Higher Human Biology

UNIT 1

BRIGHT MINDS MENTORING

Revision notes

1.Somatic/Germline Stem cells

Stem Cells

Unspecialised cells that:

1. **Reproduce** themselves to produce more stem cells and **remain undifferentiated.**
2. **Differentiate** into **specialised** cells.

Somatic cells

Cells in the body that are **not involved in reproduction** (e.g. muscle, skin, bone, blood etc).

They have **two sets** of chromosomes (**diploid** cells).

Somatic stem cells divide by **mitosis** to form more somatic cells.

Germline cells
Haploid **gametes** (sperm and ova) & **stem cells** that divide to form gametes.

Germline stem cells can divide by:

1. **MITOSIS**

To produce **more germline stem cell** to maintain the **diploid chromosome number**.

Diploid cells have **23 pairs of homologous chromosomes** (46 single chromosomes).

2. MEIOSIS
To produce haploid gametes. The nucleus undergoes **two divisions**.

First division: **separates homologous chromosomes** (diploid to two haploid cells).

Second division: **separates chromatids** to produce **more haploid gametes.**

Haploid gametes contain **23 single chromosomes**.

1. Stem Cells

Cell differentiation

The process by which a cell **expresses certain genes** to produce **specific proteins characteristic** for that type of cell.

This allows a cell to carry out **specialised functions**. This **saves ATP/resources**.

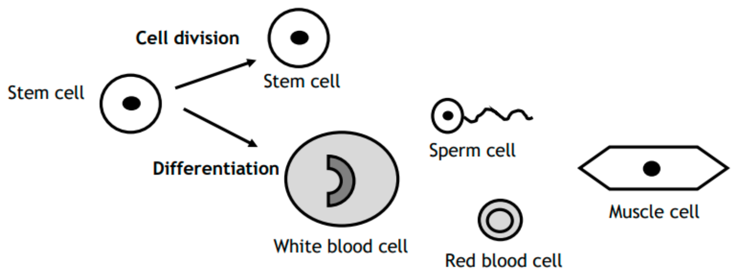
Types of Stem Cells

1. Embryonic Stem Cells

Cells in the **very early embryo** can differentiate into **all** the cell types that make up the individual

All the genes in embryonic stem cells can be switched on so these cells can differentiate into **any** type of cell aka **pluripotent.**

Pluripotent Embryonic Stem Cells



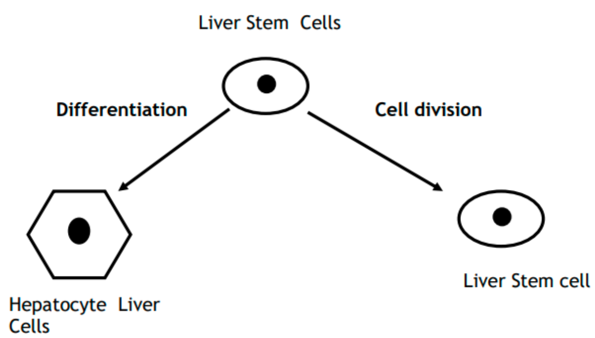
2. Tissue stem cells

Involved in the **growth, repair and renewal** of the cells found in **one tissue** and so are called **multipotent.**

Example 1: Blood stem cells in bone marrow can give rise to **ONLY a few types of blood cells.**

Example 2: Liver Stem Cells produce **only 1 type** (liver hepatocytes)

Multipotent Liver Stem Cells



1. Therapeutic/Research uses & Cancer Cells

Research Uses of Stem Cells

1. Provide information of **cell growth/cell differentiation**
2. **Model cells** for studying how **diseases develop**.
3. **Model cells** for **drug testing**

Therapeutic Uses of Stem Cells

Involve the **repair of damaged/ diseased** organ or tissues.

1. Corneal Repair
2. Regeneration of damaged skin

Ethics surrounding Embryonic Stem Cell

Embryonic stem cells can **self renew under right conditions in the lab** and be used as a **potential therapeutic use** of stem cells.

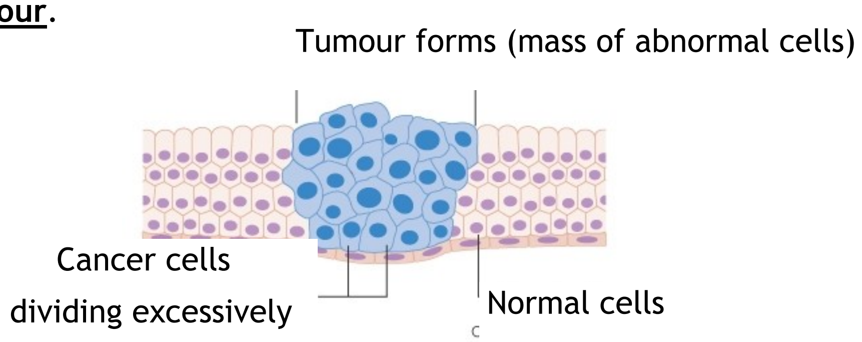
Advantage
Offer **effective treatment** for disease/injury.

Disadvantage
Involves **destruction** of the embryo.

Cancer Cells

Divide excessively as they fail to respond to **regulatory signals**.
This results in a **mass of abnormal cells** called a **tumour.**

If **tumour cells** fail to attach to each other they can **spread throughout the body** causing a **secondary tumour**.



2. Structure of DNA

The base sequence of DNA forms the **genetic code** for producing **specific proteins**.

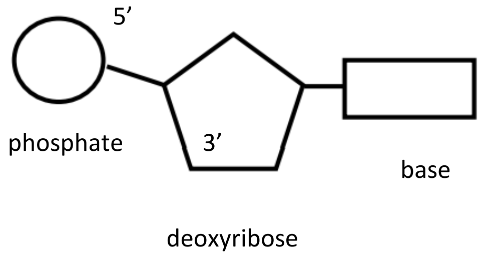
3D Structure

DNA is made of **2 strands** of nucleotides that coil up to form a **3D structure** called a **double helix.**

Nucleotide

Smallest individual unit of DNA made up of:

1. **Phosphate** on carbon 5 (C5)
2. **Deoxyribose sugar** on carbon 3 (C3)
3. **Base** (Adenine, Thymine, Guanine or Cytosine)

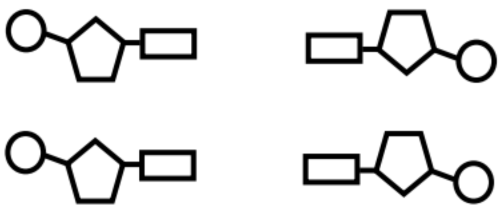


Complementary Base Pairing

Adenine pairs with **Thymine**.

Guanine pairs with **Cytosine**.

* ALWAYS USE FULL NAMES *

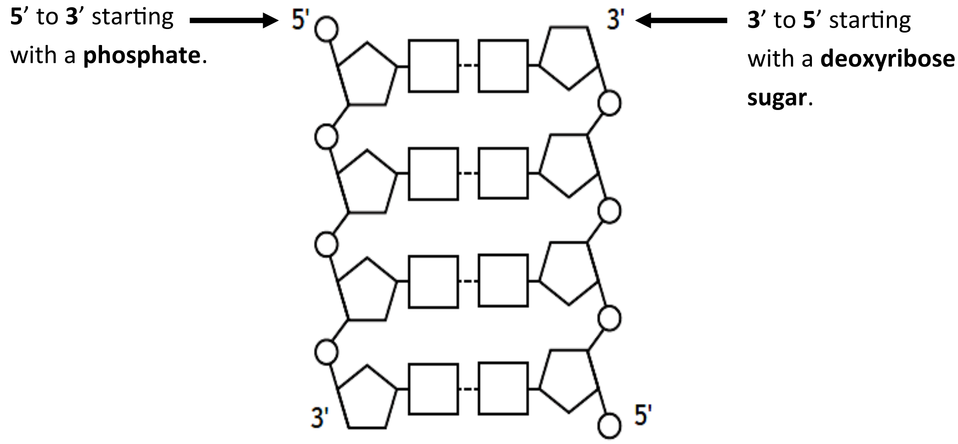


2. Structure of DNA

Antiparallel Structure

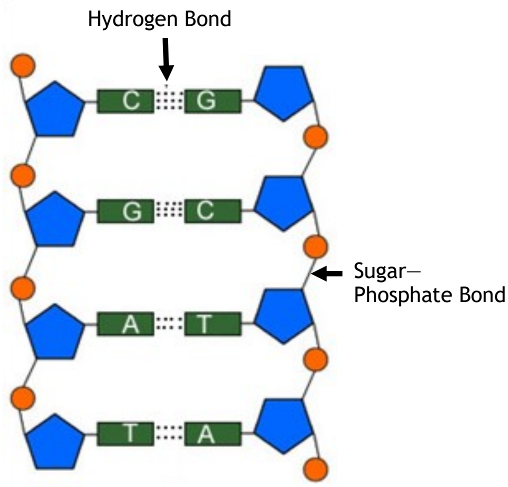
One strand runs from **5’ to 3**’ starting with a phosphate.

The other strand runs from **3’ to 5’** starting with a deoxyribose sugar.



Hydrogen Bonds

Bonds between **complementary bases** hold the two strands together.



Sugar Phosphate Backbone

Sugar-phosphate bond between C3 on Deoxyribose sugar and C5 on phosphate creates the DNA backbone.

DNA Calculations

1. If there are 300 bases in total and 20% are guanine, calculate the number that are Adenine.

Adenine - 30% Thymine - 30%

Guanine - 20% Cytosine - 20%

Adenine - 30% of 300

300/100 = 3 (1%)

3 x 30% = **90 bases**

2. There are 300 bases in total. On the original strand there are 50 Adenine and 40 Guanine bases. On the complementary strand there are 30 Guanine bases. How many thymine bases are there on the original strand?

A 50	50 T
T	A
G40	40 C
C 30	30 G

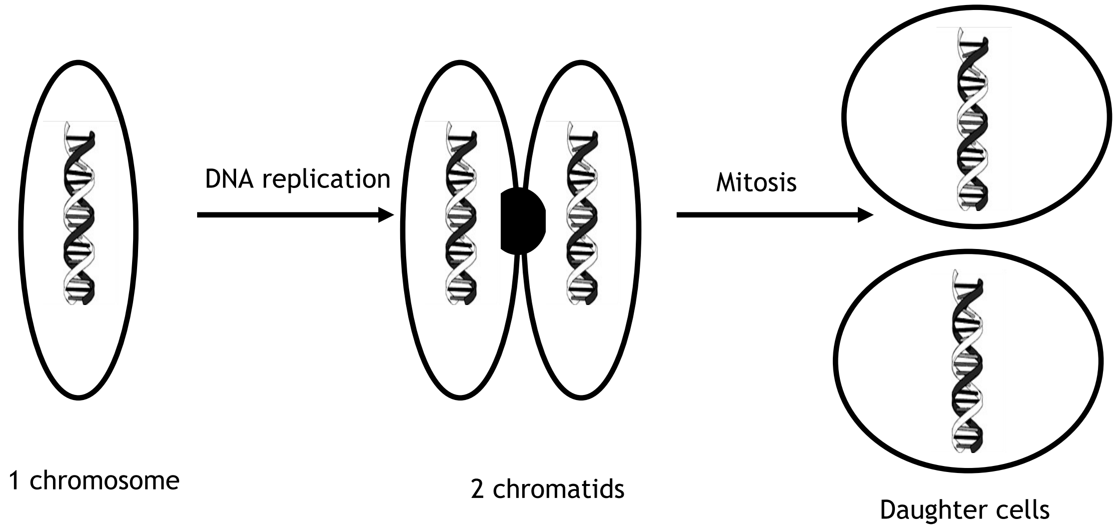
= 240 bases

300—240 = 60 bases

Thymine = 30 bases

2. Replication of DNA

DNA is replicated **before cell division** occurs to form two identical DNA double helixes.



Importance of DNA Replication

To ensure that each daughter cell has the **correct number of chromosomes** to ensure that no genetic information is lost.

