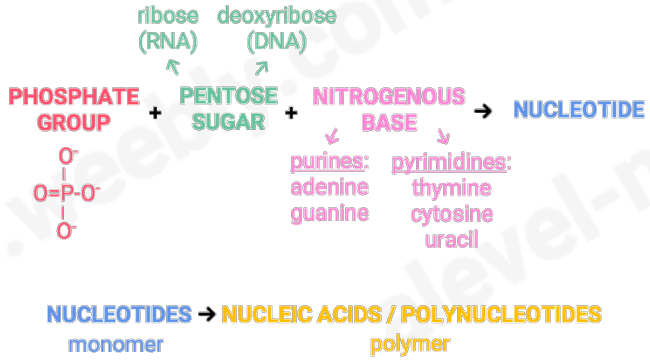
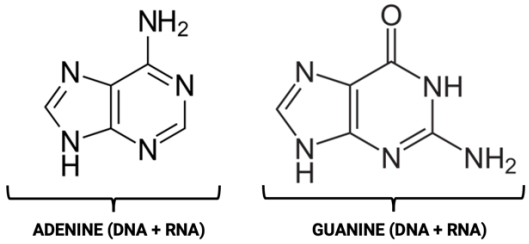
# 6 Nucleic acids and protein synthesis

## 6.1 Structure and replication of DNA



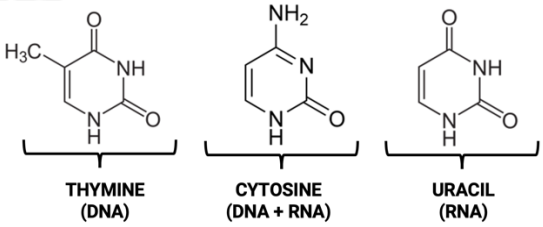

### Purines

Larger, double-ringed molecules (adenine, guanine)

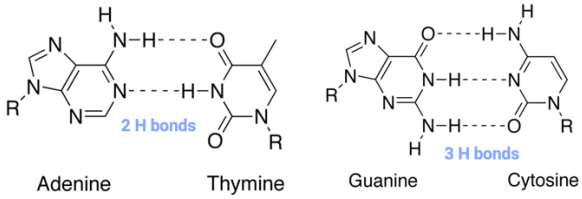



### Pyrimidines

Smaller, single-ringed molecules (thymine, cytosine, uracil)




- to form the polynucleotides DNA and RNA, nucleotides are linked into a long chain
- nucleotides are linked together by covalent bonds called **phosphodiester bonds**
- this takes place inside the nucleus during interphase
- purines combine with pyrimidines




- in RNA, adenine pairs with uracil

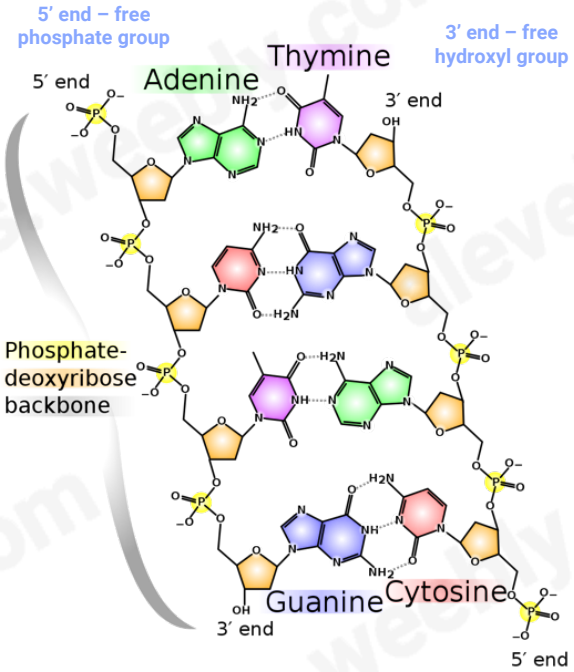



Image: By Madprime (talk · contribs). https://commons.wikimedia.org/w/index.php?curid=1848174

- sides of the ladder of DNA are made up of alternating molecules of phosphate and deoxyribose
- nitrogenous bases that make up rungs of ladder have hydrogen bonds between them
- they link bases and hold 2 strands together
- DNA molecules are made of 2 polynucleotide strands lying **anti-parallel** to each other held by hydrogen bonds between bases

### Semi-conservative replication of DNA

DNA molecules replicate by semi-conservative replication – half of the original molecule is kept/conserved in each of the new molecules.

