The big picture

? Guiding question(s)

- How does a cell produce a sequence of amino acids from a sequence of DNA bases?
- How is the reliability of protein synthesis ensured?

Keep the guiding questions in mind as you learn the science in this subtopic. You will be ready to answer them at the end of this subtopic. The guiding questions require you to pull together your knowledge and skills from different sections, to see the bigger picture and to build your conceptual understanding.

The Komondor, plural Komondorok, also known as the Hungarian sheepdog, is a large white dog with corded hair, often referred to as a 'mop' dog (**Figure 1**). Komondor hair can be around 10 inches long and forms one of the heaviest coats in the dog world. Their coats, like all dog coats, are made up of a structural protein called keratin.

Overview (/study/ap 422- cid- 755105/o

Figure 1. The incredible thick coat of Komondorok is made up of protein.

Credit: Sue Thatcher, Getty Images

Proteins are also essential to the human body, being responsible for many processes such as growing, healing, forming cell structures, carrying oxygen, protecting against disease, growing hair and nails, allowing eyesight, providing energy and more. There are thousands of different proteins in the human body – complex biomolecules made up of 20 different building blocks (amino acids). How is it possible that so many different combinations are made correctly?

Prior learning

Before you study this subtopic make sure that you understand the following:

- The structure of nucleic acids (see subtopic A1.2 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43236/)).
- The structure and function of proteins (see subtopic B1.2 (/study/app/bio/sid-422-cid-755105/book/big-picture-id-43531/)).
- How enzymes work and their role in metabolism (see subtopic C1.1 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43208/)).

D1. Continuity and change: Molecules / D1.2 Protein synthesis

Transcription

D1.2.1: Transcription D1.2.2: Role of hydrogen bonding and complementary base pairing in transcription D1.2.3: Stability of DNA templates

Student view

Overview (/study/ap 422-cid-755105/o

Learning outcomes

By the end of this section you should be able to:

- Describe transcription as the synthesis of RNA using DNA as a template.
- Describe the use of hydrogen bonding and complementary base pairing in transcription and the replacement of thymine with uracil in RNA.
- Describe how DNA used as a template for transcription, remains stable and unchanged.

After you've eaten some food and digested it, amino acids along with the other nutrients from your last meal will begin circulating through your body via your bloodstream. The amino acids are then absorbed into your cells where they will act as the building blocks of new proteins. Where does this process start?

Transcription: the synthesis of RNA using a DNA template

DNA is your cell's set of instructions to build any protein it might need. The first step in this process is transcription. This is the production of messenger RNA (mRNA) using your DNA as a template. As DNA is kept in the cell nucleus in eukaryotic cells, transcription must take place there as well. In prokaryotes transcription takes place in the cytoplasm.

As in DNA replication, enzymes are involved in protein synthesis. The enzyme responsible for transcription is RNA polymerase (**Figure 1**). Transcription occurs in three stages. In the initiation stage RNA polymerase binds to the DNA at the start of a gene. It then separates the two strands of the DNA by breaking the hydrogen bonds, exposing the bases. During the elongation stage, RNA polymerase builds a molecule of mRNA on one of the strands of DNA. The strand used is known as the template or antisense strand, while the other strand is known as the coding or sense strand. The RNA polymerase moves along the DNA reading it one base at a time, adding free RNA nucleotides to the growing mRNA. Finally at the termination stage, a terminator sequence in the DNA is reached and the mRNA is released. The RNA polymerase detaches from the DNA strand, allowing the two strands to come together again.

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/big-picture-id-43547/print/) Assign

Student view

Overview (/study/ap 422- cid- 755105/o

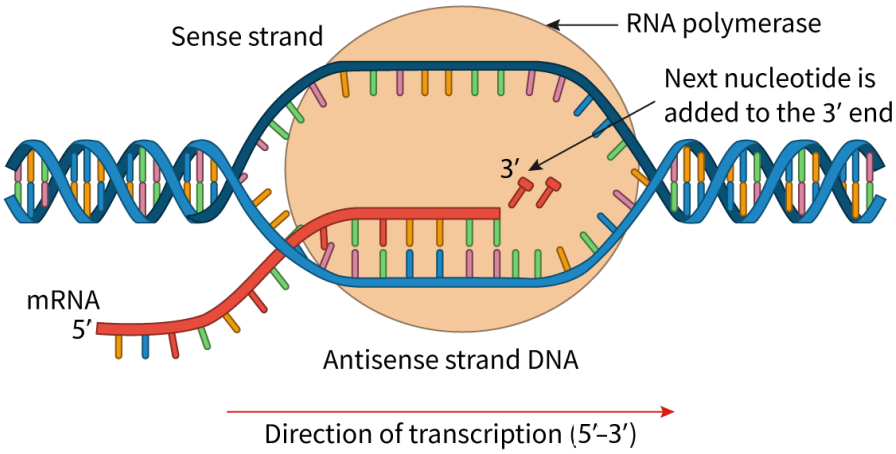


Figure 1. DNA transcription.

