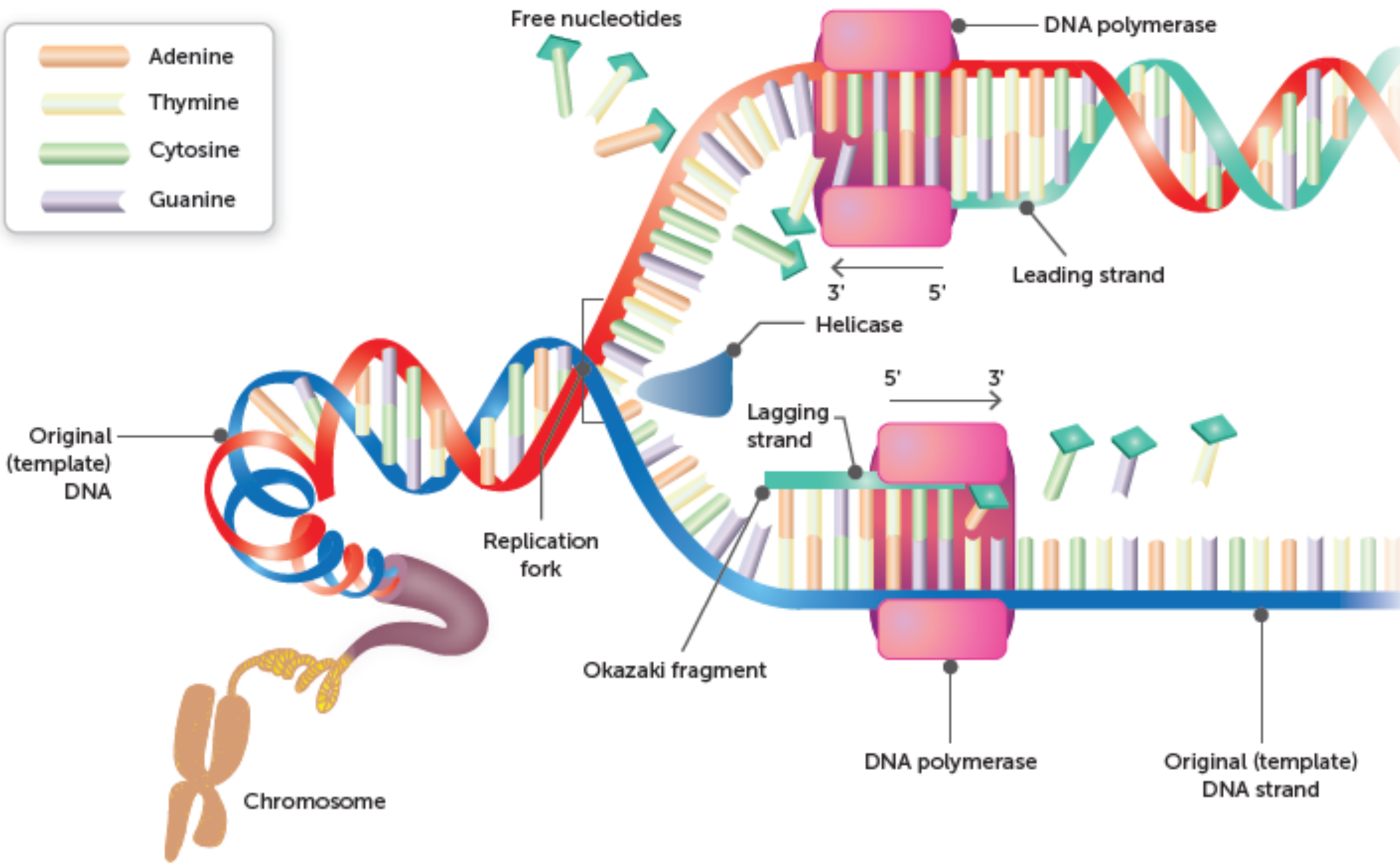
DNA replication – process



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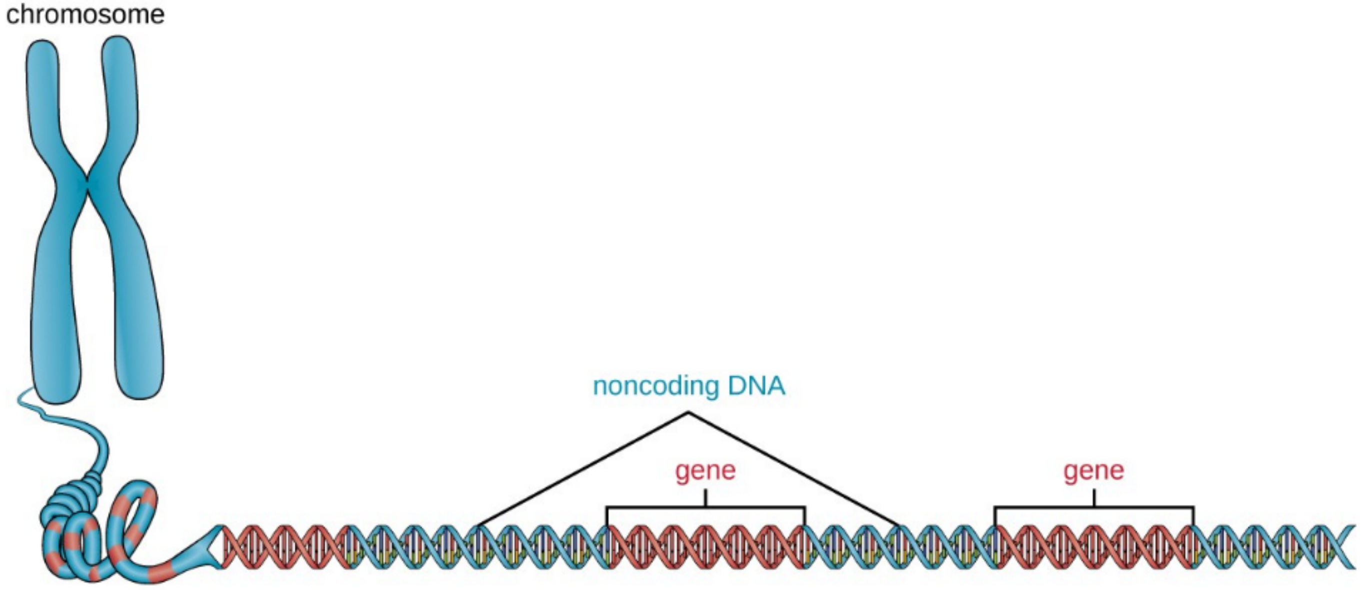
What is coding and non-coding DNA?

Some sections of the genome sequence code for a