1) double helix of DNA is unwound by enzyme **helicase**
   - it does this by splitting hydrogen bonds between bases
   - the unwinding of DNA strands creates a 'replication fork' (a y-shaped structure)

2) enzyme **primase** synthesises a short piece of RNA called primer which marks the starting point for synthesis of new strand

3) **DNA polymerase** uses the primer and synthesises new strand
   - DNA strands are anti-parallel to each other, and DNA polymerase can only add bases in one direction which is 5' to 3'

- one of the new strands, **the leading strand,** is made continuously
- DNA polymerase progresses down the strand adding bases in a 5' to 3' direction
- when using the lagging strand as a template, DNA polymerase adds nucleotides in short stretches called **okazaki fragments** to overcome directionality problem

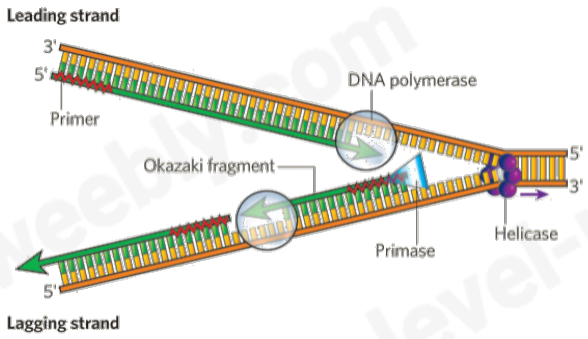



*Image: https://www.nature.com/*

**4) DNA ligase** seals up fragments of DNA in both to form a continuous double stranded helix

## 6.2 Protein synthesis

A polypeptide is coded for by a gene and that a gene is a sequence of nucleotides that forms part of a DNA molecule.

- DNA controls protein synthesis by determining the order of amino acids when proteins are synthesised in cells
- sequence of nucleotide bases in a DNA molecule is code for sequence of amino acids in a polypeptide
- each sequence of 3 bases (a codon) codes for 1 amino acid

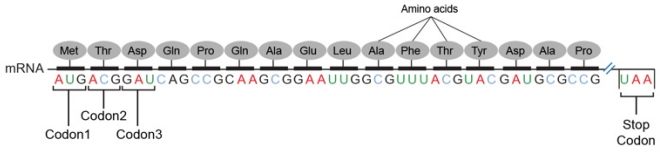



*Image: https://www.genome.gov/*

- **Gene** – part of a DNA molecule where the nucleotide sequence codes for just one polypeptide
- **Gene mutation** – a change in the sequence of nucleotides that may result in an altered polypeptide
  - types of gene mutations: substitution, deletion, insertion, inversion, frameshift
  - **alleles** – variants of genes (caused by mutations)

### Sickle cell anaemia

- caused by a change in the base sequence of amino acids in the β-polypeptide chain
- adenine replaces thymine in CTT triplet forming CAT
- this type of mutation is called substitution
- during synthesis of sickle cell haemoglobin, the amino acid valine (GTG), which is non-polar, is incorporated instead of glutamic acid (GAG)
- having this non-polar R group on the outside of the molecule makes the cell less soluble
- individuals with 2 copies of $Hb^S$ allele inherit the disease *(recessive)*

### Protein synthesis

#### a) Transcription

Process by which enzymes use the sense strand of DNA as a template to produce a messenger RNA (mRNA) molecule.

1) **RNA polymerase binds to a region of gene called promoter**
   - this signals DNA to unwind so bases can be read from one strand
   - the strand that's read is the sense-strand

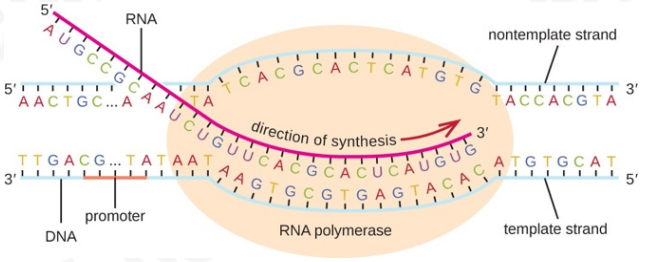



*Image: https://courses.lumenlearning.com/*

2) **RNA polymerase reads sense strand in a 3' to 5' direction and generates mRNA from 5' to 3'**
3) **when RNA polymerase has reached the terminator sequence at the end of the gene, transcription stops**
   - enzyme detaches from gene and DNA returns to original structure
4) **last triplet transcribed to mRNA is a DNA triplet coding for STOP e.g., ATT, ATC, ACT** *(in DNA the stop codons are UAA, UGA, UAG)*