More information for figure 1

The image is a diagram illustrating the process of DNA transcription. It shows a segment of a DNA double helix partially unwound. In the center, an open section of the DNA is surrounded by a circular area indicating the active site of transcription. Here, the two strands of DNA are separated, and the bases are exposed.

A red strand representing mRNA is being synthesized by the RNA polymerase. The mRNA is complementary to one of the DNA strands, known as the template strand. This new mRNA strand is shown extending from the opened part of DNA.

There are labels within the image indicating the 3' end of the growing mRNA strand, and arrows suggest the direction of transcription and movement of RNA polymerase along the DNA. Additionally, there are illustrations of nucleotides being added to the mRNA strand.

[Generated by AI]

Watch **Video 1** for an overview of transcription.

Student view

Overview (/study/ap 422- cid- 755105/o

Video 1. The basics of DNA transcription.

Hydrogen bonding and complementary base pairing

RNA polymerase unzips the two strands of DNA by breaking the hydrogen bonds between the nitrogenous bases. In DNA adenine (A) is always bonded to thymine (T), and cytosine (C) is always bonded to guanine (G). RNA polymerase then adds the free RNA nucleotides along the template strand based on the complementary base pairing rule. You may recall that one of the differences between DNA and RNA is that DNA contains the base thymine while in RNA this is replaced with uracil which now pairs with adenine. This means that the RNA polymerase will add uracil to the mRNA strand when it encounters adenine on the DNA template strand (**Figure 2**).

The complementary base pairing rule continues to be essential to the functioning of transcription just as it is for DNA replication. It is only through the base pairing rule that the correct placement of bases, which makes up the code or message within these molecules, can be assured. When the correct RNA nucleotide is placed by RNA polymerase, it will temporarily form hydrogen bonds with the complementary base on the DNA template strand. Two hydrogen bonds form between A and T/U and three hydrogen bonds form between C and G.

Student view

Overview (/study/ap 422- cid- 755105/o

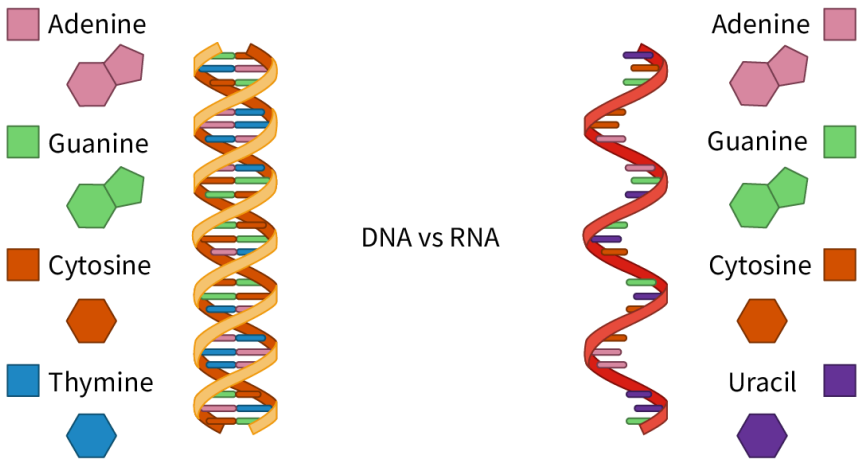


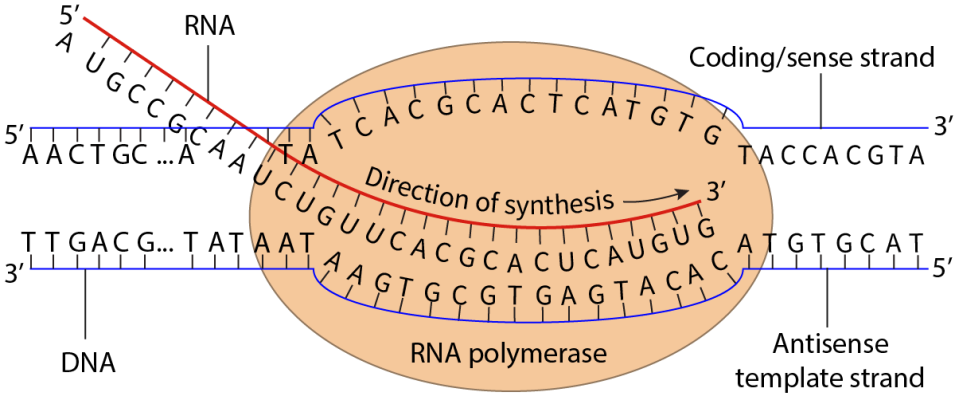
Figure 2. A comparison between DNA and RNA.