DNA Replication - Requirements

1. Primers
2. Enzymes (DNA Polymerase and Ligase)
3. DNA Template
4. Free complementary DNA nucleotides
5. ATP

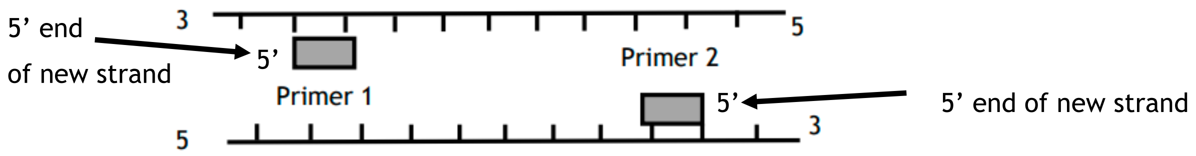
Primers

Short strand of nucleotides **complementary** to target DNA.

Function of Primers

Start DNA replication by binding to **5' end** of newly synthesised strand.

This allows DNA polymerase to start replication of the new DNA strand.



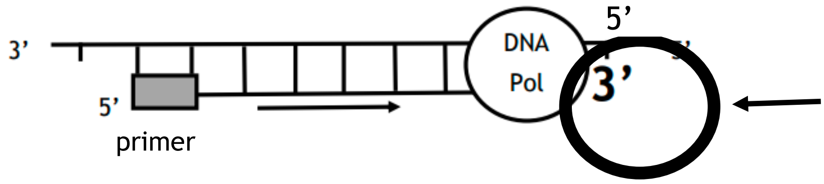
2. Replication of DNA

<u>DNA Polymerase (enzyme)</u>

Adds **<u>free complementary DNA</u>** nucleotides to the **<u>3' end</u>** of the new DNA strand

<u>Free Complementary DNA Nucleotides</u>

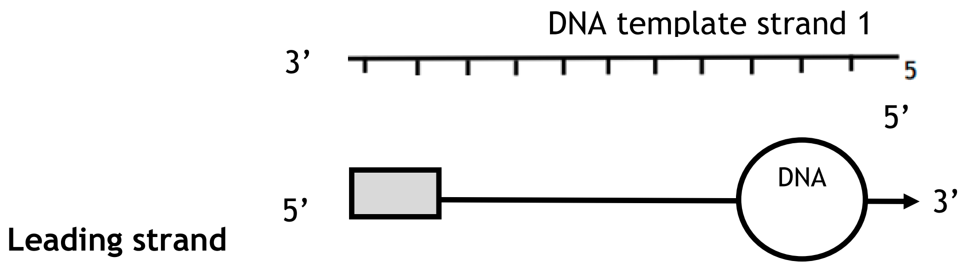
Added to the <u>3'</u> end to create the **<u>new</u>** strand.



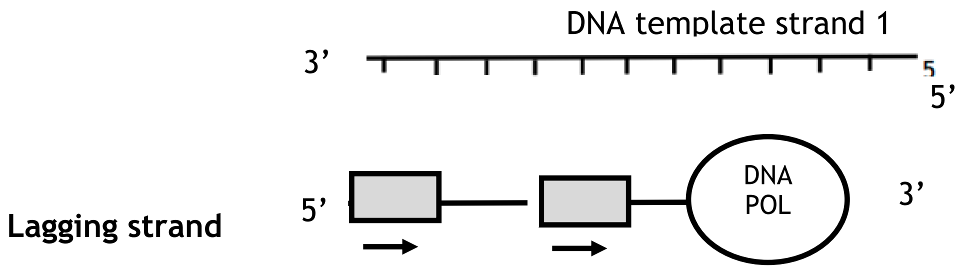
<u>Leading & Lagging Strand</u>

Leading strand **<u>replicated continuously</u>**

Lagging strand replicated in **<u>fragments</u>**



Newly synthesised single leading strand from **<u>5' to 3'</u>**



Newly synthesised DNA fragments in lagging strand from **<u>5' to 3'</u>**

<u>Ligase (enzyme)</u>

<u>Joins</u> fragments of DNA together.

2. Replication of DNA

DNA Replication

Stage 1

DNA **unwinds** and separates into **two template strands**, breaking **hydrogen bonds** between the bases.

Stage 2

Primers bind to the **5' end** of the new strand, **starting DNA replication** by allowing DNA polymerase to add DNA nucleotides.

Stage 3

DNA polymerase adds **free** complementary **DNA nucleotides** to the **3'** end of the new DNA strand.

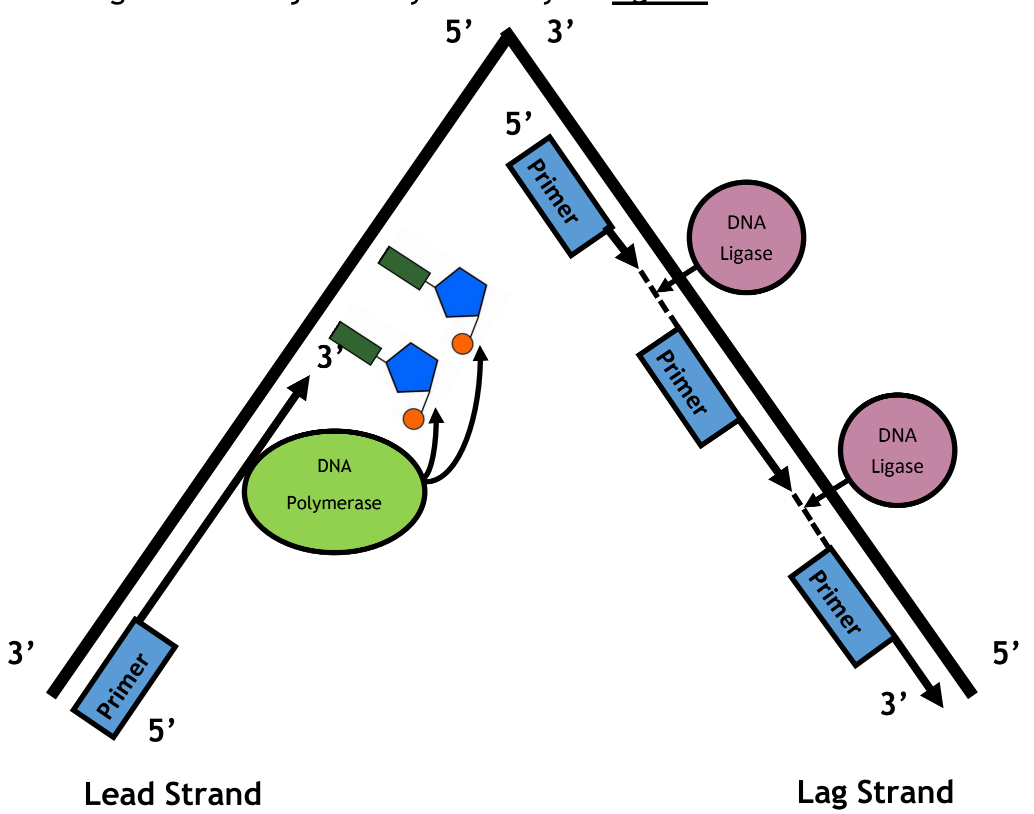
Stage 4

DNA polymerase only adds nucleotides from **5' to 3'** on the new strand and as DNA is **antiparallel**

1. The **leading** strand being replicated **continuously**
2. The **lagging** strand replicated in **fragments.**

Stage 5

Fragments in the lag strand are joined by the enzyme **ligase.**



2. PCR

Polymerase Chain Reaction (PCR) Function

Amplifies target DNA.

Practical Applications (Uses)

1. Help solve crimes
2. Settle paternity suits
3. Diagnose genetic disorders

Requirements for PCR

1. Template DNA sample
2. Free complementary DNA nucleotides
3. Primers
4. Heat Tolerant DNA Polymerase
5. ATP

Stages of PCR.

There are **3 stages** per cycle of PCR with 30-60 cycles needed.

Repeated heating and cooling occurs in each cycle to **double** DNA content.

Stage of Cycle	Description	Temperature Range
Heating	Separate the DNA strands	92˚C and 98˚C
Cooling	Allow primers to bind to target sequences to **start DNA replication**.	50˚C and 65˚C
Heating	Heat-tolerant DNA polymerase **replicates the DNA**	70˚C and 80˚C

2. PCR

Primers

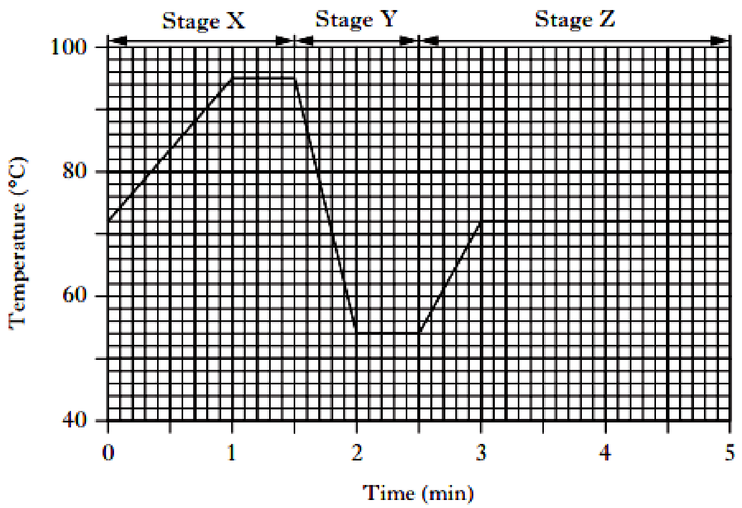
Short sequences of DNA which bind to **complementary target sequences** on **one end** of each template strand.

Two types of primers are needed per PCR reaction. One for each of the two template strands.

Heat Tolerant DNA Polymerase

To ensure enzymes **do not denature** at high temperatures of PCR

Easy Graphs



PCR Calculations

1. How long does one cycle of PCR last from the graph above.

   5 minutes

2. How long will it take to make four DNA molecules from one original DNA molecule using graph 2 above.

   1 $\xrightarrow{\text{5 minutes}}$ 2 $\xrightarrow{\textbf{10 minutes}}$ 4 DNA molecules

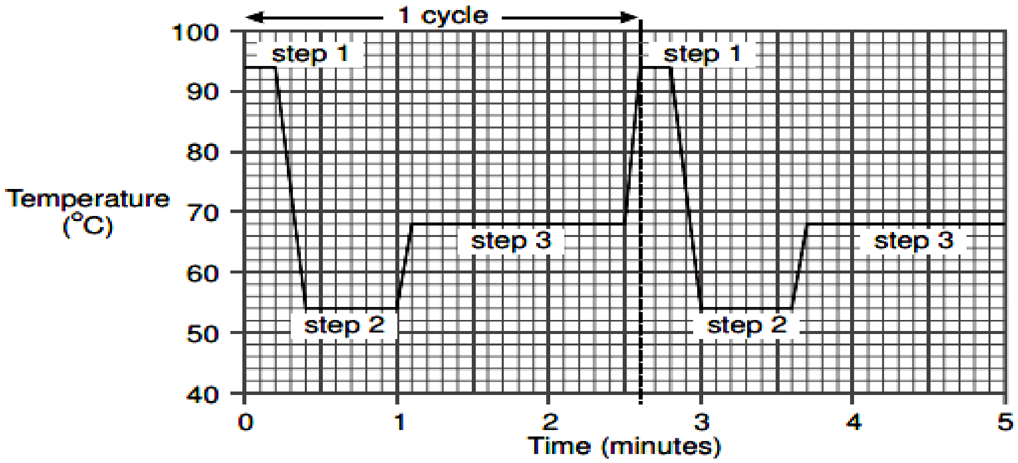
3. During step Z, DNA polymerase extends the DNA rate of 500 base pairs per minute. Calculate the length of the DNA fragment produced each time from the graph.

   Step Z is 2.5 minutes in length from graph.

   2.5 x 500 base pairs = 1250 base pairs

2. PCR

Difficult Graphs



PCR Calculations

1. How long does one cycle of PCR last from the graph above.

   2.6 minutes

2. How long will it take to make four DNA molecules from the original DNA molecule using graph 2 above.

   5.2 minutes

3. During step 3, DNA polymerase extends the DNA rate of 500 base pairs per minute. Calculate the length of the DNA fragment produced each time from the graph.