protein and are known as **coding DNA**. The sections of DNA that do not code for a protein are classified as **non-coding DNA**.



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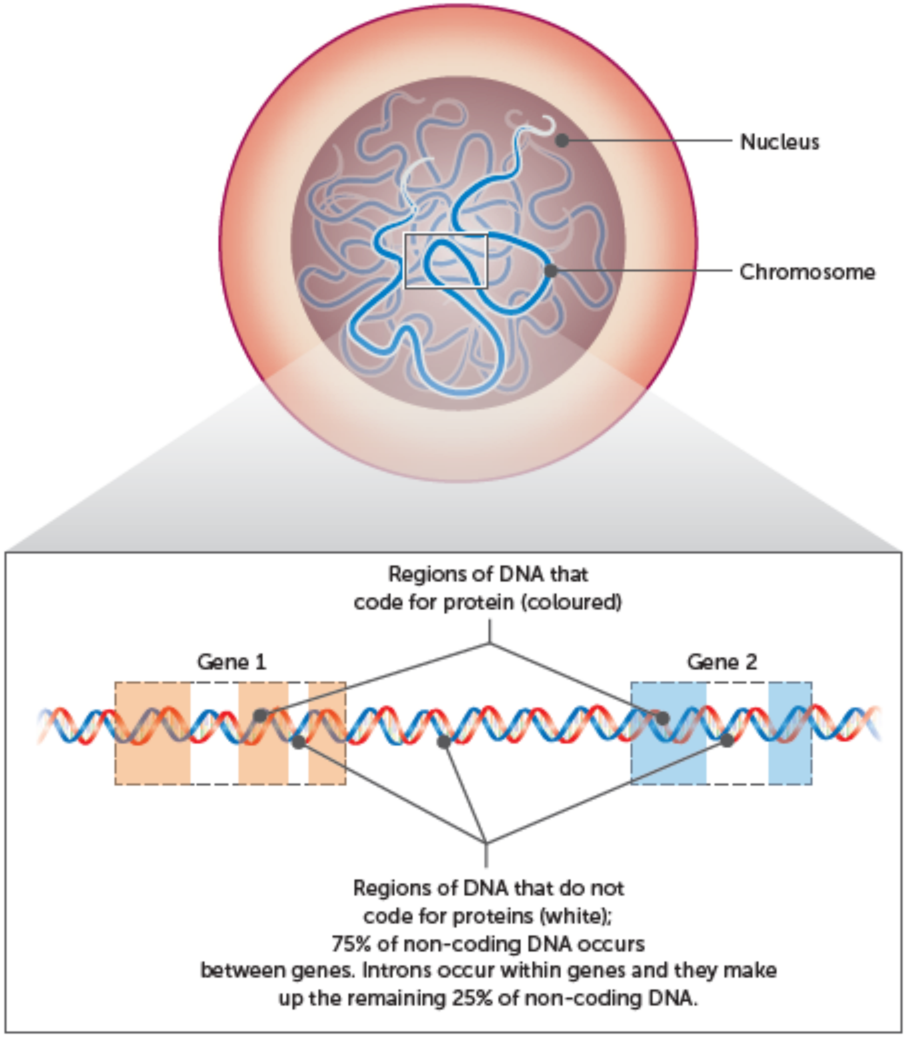
Coding and non-coding DNA