More information for figure 2

The image shows a side-by-side comparison of DNA and RNA structures. On the left, there is a DNA double helix with a ladder-like twist, with colored shapes representing different nucleotide bases: Adenine (pink squares), Thymine (blue hexagons), Guanine (green pentagons), and Cytosine (orange hexagons). On the right, RNA is illustrated as a single helix with similar base structures, but instead of Thymine, it has Uracil (purple hexagons) paired with Adenine. The depiction helps visualize base pairing rules, where Adenine pairs with Thymine (or Uracil in RNA) and Cytosine pairs with Guanine. The image highlights structural differences between DNA's double helix and RNA's single helix and the substitution of Uracil for Thymine in RNA.

[Generated by AI]

It is possible to determine the sequence of bases on either strand of DNA or the mRNA produced by the RNA polymerase using the base pairing rule (**Figure 3**).



Student view

Overview (/study/app/bio/sid-422-cid-755105/o

Figure 3. Transcription and the relationship between base sequences.

More information for figure 3

The diagram illustrates the process of DNA transcription, focusing on the relationship between base sequences in DNA and RNA. The image features two strands of DNA: the coding/sense strand and the antisense/template strand. Arrows and labels indicate the direction of synthesis by RNA polymerase. The antisense strand is shown with sequence T-A-C-C-A-C-G-T-A, and the corresponding RNA sequence A-U-G-G-U-G-C-A-U is generated through base pairing rules. The RNA is synthesized in the 5' to 3' direction. The coding strand, shown in blue, reads from 5' to 3' and is parallel to the antisense strand. The RNA polymerase enzyme is depicted as an oval where base pairing occurs. Key labels include 'RNA', 'DNA', 'Coding/sense strand', and 'Direction of synthesis', providing a visual representation of transcription dynamics.

[Generated by AI]

For example, if the template or antisense strand of DNA had the following sequence of bases:

ATCGGCTATTAGCCGCTATCGATGATGCTAGCTTAGCTA

the base sequence on the coding or sense strand, which is complementary to the template strand would be:

TAGCCGATAATCGGCGATAGCTACTACGATCGAATCGAT

In addition, the base sequence of the mRNA produced by the RNA polymerase using that template strand would be:

UAGCCGAUAAUCGGCGAUAGCUACUACGAUCGAAUCGAU

Making connections

See section A1.2.8—10 (/study/app/bio/sid-422-cid-755105/book/complementary-base-pairing-id-43801/) to learn about the role of complementary base pairing in allowing genetic information to be replicated and expressed.

Student view

Overview (/study/ap 422-cid-755105/o

Stability of DNA templates

It is important that the DNA strands are stable and remain unchanged by the transcription process. The DNA within a cell is often transcribed many times and, for cells that do not go through regular cell divisions, the DNA needs to remain intact throughout the life of the cell. If the DNA was to be degraded by the transcription process it would not be able to continue producing functioning proteins, which could stop the cell from functioning and even lead to the cell dying.

Try the activity to practise determining mRNA and DNA base sequences.

Activity

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Thinking skills — Providing a reasoned argument to support conclusions
- **Time required to complete activity:** 15 minutes
- **Activity type:** Individual/pair activity

Due to the complementary base pairing rule, you should be able to deduce the sequence of bases in either strand of DNA or the mRNA strand given any other.

Work out the missing base sequences using the base sequences given in the following questions.

1. If the following DNA sequence is the sense or coding strand, what would the resultant mRNA base sequence be?

   TTGACGAACTATTTGACAAAACCATGTGA

2. If the following is the mRNA sequence, what would the resultant DNA base sequence of the antisense or template strand be?

   UAGGAUACCCUUAGGCUCGUGCUCAAUUGCCC

3. If the following is the mRNA sequence, what would the resultant DNA base sequence of the sense or coding strand be?

   AUGGGCACUUGCCAACGUGGCUCGAGAUCUGC

4. You will need three index cards or pieces of paper. On each one you will be creating a base sequence of between 20 and 30 bases. On the first one, create a DNA coding strand. On the second, create a DNA template strand and on the third create a mRNA

Student view

Overview (/study/ap 422-cid-755105/o

sequence. When finished, exchange these with a partner to solve for the other two strands for each.

5 section questions

Translation

D1.2.4: Transcription as a process required for the expression of genes D1.2.5: Translation
D1.2.6: Roles of mRNA, ribosomes and tRNA in translation

Learning outcomes

By the end of this section you should be able to:

- Explain the use of transcription and its control of gene expression.
- Describe translation as the use of the mRNA produced in transcription to synthesise polypeptides.
- Describe the roles of mRNA, ribosomes and tRNA in translation.