   Step 3 is 1.5 minutes in length from graph.

   1.5 x 500 base pairs = 750 base pairs

PCR calculation (non graph)

Calculate how many copies of DNA would be produced from **100 molecules** of DNA.

(i) 3 cycles

100 $\xrightarrow[\text{Cycle 1}]{}$ 200 $\xrightarrow[\text{Cycle 2}]{}$ 400 $\xrightarrow[\text{Cycle 3}]{}$ <u>**800**</u>

Calculate the number of cycles needed to produce the following number of DNA molecules from a single molecule.

(ii) 24 molecules

1 $\xrightarrow[\text{Cycle 1}]{}$ 2 $\xrightarrow[\text{Cycle 2}]{}$ 4 $\xrightarrow[\text{Cycle 3}]{}$ 8 $\xrightarrow[\text{Cycle 4}]{}$ 16 $\xrightarrow[\text{Cycle 5}]{}$ 32

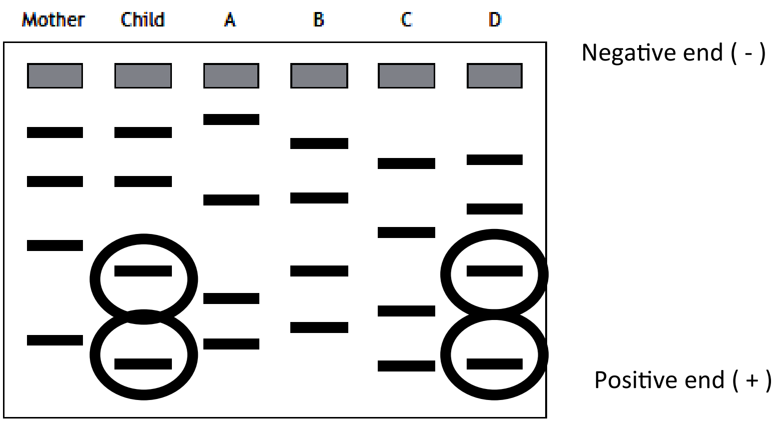
2. Gel Electrophoresis

Gel electrophoresis separates DNA fragments by **size.**

DNA is **negatively charged** and moves through the gel to the positive end

Sma**ller fragments** move **further** through the gel to the positive end.

Paternity test Gel Electrophoresis

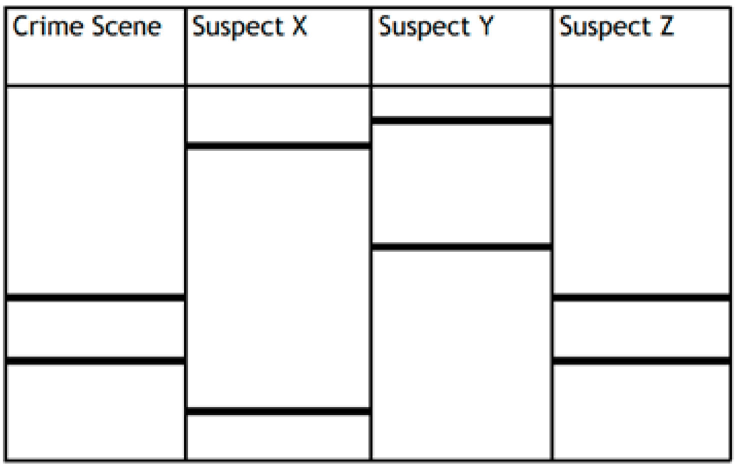


Q. Identify the father of the child from the options above.

A. **Parent D** as the last two bands of the child not belonging to the mum match up.

The first two bands of the child belong to their mother.

Solving Crimes Gel Electrophoresis



Only **suspect Z's** DNA is found at the crime scene.

The other two suspects can be eliminated from enquires.

3. The Genome & RNA

The genome is the **entire hereditary information** in our DNA.

Genome

- Genes
  - **Small %** of eukaryote genome
    - **Exons** (coding)
      Produce specific proteins
    - **Introns** (non coding)
      1. Regulate transcription
      2. Transcribed but not translated
- Other DNA Sequences
  - **Large %** of eukaryotic genome
    - **Non coding** regions of DNA

Differences between DNA and RNA

DNA	RNA
Double stranded	Single stranded
Deoxyribose sugar	Ribose sugar
2 strands of nucleotides	1 strand of nucleotides
Base Thymine	Base Uracil

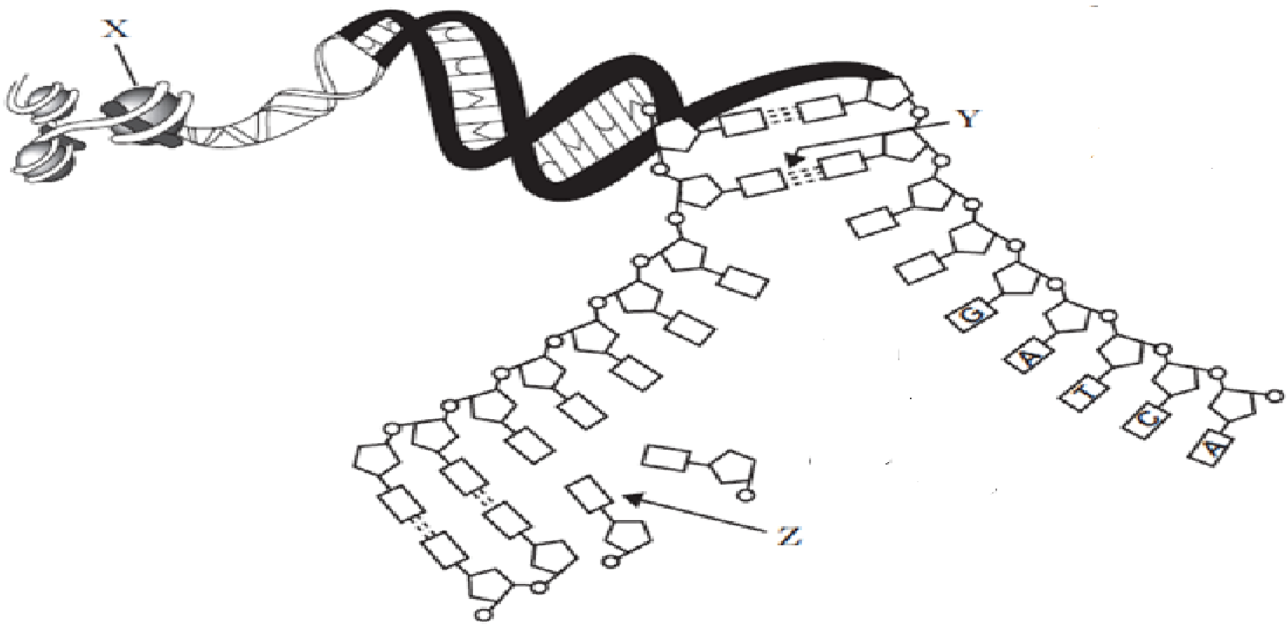
Types of RNA	Function	3 bases are called	Coding/ Non-coding for protein
mRNA	Carries a complementary copy of the DNA code from nucleus to ribosome.	CODON for 1AA	CODING
tRNA	1. binds to a specific amino acid 2. takes the amino acids to the ribosome.	ANTI CODON for 1 AA	NON– CODING
rRNA	Part of the ribosome along with protein.		NON– CODING

3. Transcription

RNA polymerase (enzyme) has two roles in transcription of DNA into primary mRNA transcripts.

1. RNA polymerase **unwinds** double helix & **breaks hydrogen bonds** between the bases on the two strands of the double helix.

2. RNA polymerase attaches free **complementary RNA nucleotides** to make the **primary mRNA transcript**.



Transcription occurs in the **Nucleus** of the cell.

DNA code $\longrightarrow$ primary transcript $\longrightarrow$ mature transcript

Primary Transcript contains:

A) **Introns** which are **non - coding** regions of the gene

B) **Exons** which are **coding regions** of the gene

Mature transcript contains:

Only exons, as the introns are removed during a process called **RNA splicing**.

Introns have 2 key roles in protein synthesis.

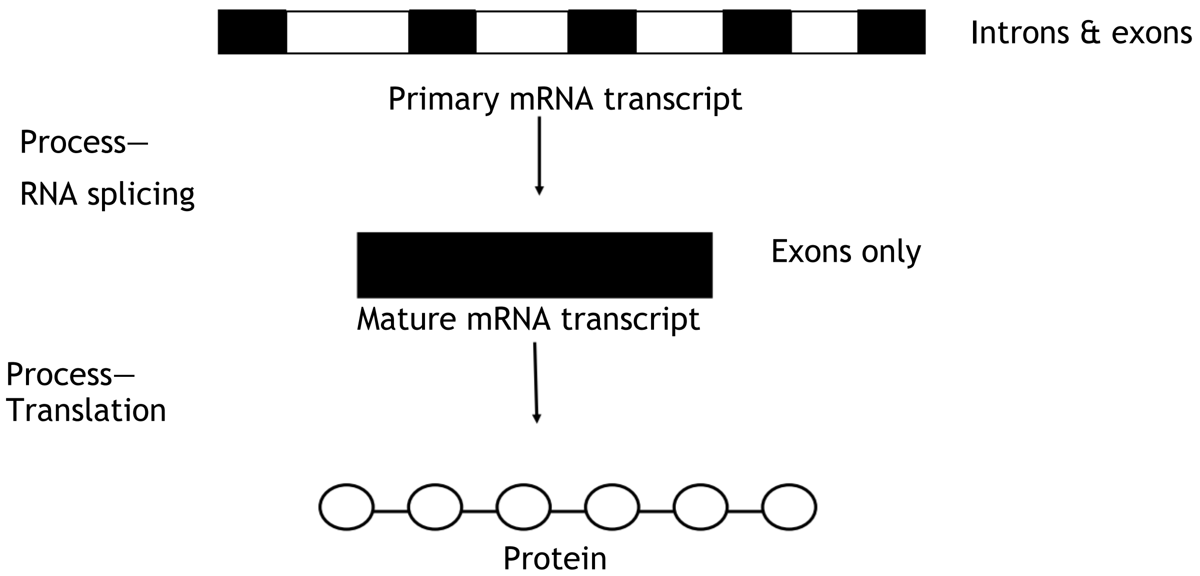
1. Transcribed but not translated.
2. Regulate transcription.

3. RNA Splicing

RNA Splicing

Introns removed from the primary transcript

The **exons** are **joined together** to form **mature mRNA transcript**.

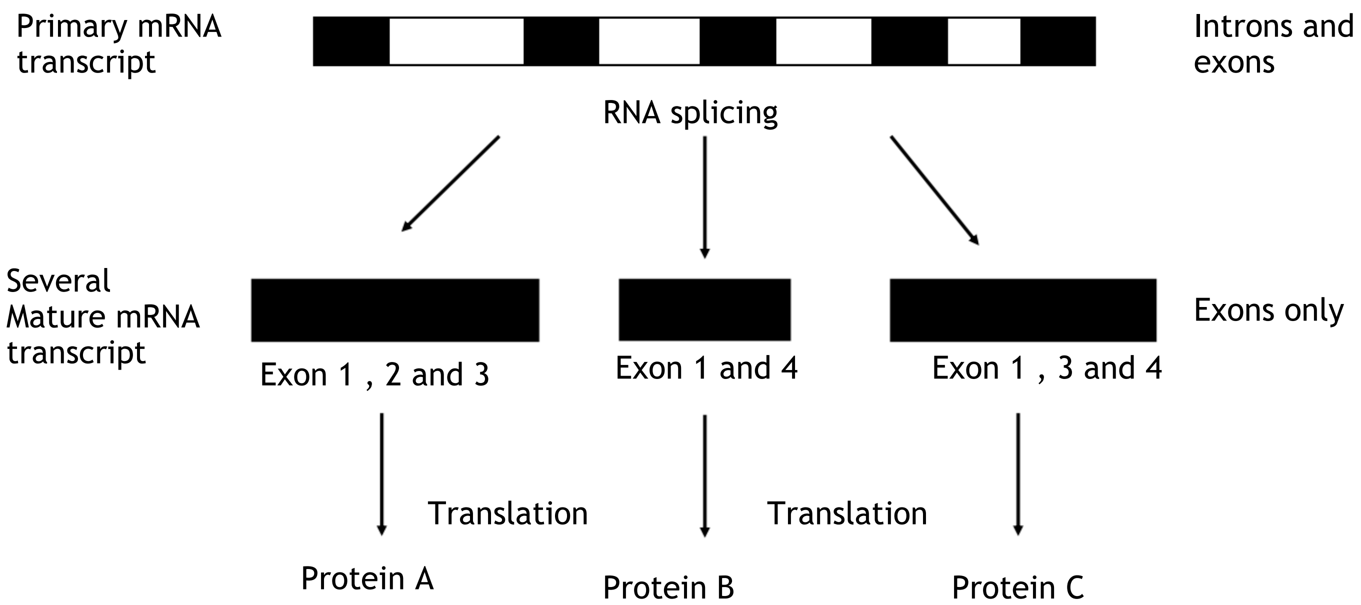


Alternative RNA Splicing

Different proteins can be expressed from **one gene**.