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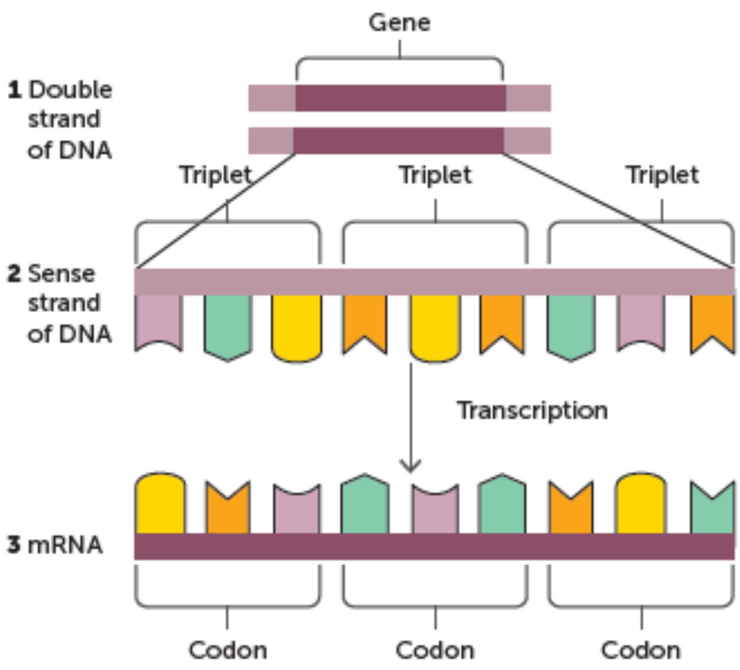
Coding and non-coding DNA

The genetic code



The **genetic code** is the term used for the way that the four nitrogenous bases of DNA are ordered. In the genetic code, each set of three DNA nucleotides in a row counts as a **triplet** and codes for an mRNA triplet called a **codon**. The mRNA codon (three nucleotides) is read by cellular machinery and is translated into a single, specific amino acid.

Introduction to protein synthesis

Protein synthesis is a process. The end product is a protein. There are two main parts to the flow of information from gene to protein: transcription and translation.

Transcription is the synthesis of mRNA using the stored DNA code. The synthesised mRNA is a chain of complementary RNA nucleotides, except that uracil (rather than thymine) is the base pair of adenine in RNA.

Translation is the synthesis of a polypeptide using the information in the mRNA. The RNA nucleotide code is translated into an amino acid sequence.

Protein synthesis

Essential materials needed for protein synthesis

Codons

A series of three nucleotides found in mRA act as a code for an amino acid. A START codon (AUG) initiates translation and a STOP codon (UAG) brings the process to an end.

Enzymes

Help break or form new bonds; e.g. RNA polymerase

Amino acids

Twenty amino acids are the building blocks of polypeptides and proteins. The sequence of amino acids is a type of code that specifies the structure and function of the protein, making it different from other proteins.

Nucleic acids

DNA stores the code. mRNA copies and delivers the code from the nucleus into the cytoplasm and the ribosome. tRNA is found in the cytoplasm. It carries amino acids to the ribosome for protein synthesis specific to the codon.

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Base pair rules

DNA nitrogenous base attached to the DNA nucleotide	RNA nitrogenous base attached to the RNA nucleotide that complements the DNA nucleotide
Adenine	Uracil
Thymine	Adenine
Cytosine	Guanine
Guanine	Cytosine

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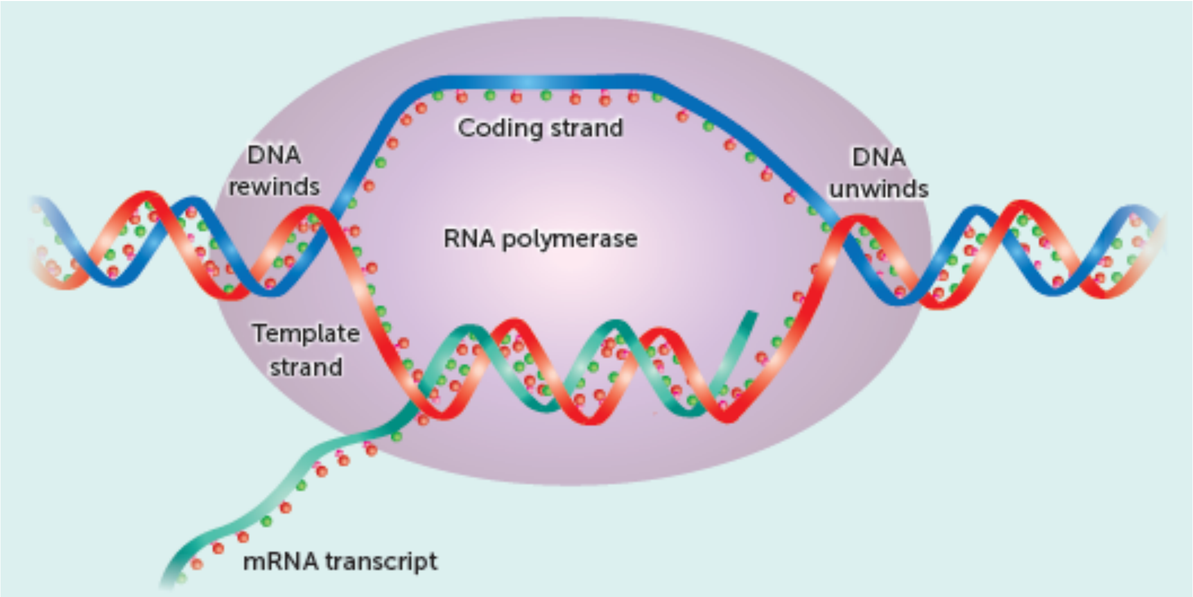
The process of transcription