Almost every cell in your body has a complete copy of your DNA in its nucleus and therefore has the instructions to produce every protein required by your body. However, we do not want all of our cells making all proteins all of the time. That would be a tremendous waste of resources and energy. Also, being complex multicellular organisms, our cells are highly specialised and are designed to carry out specific functions, requiring only a specific number of the proteins found in our genetic code.

In each cell of our body only some of the over 20 000 genes within our DNA are expressed. But what determines whether or not a gene is expressed and that protein is produced?

Transcription as a process required for the expression of genes

Gene expression is the process by which the information coded in the genes is used to synthesise proteins. Cells regulate the expression of genes by various mechanisms. A key stage of gene expression is transcription see section D1.2.1 (/study/app/bio/sid-422-cid-755105/book/transcription-id-46485/) as only genes (DNA sequences) that are transcribed are active

Student view

Overview (/study/app/bio/sid-422-cid-755105/o

within the cell. Transcription thus enables cells to 'switch on' (express) the genes whose products are needed at a particular time and 'switch off' (silence) other genes. It follows that by regulating transcription, cellular activities can be regulated. Transcriptional regulation also leads to cell differentiation due to the permanent switching off or on of certain genes within a cell.

Translation as the synthesis of polypeptides from mRNA

Once the mRNA is produced and it has migrated out of the nucleus into the cytoplasm in eukaryotic cells, the next step in protein synthesis can take place – translation. This is the step in which the code from the mRNA is read and used to synthesise polypeptides. This occurs at ribosomes either free in the cytoplasm or attached to the rough endoplasmic reticulum.

During translation the mRNA is read by the ribosome and using the code within the mRNA, amino acids are added in a specific sequence to form a polypeptide.

Roles of mRNA, ribosomes and tRNA in translation

There are three important components that interact to carry out translation: mRNA, ribosomes and tRNA. The mRNA brings the code from the DNA in the nucleus in its base sequence. This code has the instructions for the polypeptide to be produced. The site of translation is the ribosome. The structure of the ribosome brings the mRNA and the tRNA together in the correct orientation so that the process can occur efficiently and correctly.

The ribosome acts almost as an enzyme with multiple active sites. Ribosomes are very complex structures, consisting of proteins and ribosomal RNA molecules. Ribosomes have a small and a large subunit, with three binding sites for tRNA molecules (**Figure 1**). The mRNA binds to the small subunit, while up to two tRNAs can bind to the large subunit of the ribosome at a time. tRNA is a single-stranded RNA molecule that folds on itself to form a cloverleaf-shaped structure with double-stranded regions and three hairpin loops (**Figure 2**). Each tRNA has a specific corresponding amino acid attached. When a tRNA recognises and binds to its corresponding code on the mRNA in the ribosome, the tRNA transfers the appropriate amino acid to the end of the growing polypeptide where a peptide bond is formed between adjacent amino acids.

Making connections

Take a look at section B2.2.1—3 (/study/app/bio/sid-422-cid-755105/book/compartmentalisation-and-organelles-id-44250/) to learn about how organelles are discrete subunits of cells that are adapted to perform specific functions.

Student view

Overview (/study/ap 422- cid- 755105/o

View section B1.2.1—3 (/study/app/bio/sid-422-cid-755105/book/fundamentals-of-amino-acids-id-45486/) to learn about how condensation reactions occur in the formation of dipeptides and longer chains of amino acids.

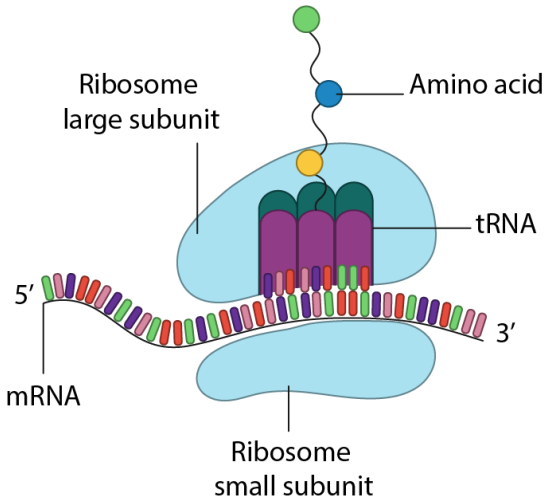


Figure 1. Structure of a ribosome.

More information for figure 1

The diagram illustrates the structure of a ribosome. It shows the mRNA strand labeled with "5'" on the left and "3'" on the right. The ribosome is divided into two subunits: the large subunit and the small subunit. The mRNA passes through these subunits. The tRNA is positioned between the mRNA strand and the large subunit, and an amino acid is attached to it, indicating the process of protein synthesis.