The introns are removed and **different combinations** of exons are spliced together, forming **alternative mature transcripts.**

Note: Note the order of the exons is unchanged during splicing.



3. Types of RNA

There are three types of RNA.

1. mRNA → Made from coding regions called **exons**
2. rRNA
3. tRNA

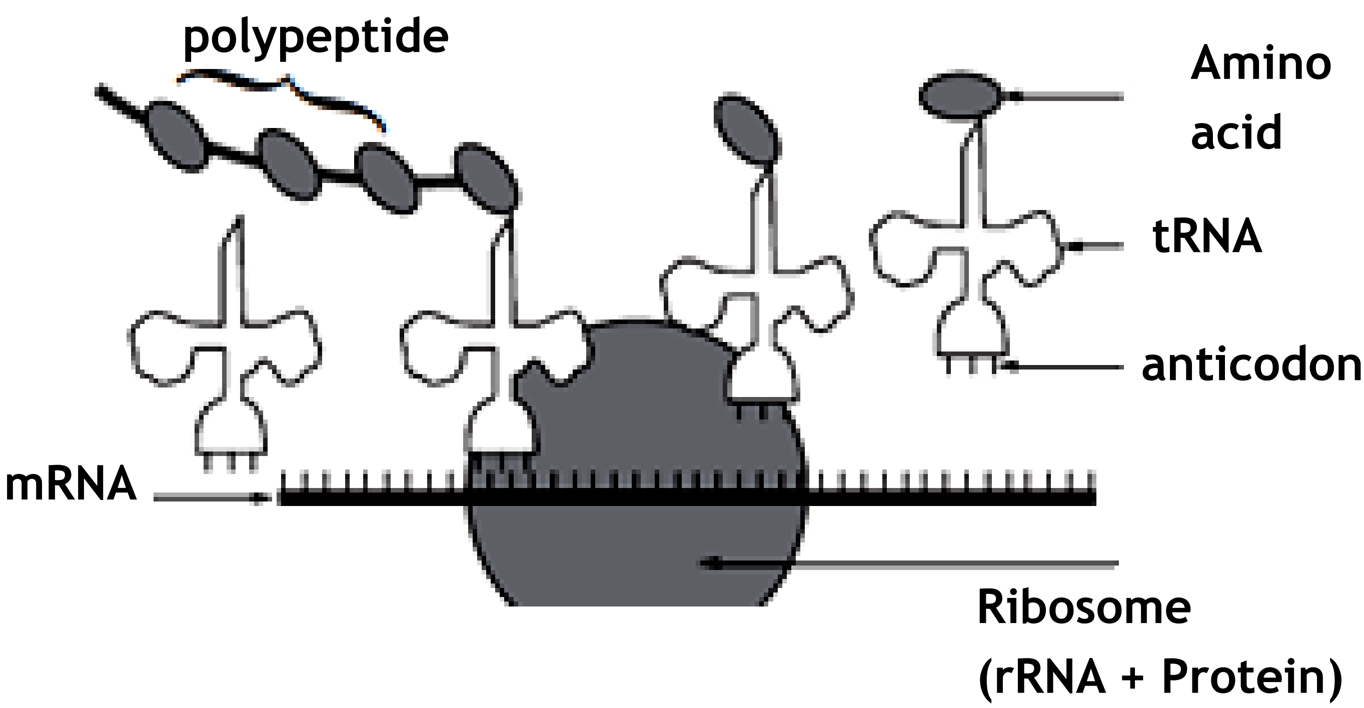
$\left.\begin{array}{l}\text{2. rRNA}\\ \text{3. tRNA}\end{array}\right\}$ Made from non - coding regions called **introns**

1. mRNA

Messenger RNA (mRNA) carries a complementary copy of the DNA code from the nucleus to the ribosome.

2. rRNA

Ribosomal RNA (rRNA) and proteins form the ribosome.



3. Types of RNA

There are three types of RNA.

1. mRNA → Made from coding regions called **exons**
2. rRNA
3. tRNA

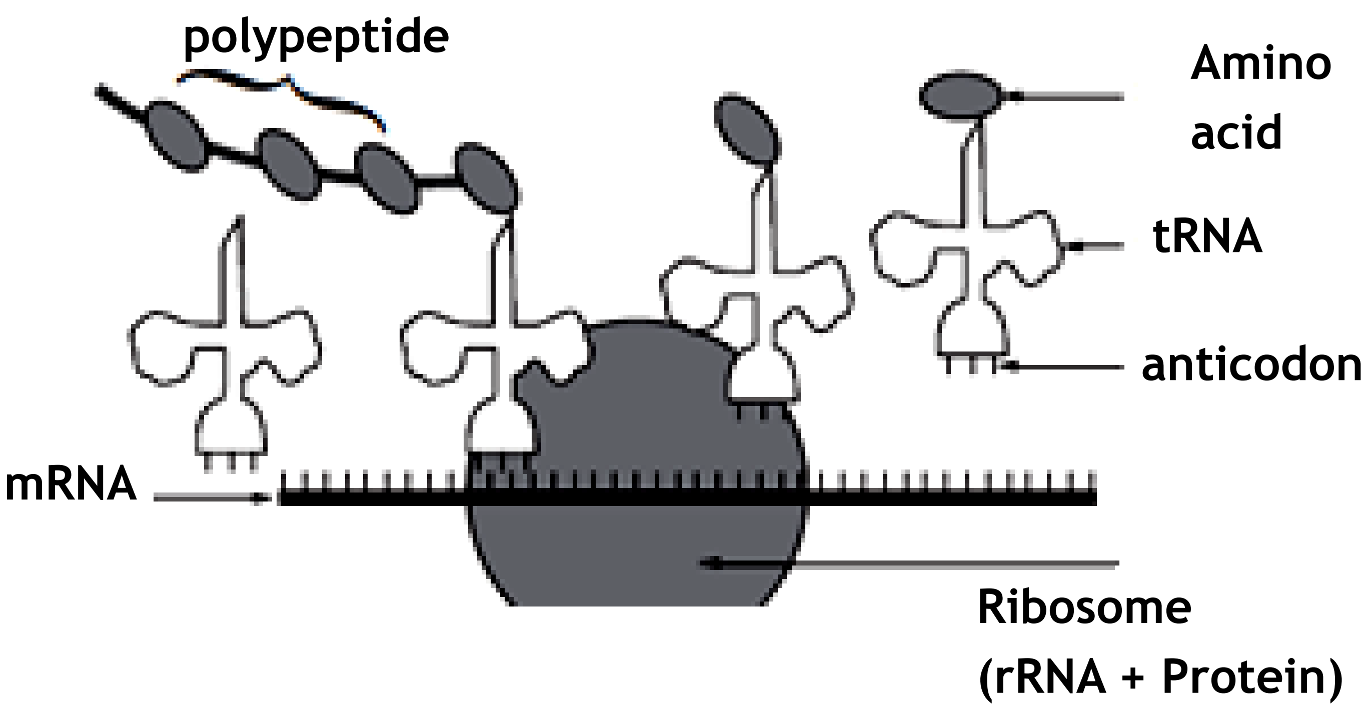
(rRNA and tRNA) Made from non - coding regions called **introns**

1. mRNA

Messenger RNA (mRNA) carries a complementary copy of the DNA code from the nucleus to the ribosome.

2. rRNA

Ribosomal RNA (rRNA) and proteins form the ribosome.