Step 1
In the nucleus, part of one gene becomes unzipped by the action of RNA polymerase, which breaks the weak hydrogen bonds. RNA polymerase then joins the complementary nucleotides.



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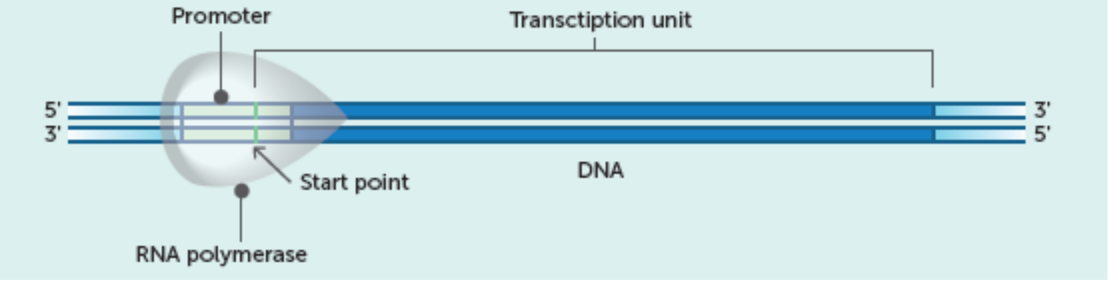
Protein synthesis − transcription

Step 2

The template strand (non-coding strand; antisense strand) is used for transcription. RNA polymerase binds to a promoter region after transcription is initiated.



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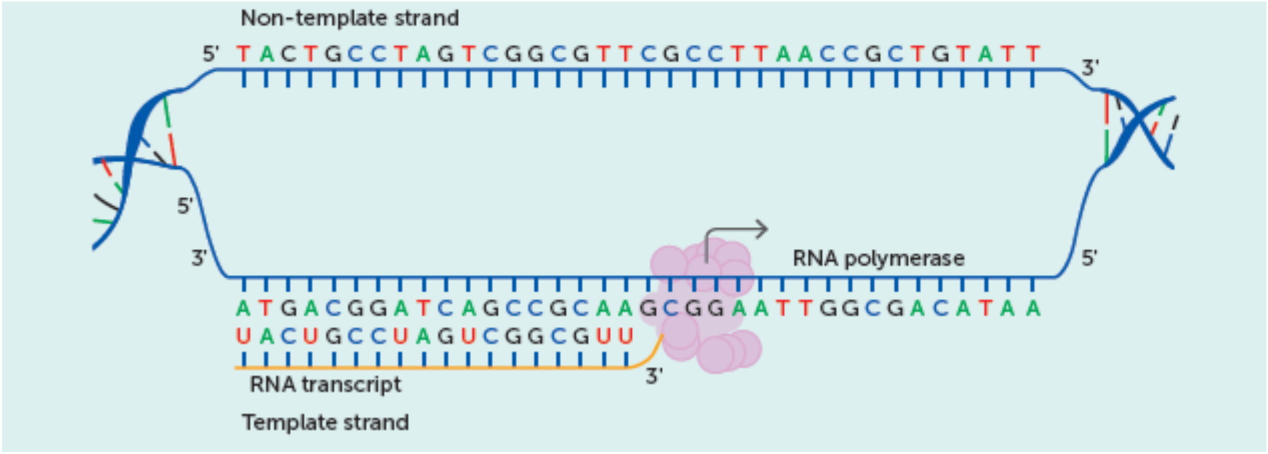
Protein synthesis – transcription

Step 3

RNA polymerase adds free-floating nucleotides according to the complementary base pair rules, but in RNA uracil pairs with adenine. The new strand of mRNA is synthesised in a 5’ to 3’ direction.