[Generated by AI]

Student view

Overview (/study/ap 422-cid-755105/o

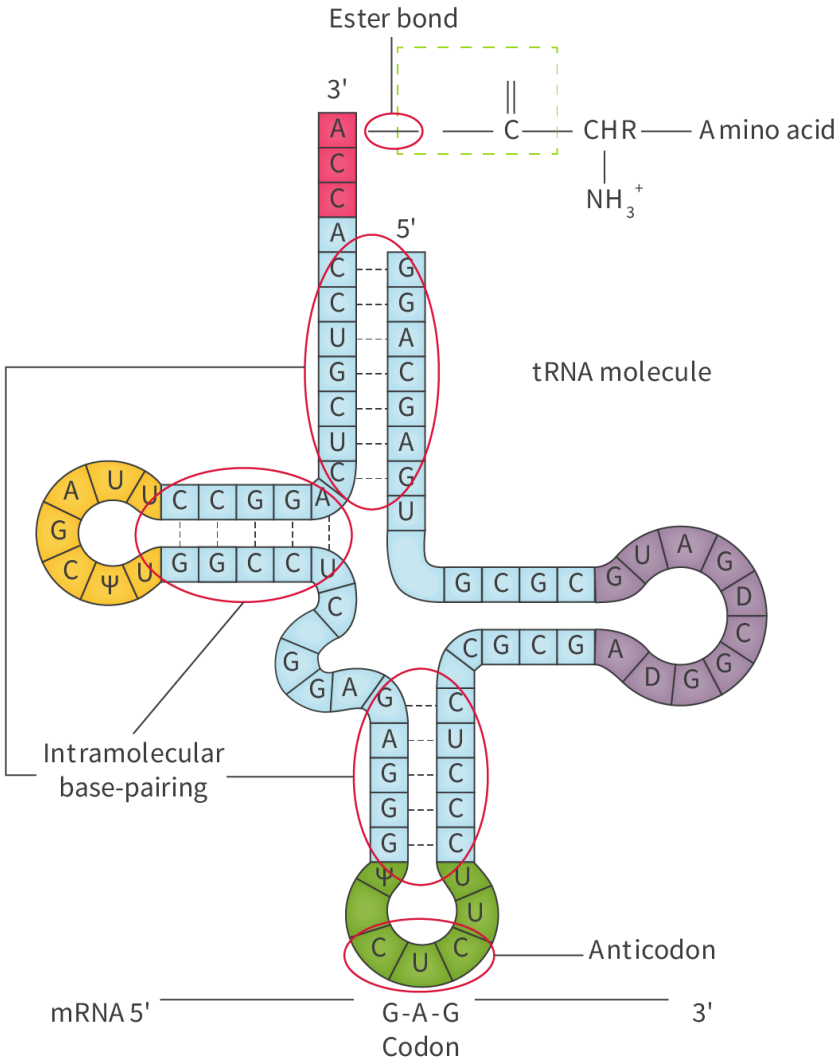


Figure 2. Structure of tRNA.

More information for figure 2

The diagram illustrates the structure of a tRNA molecule with the characteristic cloverleaf shape. The tRNA is composed of four main loops and multiple regions of intramolecular base-pairing. The top left part of the diagram shows the amino acid attachment site with an ester bond linked to the sequence 'CCA'. The right side of the molecule is labeled and shows the anticodon region with a sequence 'CUC', which pairs with the complementary mRNA codon 'GAG'. The main body of the tRNA includes the D-loop and TΨC loop, each containing specific sequences like 'GGC' and 'AUC', respectively. Intramolecular base-pairing is highlighted between sections, such as 'G-C' pairs. The diagram extensively illustrates the spatial relationship among the different components and regions within the tRNA structure.

[Generated by AI]

Student view

Overview (/study/ap 422- cid- 755105/o

This webpage (https://pdb101.rcsb.org/motm/121) shows images of the structure of ribosomes, mRNA, tRNA at each stage of protein synthesis: be sure to scroll down the page to see each stage. You may be able to use molecular visualisation software to analyse the structure of eukaryotic ribosomes and a tRNA molecule. An example is here (https://www.rcsb.org/3d-view/jsmol/4UG0/undefined).

You can also use the following link (https://pdb101.rcsb.org/motm/15) to explore the three-dimensional structure of each of these molecules.

Watch **Video 1** for an overview of the process of translation.

Video 1. The basics of translation (protein synthesis).

Try the activity to explore the Central Dogma of Molecular Biology.

Activity

- **IB learner profile attribute:** Communicator
- **Approaches to learning:** Communication skills — Using digital media for communicating information
- **Time required to complete activity:** 30 minutes
- **Activity type:** Individual activity

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/transcription-id-46485/print/) Assign

The Central Dogma of Molecular Biology is the theory which explains how genetic information flows from DNA to RNA to produce a biologically functional product, protein. DNA is transcribed to RNA and RNA is translated to protein.