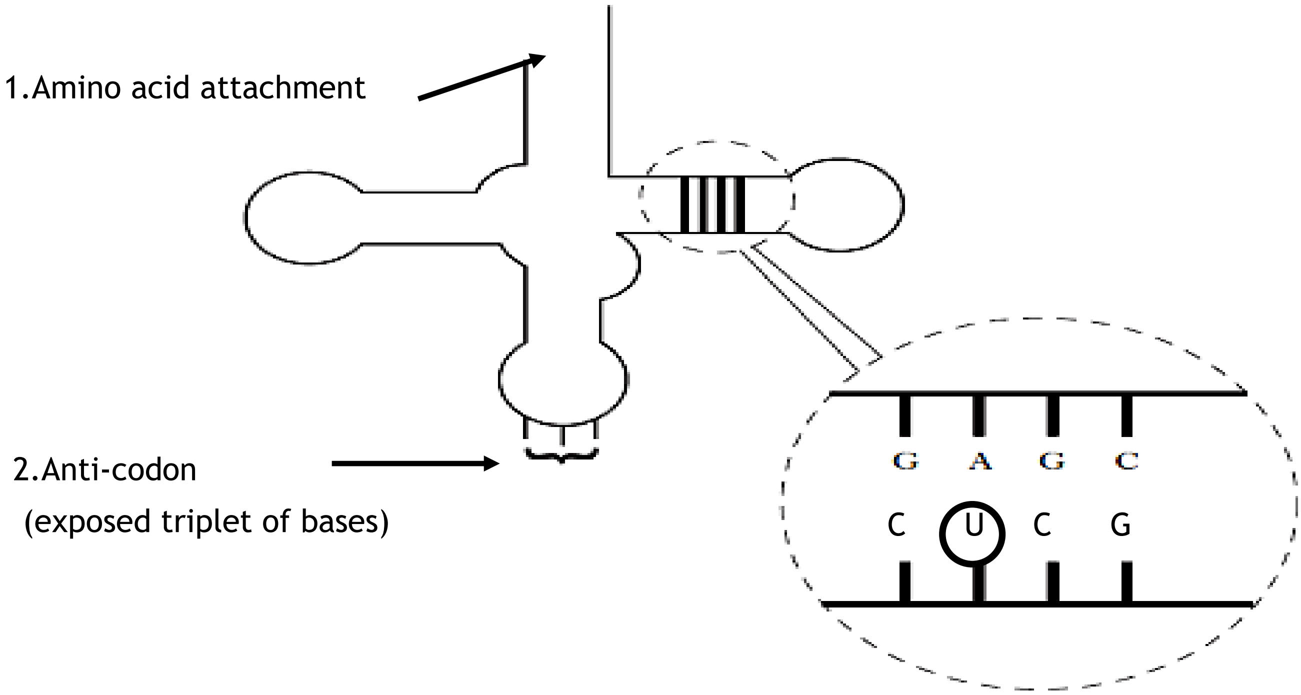


3. Types of RNA

3. tRNA

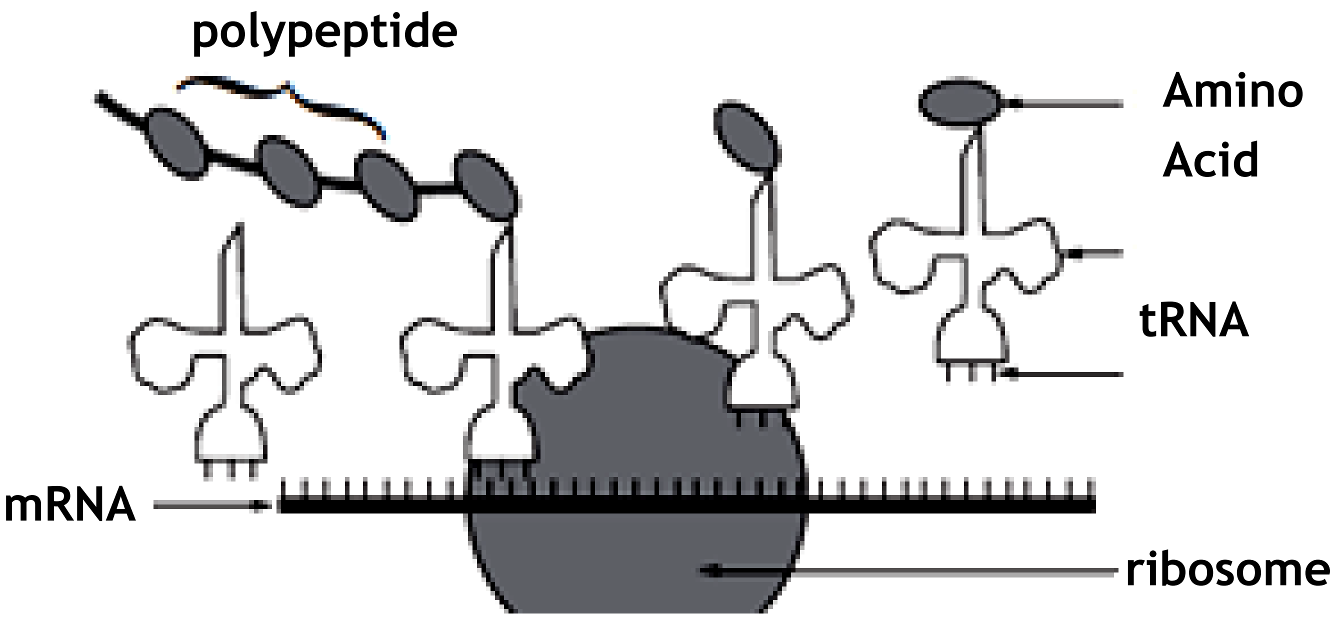
A **single stranded** molecule which is **folded** and held together by **complementary base pairs.**

tRNA is made up of 2 parts—



tRNA Function

1. **Binds** to a **specific** amino acid AND **carries** it to the **ribosome**.
2. tRNA anticodons **complementary base pair** with mRNA codons forming a **polypeptide**

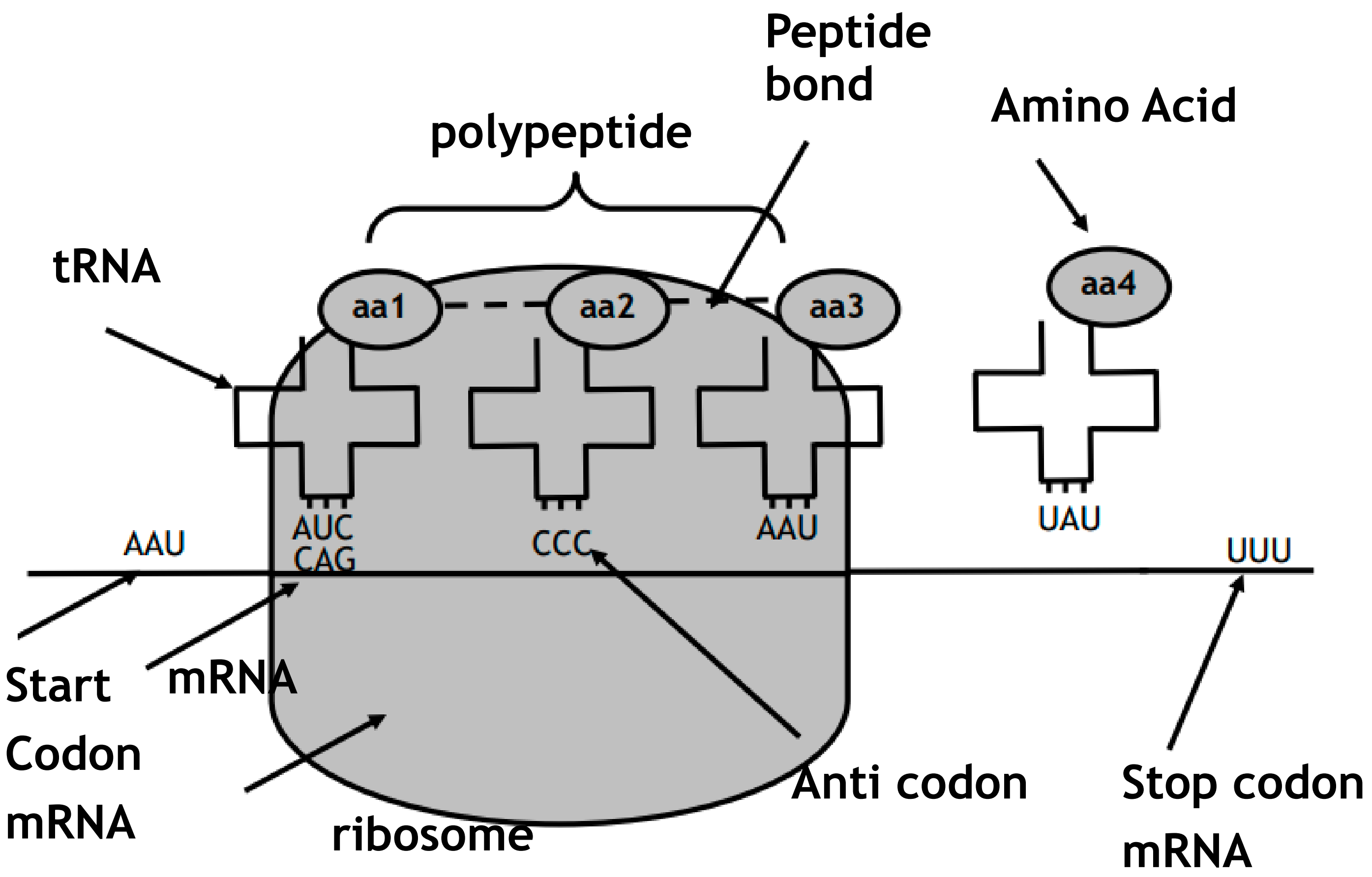


3. Translation

Translation

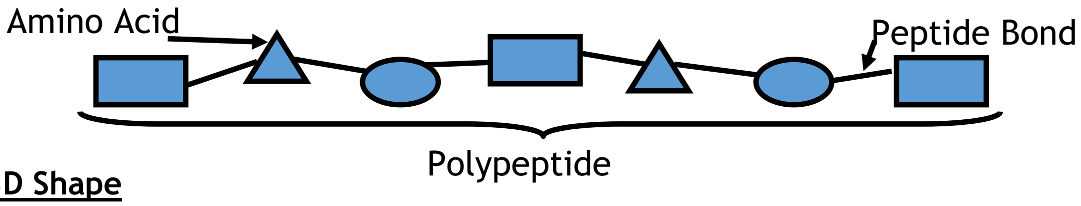
This involves the mature mRNA transcript directing protein synthesis at the **ribosome**.

1. **mRNA attaches** onto ribosome
2. tRNA **binds to a specific amino** acid and **takes it** to the ribosome
3. Translation begins at a **start codon** and ends at a **stop codon**.
4. **Anticodons** on tRNA bond to **codons** on mRNA by complementary base pairing
5. This lines the amino acid in a **specific sequence** forming a polypeptide.
6. **Peptide bonds** join the amino acids together.
7. Each tRNA then **leaves the ribosome** as the polypeptide chain is formed.



3. Protein Folding

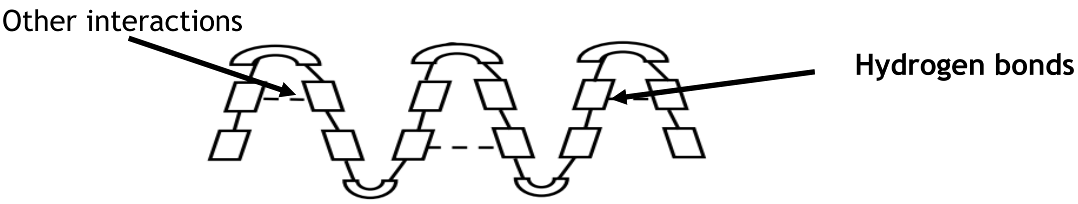
Amino acids are linked by **peptide bonds** to form **polypeptides.**



3D Shape

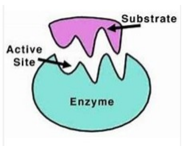
Polypeptide chains **fold** to form the **3D shape** of a protein.

These 3D shapes are held together by **hydrogen bonds** OR **other interactions** between individual amino acids.

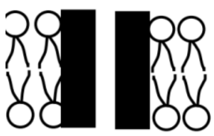


Proteins have a **large variety of shapes** which determines their **functions.**

Enzymes



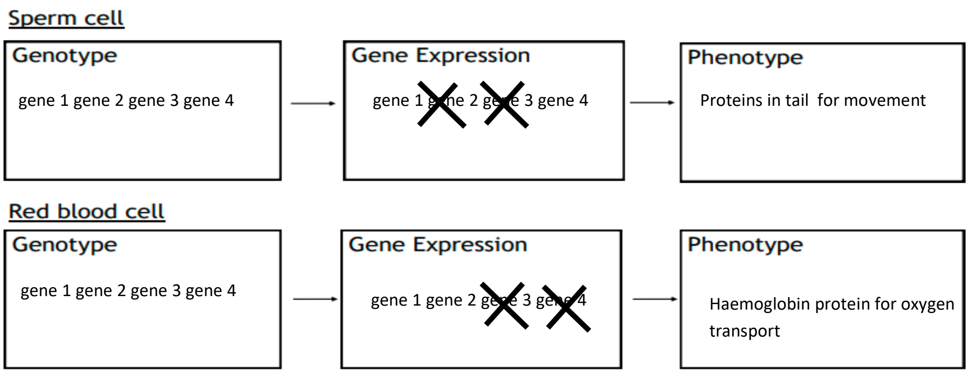
Pore (diffusion)



Pump (active transport)

Gene Expression

All cells contain the **same genes.** However only a **small percentage** are actually **expressed** in any one cell through a process called **cellular differentiation**



Phenotype is determined by

1. **Proteins** produced as a result of **gene expression**
2. **Environmental factors** also affect gene expression

4. Mutations

Mutations

<u>Changes</u> in the DNA that can result in **<u>no/altered protein</u>** being synthesised.

1. **<u>Single gene mutations</u>** - Changes to the DNA nucleotide **<u>base</u>** sequences

2. **<u>Chromosome structure mutations</u>** - Changes to a **<u>section of a chromosome</u>** (gene order).

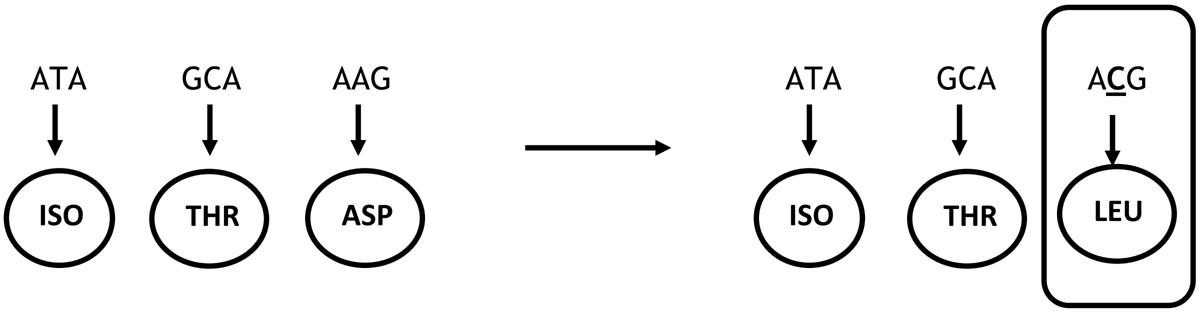
<u>Single gene mutations (SID)</u>

1. **Substitution—3 types**

1.1 Missense mutation

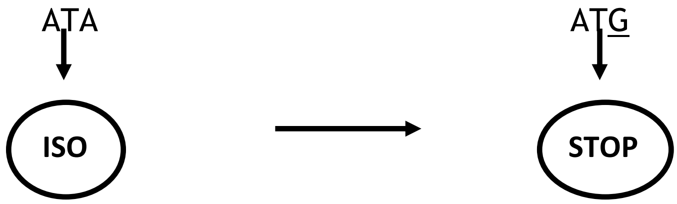
<u>Affects one codon/amino acid</u>.