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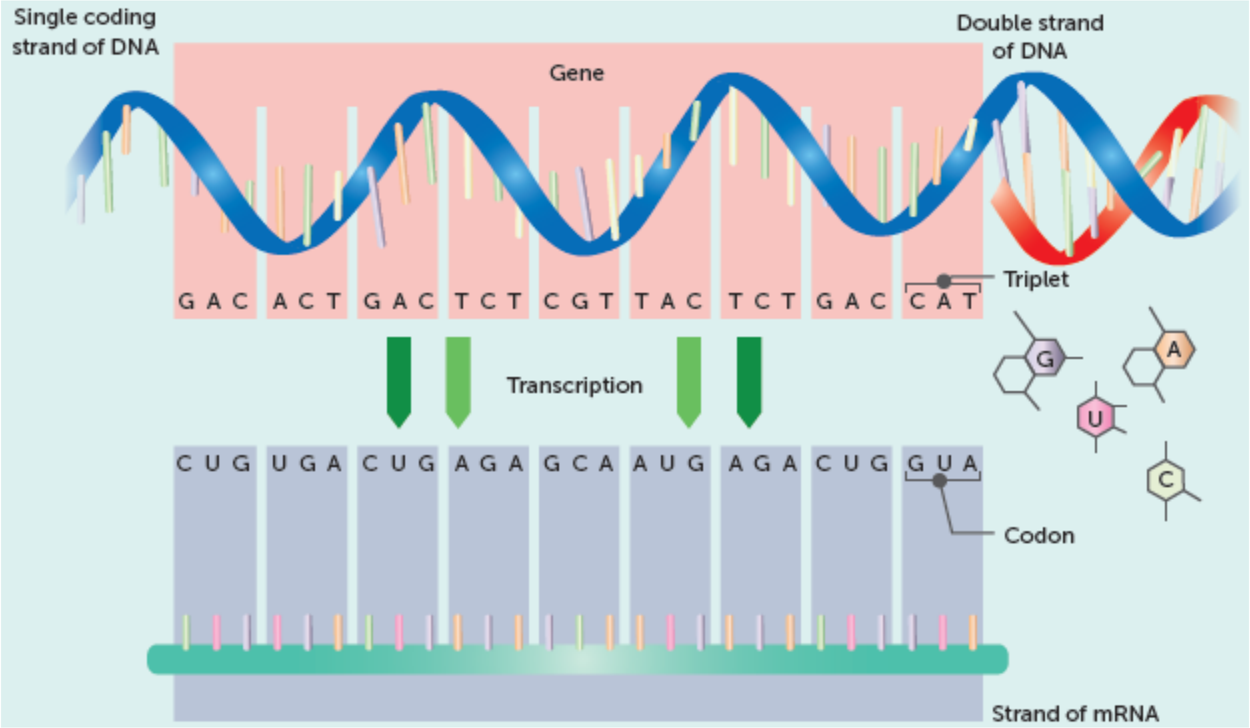
Protein synthesis – transcription

Step 4

The DNA bases are read in triplets, and the complementary mRNA triplets are called codons. The process continues until there is a termination signal and the pre-mRNA is released.



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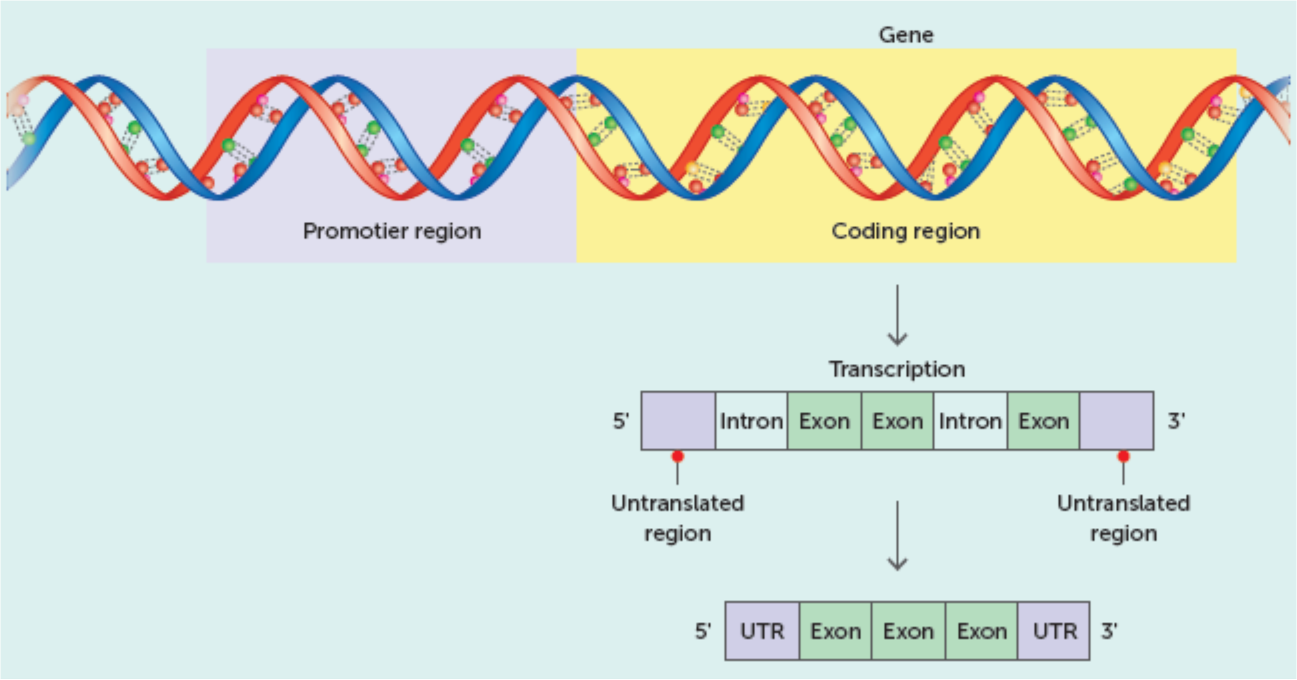
Protein synthesis – transcription