Student view

Overview (/study/ap 422-cid-755105/o

In this activity you will research and produce an infographic on the Central Dogma of Molecular Biology.

Your research and infographic should include the following and any other interesting and relevant information.

- When was the Central Dogma first proposed and by whom?
- What is its significance to molecular biology?
- Does the flow of genetic information always happen in the same direction?

5 section questions

D1. Continuity and change: Molecules / D1.2 Protein synthesis

The genetic code

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

Learning outcomes

By the end of this section you should be able to:

- Describe complementary base pairing between the codons on mRNA and the anticodons on tRNA.
- Explain the main features of degeneracy and universality of the genetic code.
- Deduce the sequence of amino acids from an mRNA strand using a table of mRNA codons.

To ensure production of functional polypeptides, it is essential that the correct amino acids are placed in the correct sequences. What is the code for creating the correct sequences?

Complementary base pairing between tRNA and mRNA

Placement of the correct amino acids in the correct sequence to produce a functional polypeptide is made possible by continuation of the complementary base pairing rule. This time the pairing is between the bases in the mRNA and those found on the tRNA molecules that are carrying the amino acids.

Student view

Overview (/study/ap 422- cid- 755105/o

The code found in the mRNA is read in groups of three. This triplet code is known as a codon. A codon can be any three RNA bases in a sequence, such as UAG or CCA. Each of these codons is the code for the placement of a specific amino acid. The tRNA molecules, each carrying their specific amino acid, have their own three-base code that is complementary to the matching codon on the mRNA. The three base code on the tRNA is known as an anticodon. The complementary nature of the codon and anticodon ensures that the correct amino acid is placed in sequence (**Figure 1**).

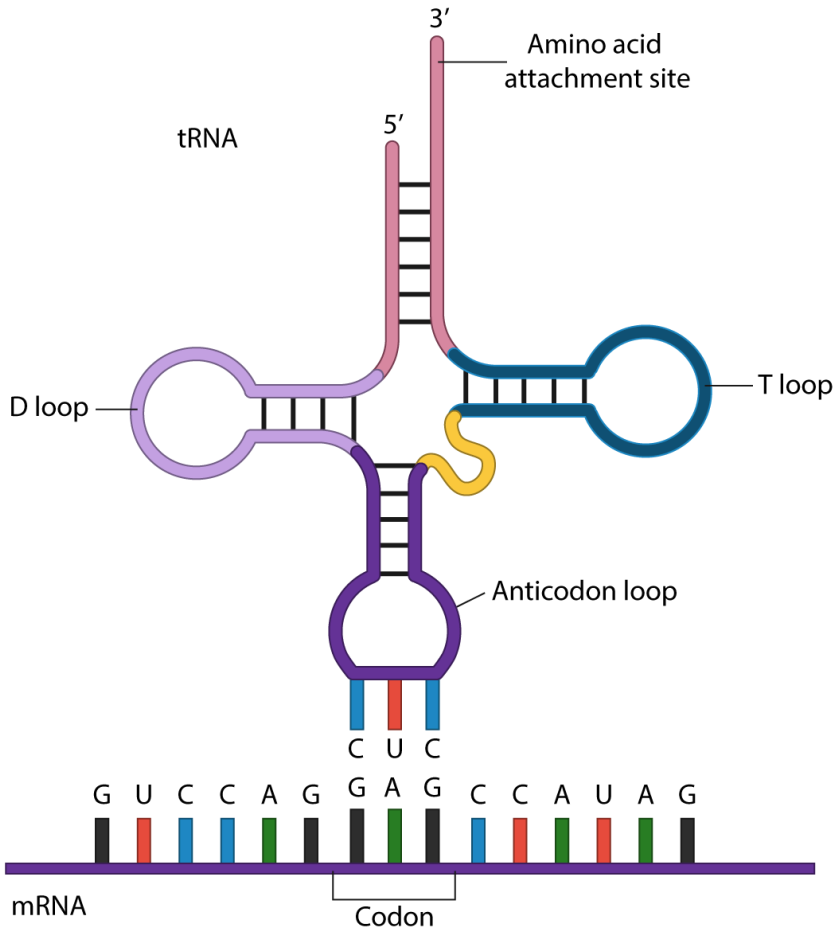


Figure 1. The matching of the tRNA anticodon and mRNA codon.