Result - **<u>non-functional</u>** OR **<u>little effect</u>** on the protein.



1.2 Nonsense mutation

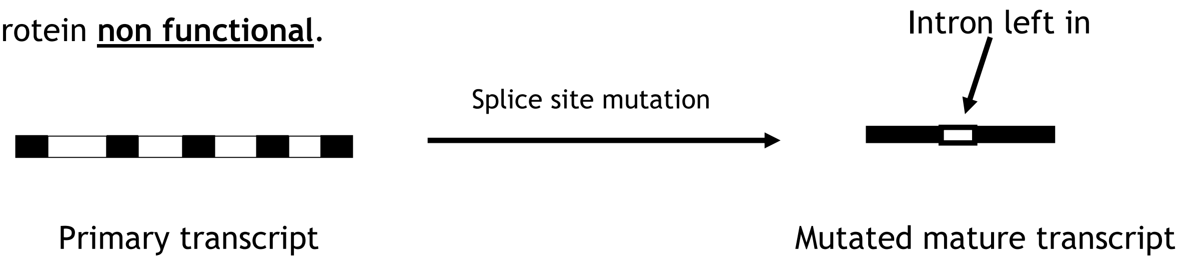
Results in a **<u>premature stop codon</u>** being produced which results in a protein that is **<u>too short</u>**. Protein **<u>non functional</u>**.



1.3. Splice-site Mutation

Result in some **<u>introns being retained</u>** and/or **<u>exons not being included</u>** in the mature transcript.

Protein **<u>non functional</u>**.



4. Single gene Mutations

2. **Insertion mutation frameshift**

A **base** has been **added** into the base sequence.

ATA GCU GAT TAA

ATA GCU GCA TTA A

3. **Deletion mutations frameshift**

A **base** is **removed** from the base sequence

ATA GCU GAT TAA

ATA GCU GTT AA

Frameshift mutations

Cause—**insertion or deletion mutations**

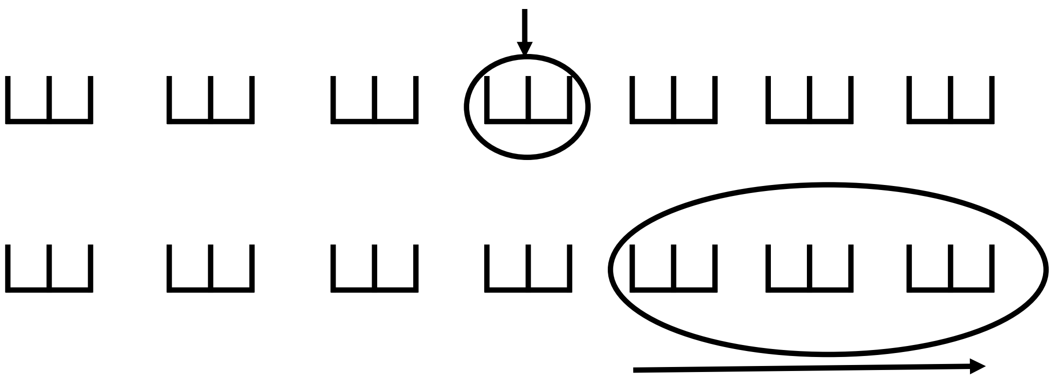
Effect on base sequence

All of the **codons/amino acids after** the mutation are changed.

This has a **major effect** on the structure of the protein produced & is **non functional**.

Remember 1 codon (triplet of bases) codes for 1 amino acid

Insertion/deletion mutation



Affects **ALL** codons **AFTER** mutation

4. Chromosome Structure Mutations

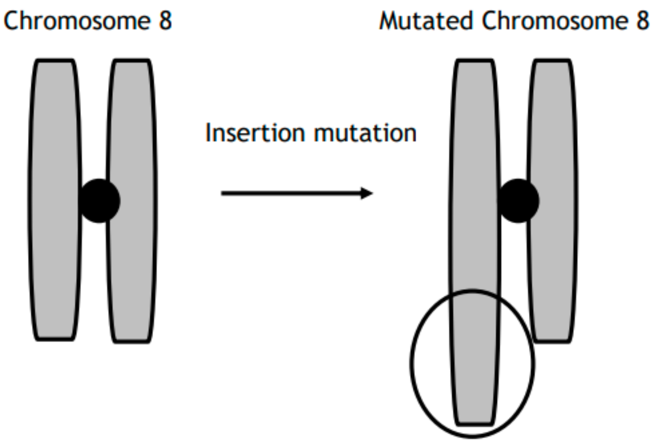
Chromosome Mutations (TIDD)

Th**e substantial changes** in chromosome mutations often make them **lethal.**

Duplication

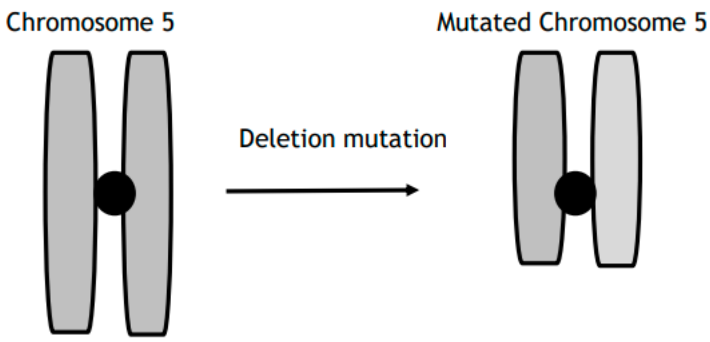
A section of a chromosome is **added** from its **homologous partner**.

C and D have been duplicated.



Deletion

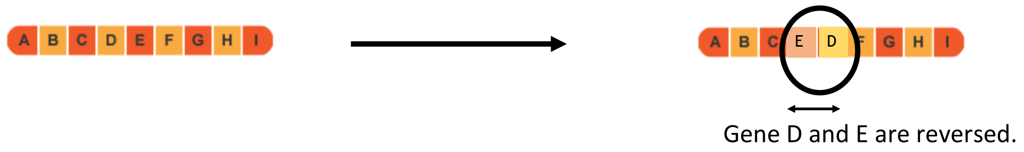
Deletion is where a section of a chromosome is **re-** **moved.**

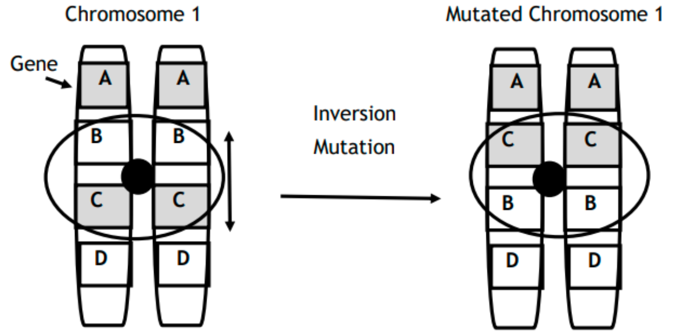


4. Chromosome Structure Mutations

Inversion

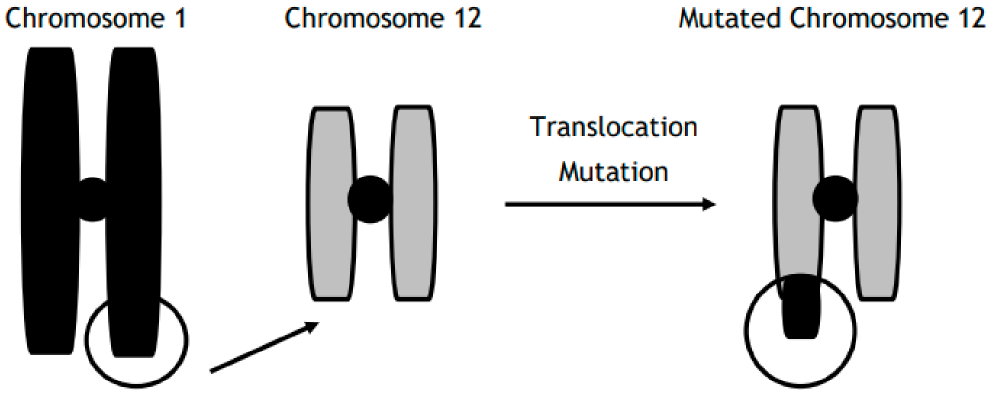
Inversion is where a section of chromosome is **reversed.**





Translocation

A section of a chromosome is **added** to a chromosome from a **NON homologous partner**.



Duplication - Importance in Evolution

Allows potential **beneficial mutations** to occur in a duplicated gene whilst the **original gene** can still be **expressed** to produce its protein.

5. Genomic Sequencing

Genomic Sequencing

The sequence of nucleotide bases can be determined for **individual genes** or **entire genomes**.

Bioinformatics

To compare sequence data, **computer** and **statistical analyses** (bioinformatics) are required.

Bioinformatics

Computer programs can be used to identify base sequences by looking for **sequences similar to known genes.**

Pharmacogenetics

Analysing an individuals genome.

This allows personalised medicine to be created to;

1. Determine the **likelihood** of developing certain diseases.

2. Used to choose the **most appropriate drug and dosage** to treat disease (**pharmacogenetics**).

Side effects

Personalised medicine is needed to make sure that patients have no side effects and the drug is beneficial to the patient.

Side effects Beneficial	No side effect Beneficial
Side effects Not Beneficial	No side effect Not Beneficial

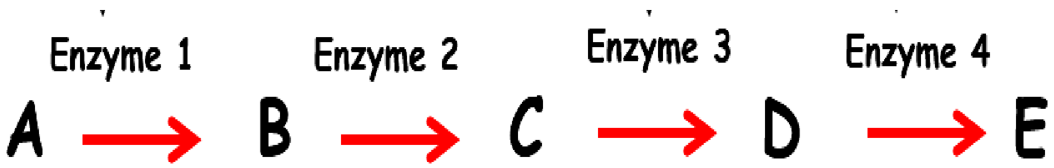
6. Metabolic Pathways

Metabolic Pathways

Integrated and **controlled** pathways of **enzyme-catalysed reactions** within a cell.