Step 5

Pre-mRNA consists of introns and exons. Introns are removed and exons are joined to create mature mRNA. Mature mRNA exits the nucleus via the nuclear pore.



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Translation

Initiation

A ribosome binds to a molecule of mRNA. A start codon signals the start of translation. Two codons enter and are bound to the ribosome. Following initiation, only one codon enters and is translated at a time.

Elongation

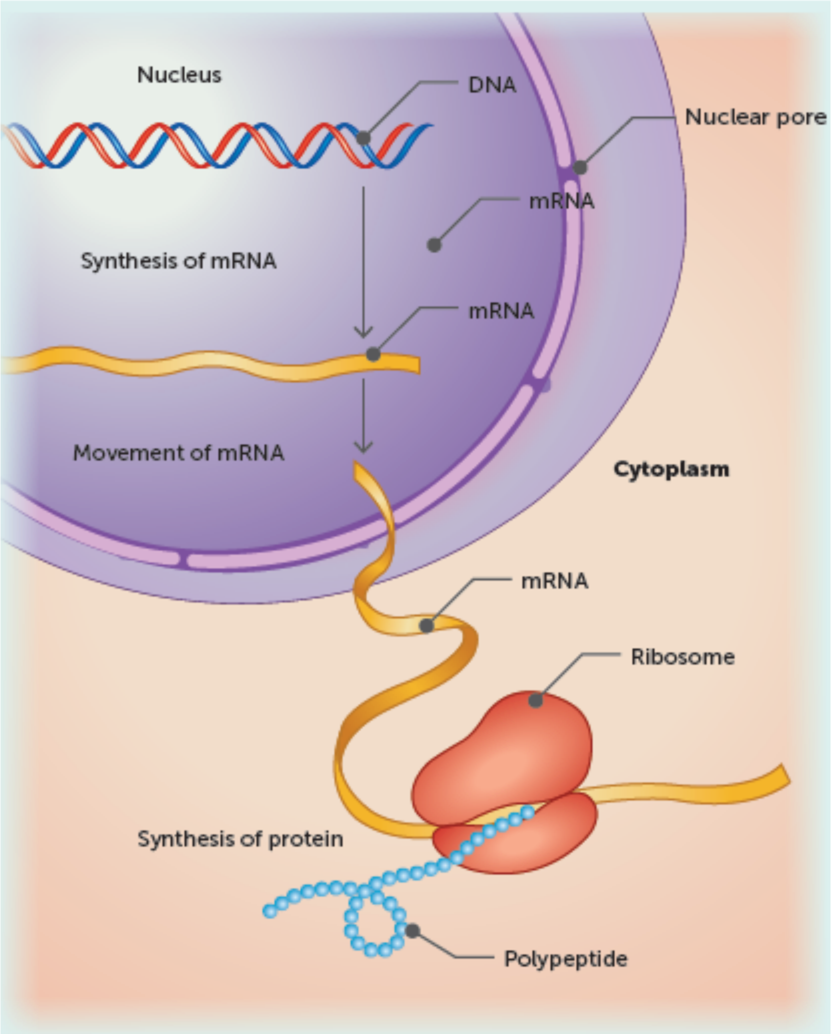
A tRNA molecule, which includes an anticodon, is attracted to the corresponding codon due to complementary base pairing. On the other side of the tRNA molecule is the amino acid specified by the codon. As one codon is read and exits, another one slides into the ribosome to be read. tRNAs transfer the amino acids to the mRNA–ribosomal complex in the order specified by the codons of the mRNA.

Termination

Elongation continues until a stop codon in the mRNA enters the ribosome.

Protein synthesis – translation

Step 1
The ribosome binds to the mRNA strand.