More information for figure 1

The image is a diagram illustrating the interaction between tRNA and mRNA during protein synthesis. It depicts the structure of a tRNA molecule, which includes three major loops and a stem. The anticodon loop, at the bottom of the tRNA structure, contains a triplet of nucleotides, represented as colored bars, which are complementary to a specific codon on the mRNA strand shown below. The mRNA strand at the bottom shows a linear sequence of codons arranged in groups of three nucleotide bases. The diagram highlights the complementary matching between the anticodon on tRNA and the codon on mRNA, which ensures the correct amino acids are incorporated into the growing peptide chain.

[Generated by AI]

Student view

Overview (/study/app/422-cid-755105/o

Features of the genetic code

The genetic code is broken down into codons found on the mRNA. Each codon represents a specific amino acid. As there are four bases in RNA and they are arranged in groups of three, this means there are 64 different possible combinations (4^3).

There are 20 amino acids in total and, as 64 codons can be formed by using the four bases, some amino acids are coded for by more than one codon, accounting for the degeneracy of the genetic code. There are also specific codons that act as a signal for the protein translation machinery to start (AUG) or to stop (UAG, UGA, UAA).

Another important feature of the genetic code is that it is universal. The same codons, code for the same amino acids in every organism on Earth with very few exceptions. This is evidence that all existing life on Earth has likely descended from a common ancestor. Otherwise there would likely be multiple ways that the mRNA code could be used to create a sequence of amino acids.

Using the genetic code expressed as a table of mRNA codons

Figure 2 shows the different base sequences making up mRNA codons. These codons make up the genetic code; in other words, they provide a dictionary for genes. The genetic code was worked out by scientists in the 1960s. The table is used by selecting the row of the first base of the codon from the left-hand side, then the column of the second base of the codon from the top and finally by selecting the correct amino acid from the list within that square based on the third base in the codon. So, for example, if the mRNA begins with AUG–CCC this would be translated into the amino acids methionine (Met) and proline (Pro).

Student view

Overview (/study/ap 422-cid-755105/o

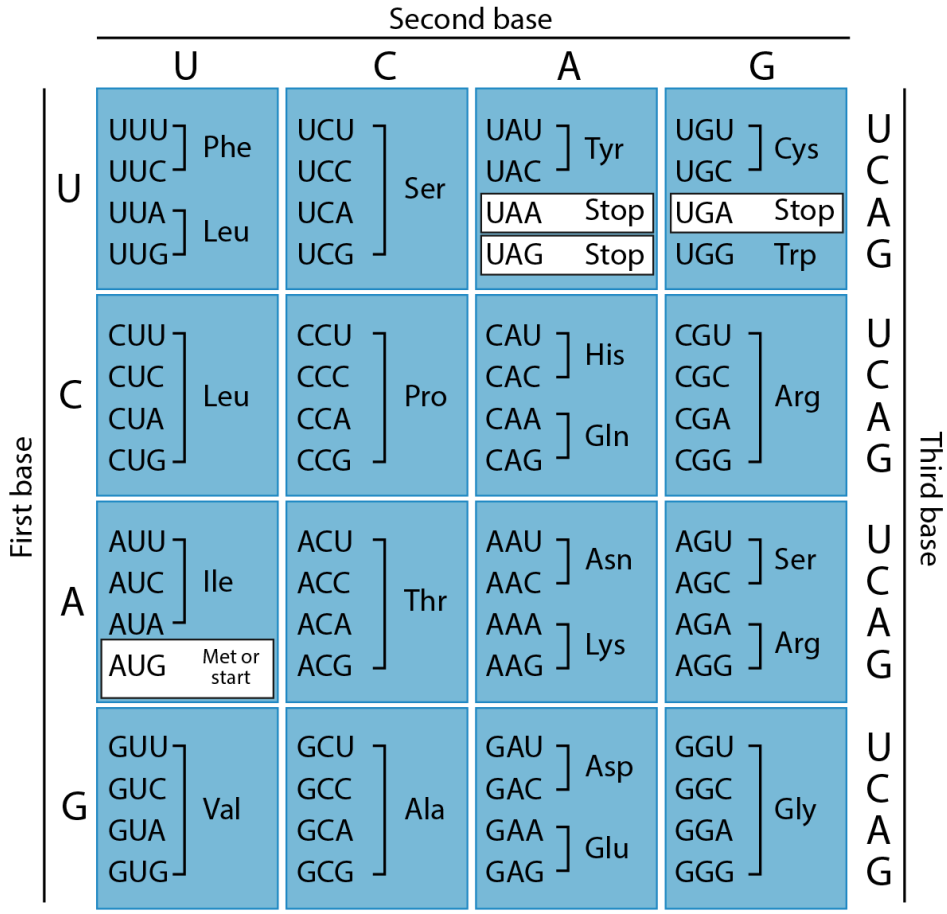


Figure 2. The genetic code.