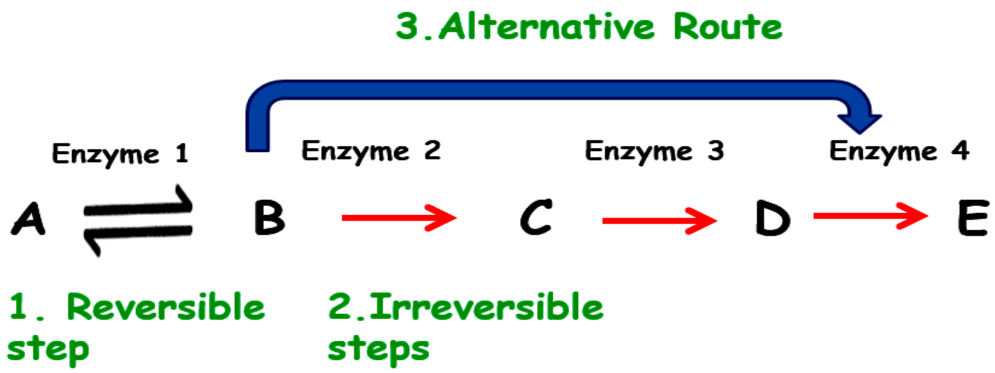
Metabolic Pathways

Each step in a metabolic pathway requires a **specific enzyme.**

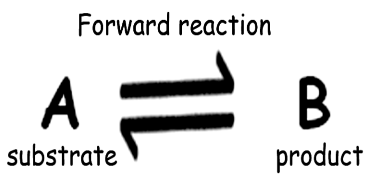


Three Steps in a metabolic Pathway

1. **Reversible** Step (2 way arrow allowing forward and backward reaction)
2. **Irreversible** Step (1 way reaction
3. **Alternative route** (skips certain steps but produces same molecule regardless)



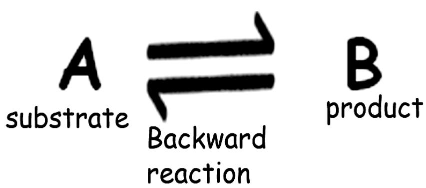
Substrate & Product Concentration in Reversible reactions



Forward Reaction of A to B is promoted by:

High substrate concentrations (A)

Low product concentration (B)



Backward Reaction of B to A is promoted by:

High product concentrations (B)

Low substrate concentration (A)

6. Metabolism and Enzymes

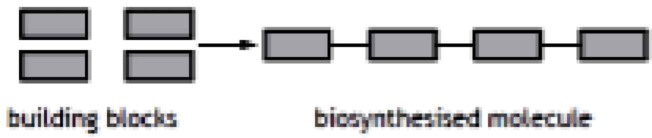
Types of Metabolic Reactions

1. Catabolic reactions **breakdown** larger molecules into smaller ones **RELEASING energy.**

   Example glycogen/starch → glucose protein → amino acids

2. Anabolic reactions involve the **BIOSYNTHESIS** of larger molecules into smaller ones **REQUIRING** energy to undertake this process.

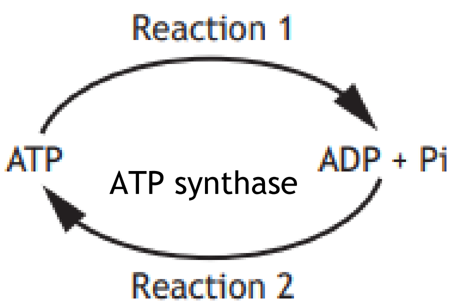
   Example glucose → starch amino acids → polypeptides (proteins)



ATP Example

Reaction 1: ATP is broken down is **catabolic** and **releases** energy.

Reaction 2: ATP is synthesized by the enzyme ATP synthase. **Anabolic** and **requires** energy.

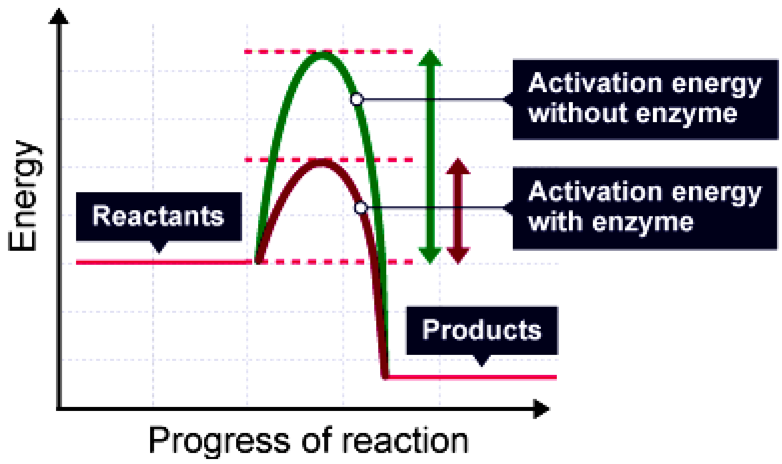


6. Enymes

Activation Energy

The **energy** required to **BREAK chemical bonds** in the reactants to allow products to be made.

Enzymes speed up reactions as they **lower the activation energy** required to form products .



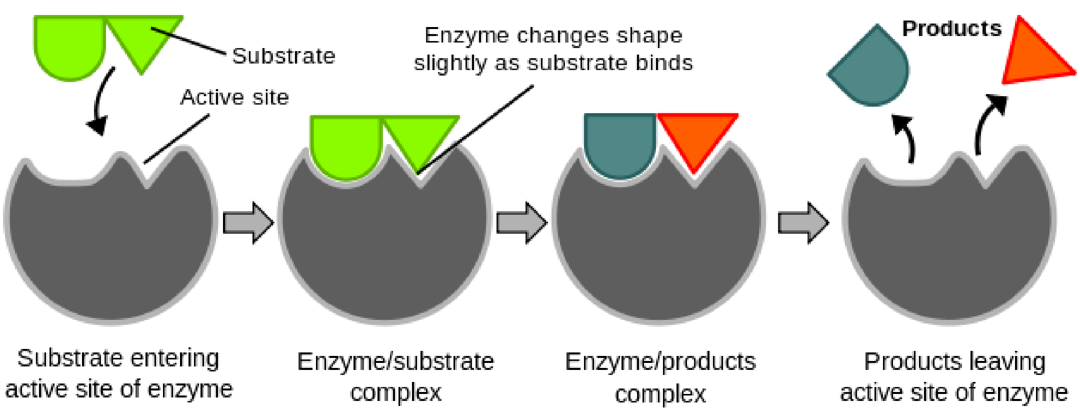
Induced Fit model

After the **substrate has bound** to the active site, the **ACTIVE site changes shape** to better fit the substrate.

Affinity for Active site

Substrate—**high affinity** for active site

Product—**low affinity** for active site



6. Substrate Concentration Graphs

Substrate Concentration

1. Low substrate concentration = Low enzyme activity

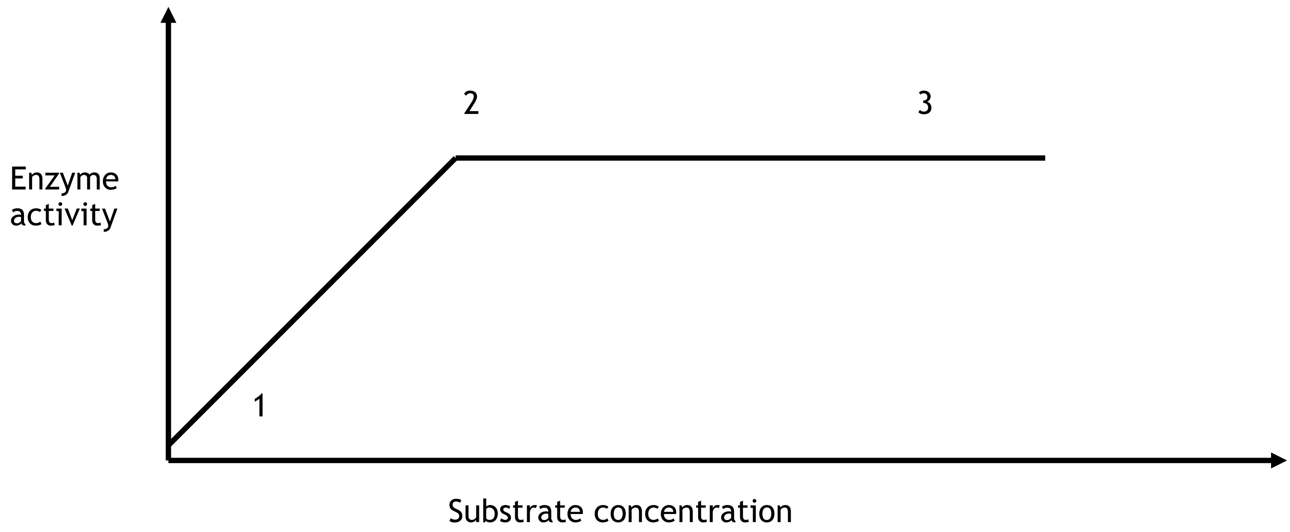
There are not enough substrate molecules to fill all the active sites.

2. High substrate concentration = Higher enzyme activity

<u>All</u> active sites are filled by substrates due to increased concentration of substrates.

3. Very High substrate concentrations = No further increase in enzyme activity

Enzyme working at maximum and all active sites are filled by substrates.
No further increase in reaction rate.



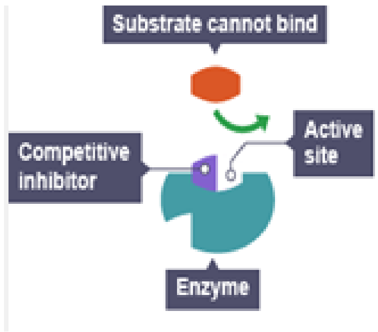
6. Inhibitors

Inhibitors

Inhibitors reduce enzyme activity.

3 types of enzyme inhibitors

1. Competitive Inhibitors 2. Non Competitive Inhibitors 3.Feedback Inhibition



Competitive Inhibitors

Bind at the active site and prevent substrate from binding.

Competitive inhibitor molecule resembles substrate.

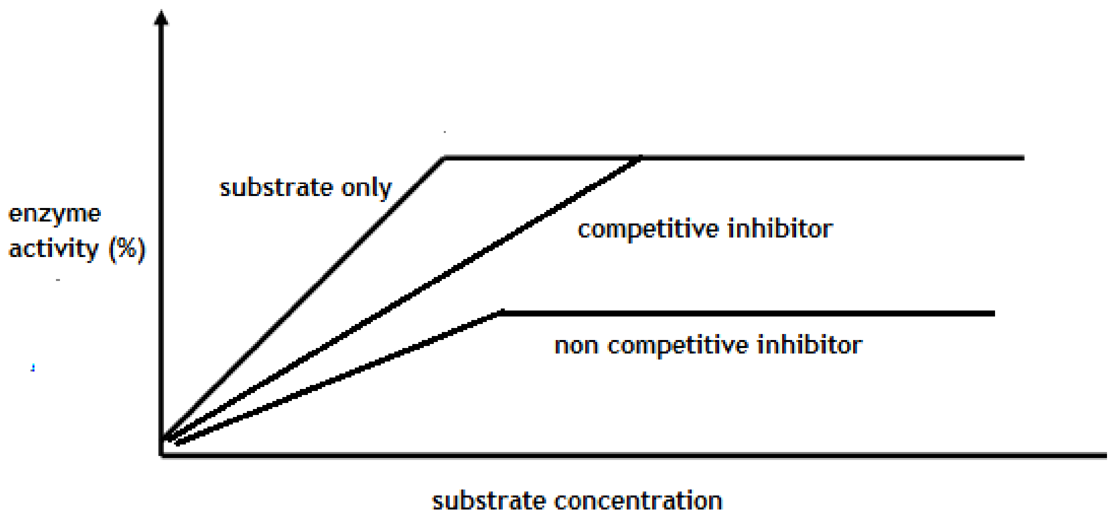
Inhibition reversed with increasing substrate concentration.

Non competitive Inhibitors

Bind AWAY from active site and **change shape** of active site preventing substrate from binding.

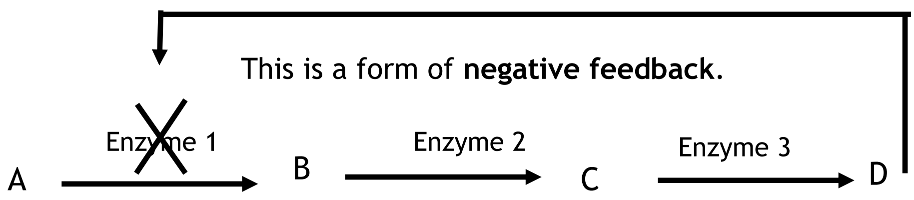
Action irreversible—**no effect** when increasing substrate concentration.

Enzyme Inhibitor Graph



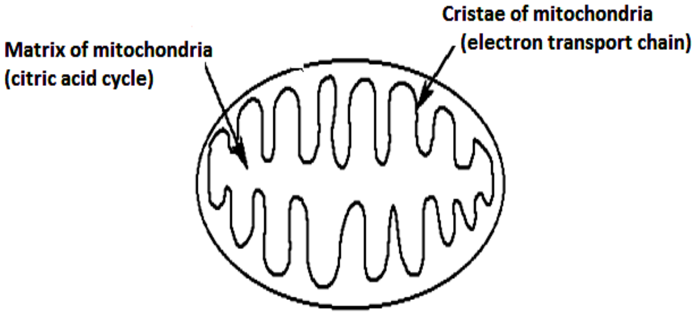
Feedback Inhibition

When the end product concentration reaches a **critical concentration** (too high), it binds to an **earlier enzyme** in the pathway, preventing its own synthesis. **Saves ATP**.