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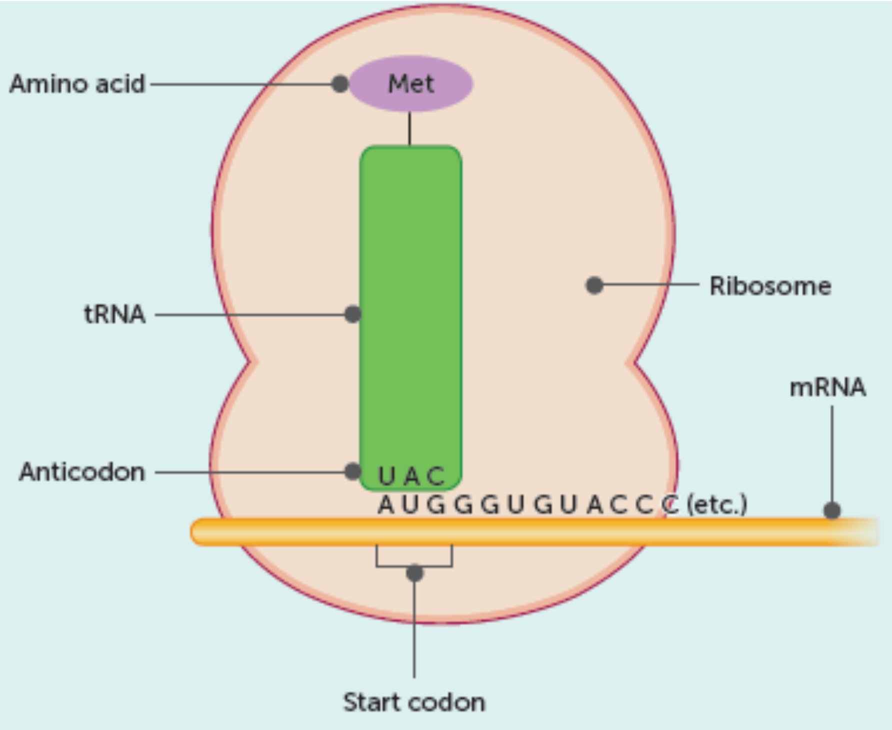
Protein synthesis – translation

Step 2

The start codon in mRNA is usually ‘AUG’.



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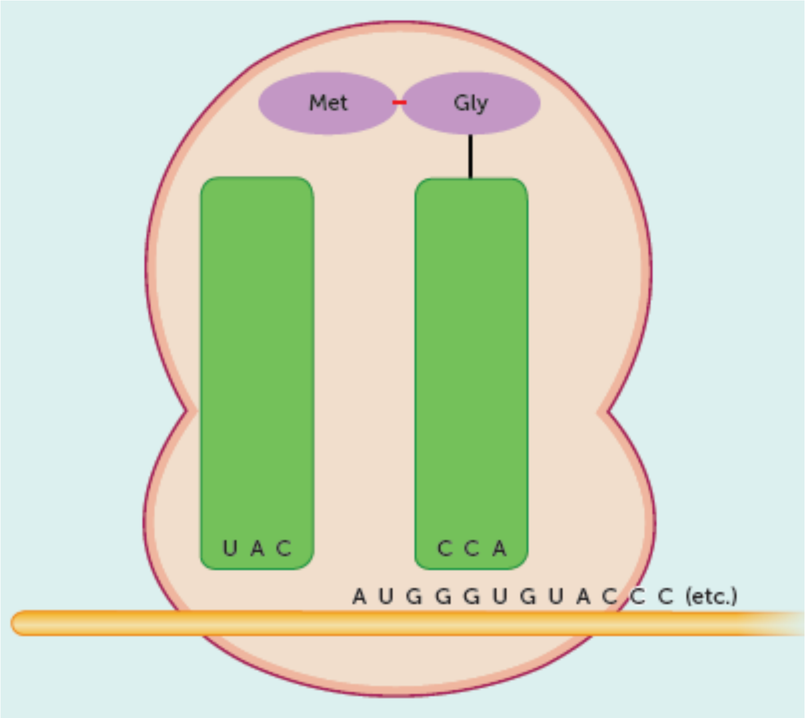
Protein synthesis – translation

Step 3

Amino acids are attached in order according to the order of the codons.