#### STOP codons

- codons that terminate translation
- does not specify any amino acid
- has no complementary tRNA/anti-codon
- causes the release of a completed polypeptide chain

#### b) Translation

Process by which the genetic code in mRNA is read to make a protein.

1) **mRNA leaves the nucleus and binds to the smaller ribosomal unit**

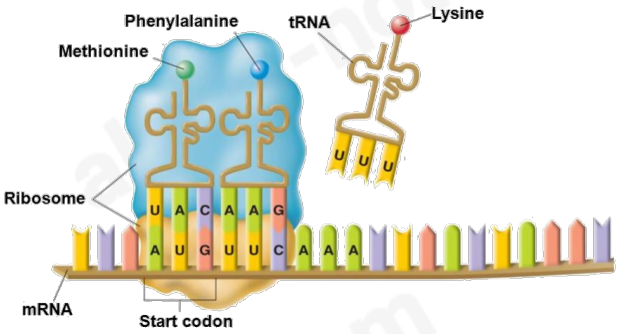



Image: https://slideplayer.com/slide/16525143/

2) every 3 bases (a codon) on mRNA codes for a specific anti-codon which is carried by a transfer RNA (tRNA) molecule

- each different tRNA is covalently linked to a particular amino acid

| | | | |
|---|---|---|---|
| **mRNA** | **AUG** | **UGC** | **AAG** |
| **tRNA** | **UAC** | **ACG** | **UUC** |
| | Met | Cys | Lys |

- since there are 4 bases (A, T, G, C) and each codon has 3 bases –

$$4^3 = 64$$

- there are 64 possible codons, more than enough to code for 20 amino acids
- some codons are 'special', e.g., AUG is a START codon and initiates translation by coding for methionine

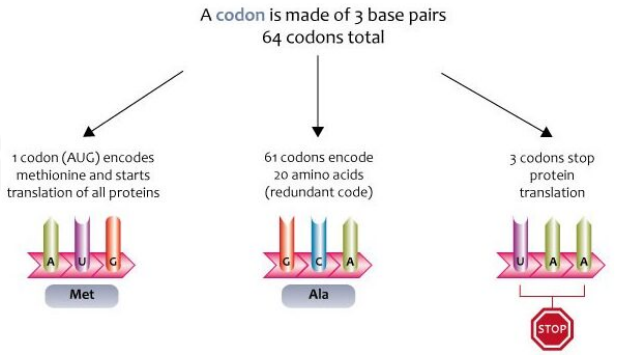



Image: https://www.differencebetween.com/difference-between-start-codon-and-stop-codon/

3) an initiator tRNA adheres to a START codon

4) the tRNA that corresponds to the next codon after the START codon enters the ribosome carrying an amino acid with it which becomes covalently bound to methionine from the initiator tRNA

5) the first tRNA detaches and leaves the ribosome which has shifted over making room for the next tRNA molecule

- new amino acid from new tRNA links the first two
- this process continues all the way down the mRNA strand
- this polypeptide chain continues to grow till a STOP codon is reached

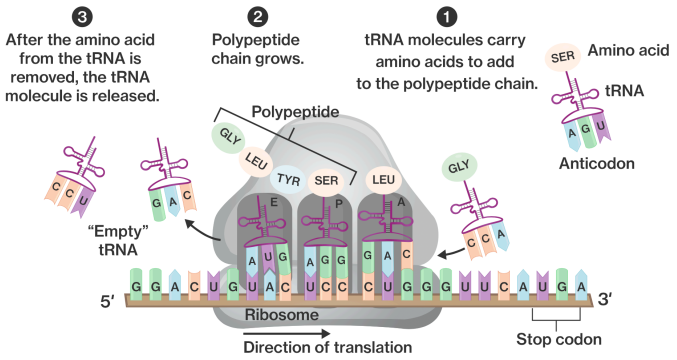



Image: https://www.coursehero.com/sg/cell-biology/translation/