7. Respiration

Stages of respiration



1. Glycolysis (**<u>cytoplasm</u>**)

2. Citric Acid Cycle (Kreb Cycle)
   (**<u>matrix of mitochondria</u>**)

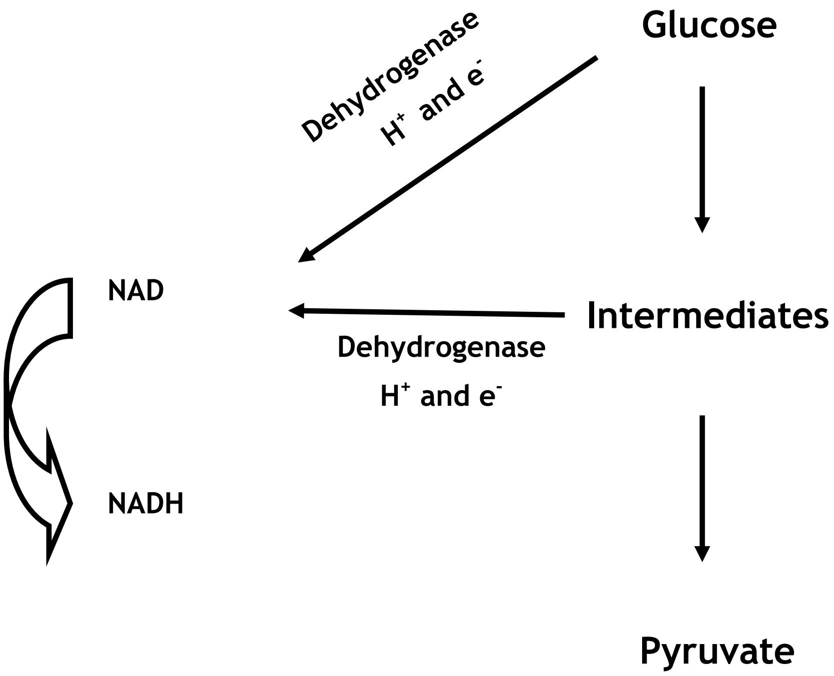
3. Electron Transport Chain
   (**<u>cristae/inner mitochondria membrane</u>**)

ATP production

The <u>majority of the ATP</u> is produced during the **<u>electron transport chain</u>** although **ALL stages** generate some ATP.

<u>Glycolysis</u>

Location—cytoplasm Process does **<u>not require oxygen</u>** **<u>Net</u>** <u>gain</u> **<u>of 2ATP</u>**



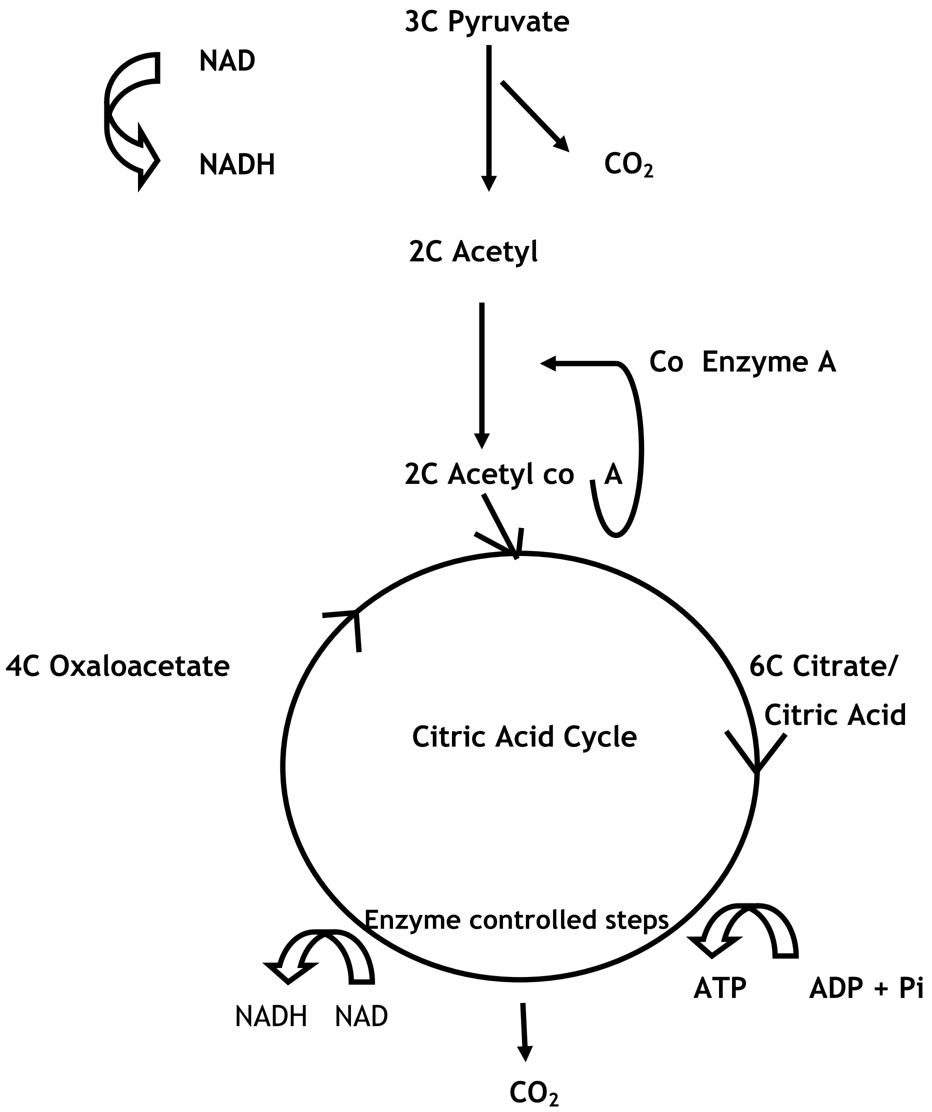
1. **Energy Investment Stage**
   2 ATP IN to p<u>hosphorylate</u>
   glucose & intermediates

2. **Energy Payoff stage**
   4 ATP produced after 2 ATP in
   = **Net gain of 2 ATP**

7. Aerobic Respiration

Aerobic Stage of Respiration

Process **requires oxygen** to move beyond pyruvate and is **controlled by enzymes** called **dehydrogenases**.



Summary of steps

1. In aerobic conditions, **pyruvate** is broken down to an **acetyl group**.
2. Acetyl combines with recycled coenzyme A forming **acetyl coenzyme A**.
3. In the citric acid cycle, the **acetyl group** from acetyl coenzyme A combines with **oxaloacetate** to form **citrate**.
4. During a series of **enzyme-controlled steps**, **citrate** is gradually **regenerated** back into **oxaloacetate.**
5. **ATP, NADH and CO_2** are all produced during these enzyme-controlled steps.

7. Dehydrogenases and Co enzymes

Role of dehydrogenase

Removes hydrogen ions and electrons from substances and **passes to coenzyme** NAD to form NADH.

Location—**Glycolysis and Citric Acid Cycle**.

Role of Co enzymes

Accepts hydrogen ions and electrons and **takes them to the electron transport chain** on inner mitochondrial membrane.

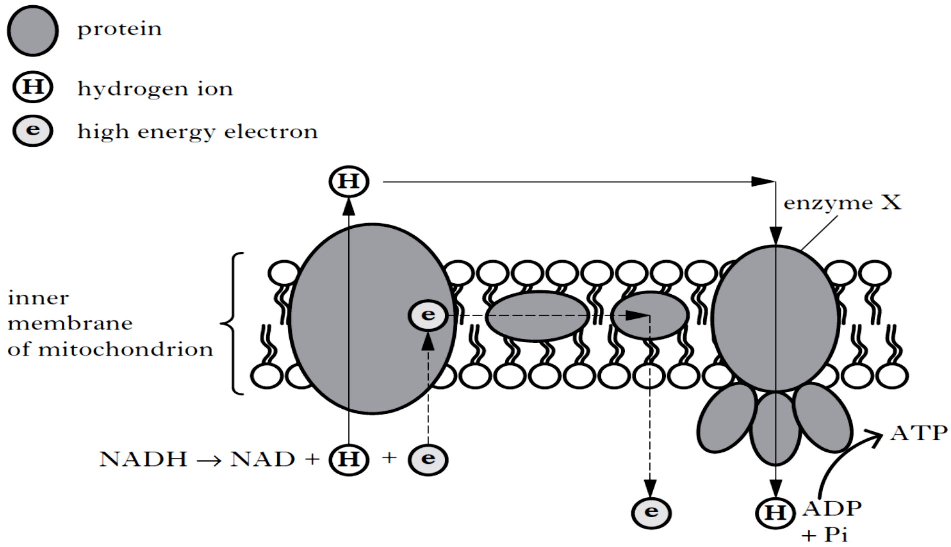
Location—**Glycolysis, Citric Acid Cycle and Electron Transport Chain**

7. Electron Transport Chain

Electron Transport Chain

The electron transport is a series of **carrier proteins** attached to the **inner mitochondrial membrane.**

Location—Inner membrane of mitochondria (Cristae).



Summary of Process

1. The co enzyme NADH **releases electrons and hydrogen ions** in the inner mitochondrial membrane.
2. **Electrons pass along** the electron transport chain and **release energy**.
3. The energy released by electrons pumps H ions across the membrane by active transport.
4. **H diffuses back across ATP synthase** causing it to rotate to **make ATP** from ADP + Pi.
5. Oxygen is the **final hydrogen ions and electron acceptor** forming **water.**
1. **Most of the ATP** produced during respiration occurs during this stage.

High/Low Cristae

Lots of folds in the inner mitochondrial membrane are needed for **active cells** as they need lots of ATP e.g. muscle/brain/sperm cells.

More folds/cristae mean **more electrons pass down chain/more H is released & more ATP is produced by ATP synthase.**

Lots Cristae/ High surface area
Lots ATP produced

Less Cristae/ Less surface area
Less ATP produced

8. Energy systems in muscles

Vigorous exercise

Muscle cells get **insufficient oxygen** to support the **electron transport chain**.

NADH ← NAD

Pyruvate ⇌ lactate.

NADH → NAD

To compensate, muscle cells convert pyruvate into lactate via the **transfer of H^+ ions** from **NADH** which **regenerates NAD .**

NAD is needed to maintain **ATP production** through **glycolysis**.

Lactate accumulates & **muscle fatigue** occurs, creating an **oxygen debt** .

The oxygen debt is **repaid** when **exercise stops**. This allows respiration to provide the energy to **convert the reverse reaction of**

lactate ⟶ **pyruvate** + **glucose (**liver)

Types of Skeletal muscle fibres

1. Slow-twitch muscle fibres

Contract relatively slowly, but can sustain **contractions for longer.**

Rely on **aerobic respiration** to generate ATP.

For **endurance** activities such as **long-distance running, cycling or cross-country skiing**

Features of slow twitch muscle fibres

(a) M**any** mitochondria

(b) **Large** blood supply

(c) **High concentration** of myoglobin (**O_2** storing protein).

8. Muscle Fibres

2. Fast- Twitch Muscle Fibres

Fast-twitch muscle fibres **contract relatively quickly**, over **short** periods.

Generate ATP through **glycolysis only**

Useful when **sprinting** or **weightlifting**

Features of Fast-Twitch Muscle Fibres

(a) **Fewer** mitochondria
(b) **Lower** blood supply compared to slow-twitch muscle fibres.
(c) **Lower** concentration of myoglobin
(d) **Glycogen** is major storage fuel

Muscle Fibre Composition

Most human muscle tissue contains a **mixture** of both slow & fast-twitch muscle fibres.

Athletes show **distinct patterns** of muscle fibres that **reflect their sporting activities**.