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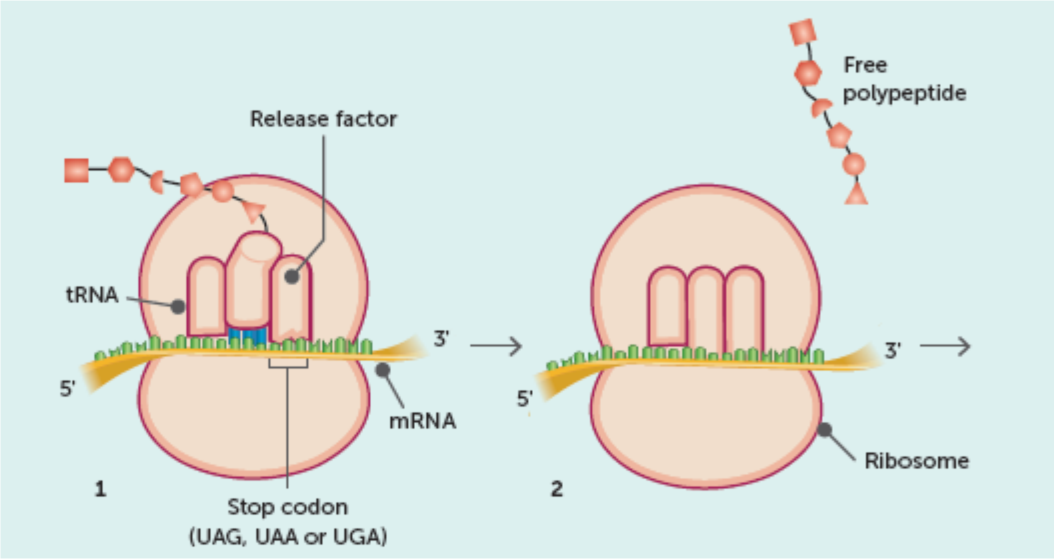
Protein synthesis – translation

Step 4
The polypeptide forms.



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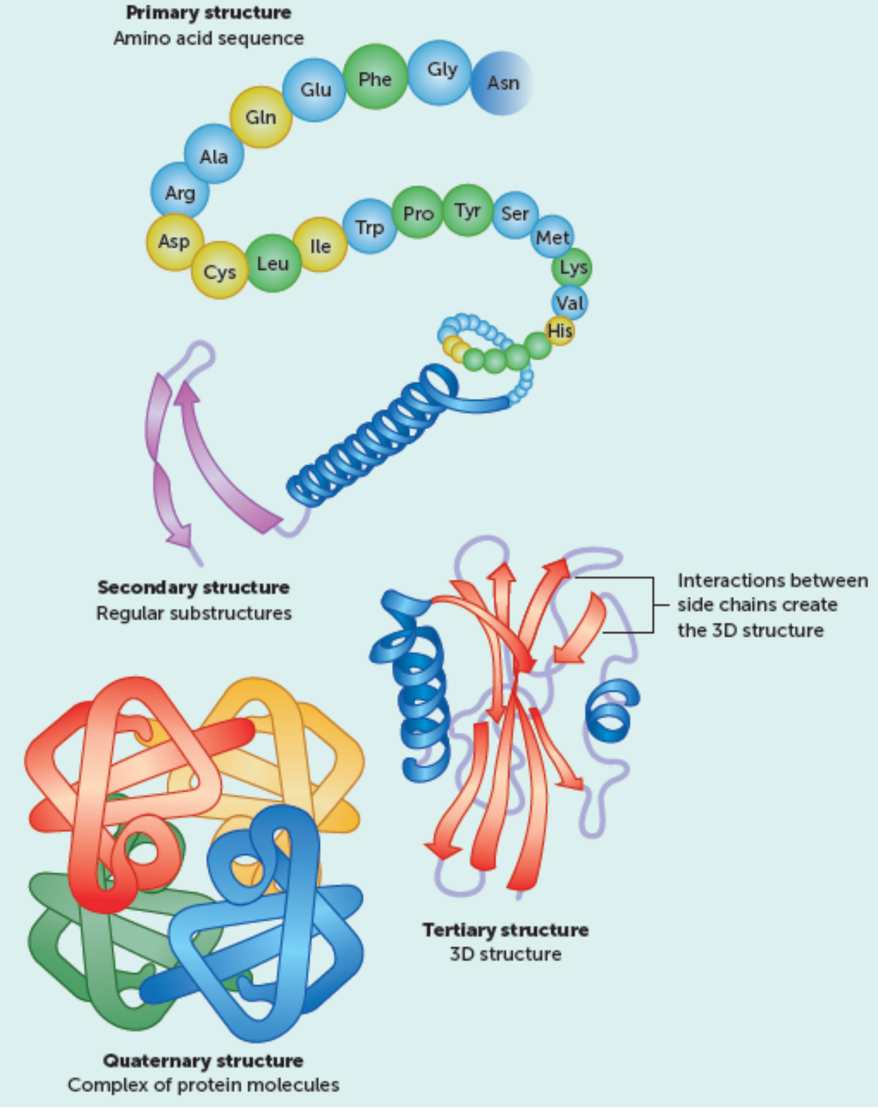
Protein synthesis – translation

Step 5
Translation is complete.



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Proteins

Amino acids

Proteins are built from a selection of 20 different **amino acids**. The amino acids are linked together by peptide bonds to form **polypeptide chains**, which fold and/or are modified to form the protein.

An amino acid table (**codon table**) is a translation table.
To find the amino acid coded for by an mRNA codon, look for the three nitrogenous base letters in the table. There are 64 possible base triplets and three of these are stop codons that signal for translation to stop.

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

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