More information for figure 2

The image is a table representing the genetic code, used to translate mRNA codons into amino acids. The table is organized with rows and columns that correspond to the first and second bases of the mRNA codons, while the individual squares within the table show the third base of the codon. Each square lists the possible triplet sequences and the amino acids or functions they correspond to. For example, if the first base is U, the second is U, and the third base is C, then the codon UUC corresponds to the amino acid Phenylalanine (Phe). Similarly, AUG is indicated as "Met or start," signifying the start codon for Methionine. Stop codons are listed as UAA and UGA.

[Generated by AI]

Study skills

You do not need to know the full names of the amino acids. **Figure 2** shows the abbreviations of their names that are widely used and recognised by scientists.

Although you do not need to know the names of all the amino acids and their abbreviations, you must be able to:

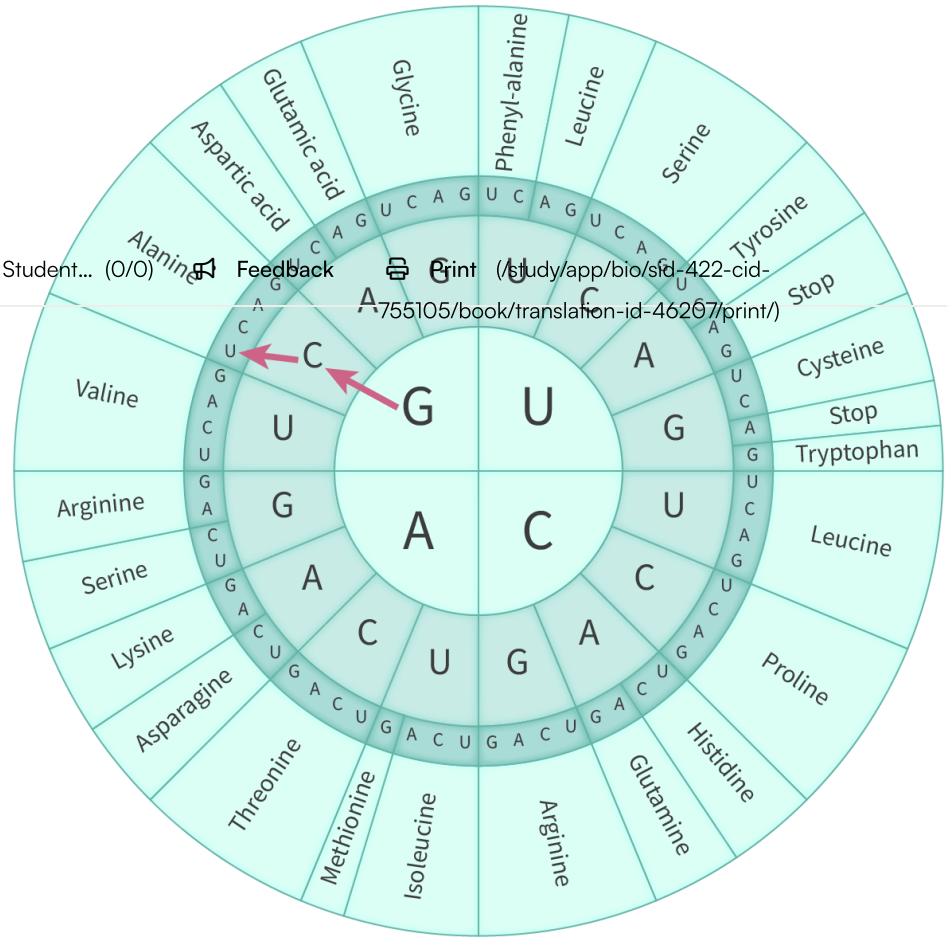
- Read the genetic code.

Student view

Overview (/study/ap 422-cid-755105/o

- Deduce which codon(s) corresponds to which amino acid.
- Deduce the sequence of amino acids coded by a short mRNA strand of known base sequence.

The genetic code can be also read using another circular version of the diagram with codons. Using the diagram in **Figure 3**, if you want to find out which amino acid is coded by GCU, you start off in the centre of the circle with the G. Then, you move outwards and find C (the second circle) and lastly U (the last circle). The amino acid coded by GCU is alanine.



Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/translation-id-46207/print/) Assign

Figure 3. A circular representation of the genetic code.

More information for figure 3

This image is a detailed diagram of the circular genetic code, illustrating the relationship between codons and corresponding amino acids. The diagram is structured in concentric circles. The innermost circle represents the first base of the codon, followed by the second base in the next circle outward, and the third base in the outermost circle.

Starting with the center circle, there are four letters: G, U, A, and C, representing the nucleotides. These lead outward to the next circle, which lists combinations of these letters: G, C, A, U in arrangements corresponding to the nucleotides. Finally, the outermost section contains the names of the amino acids or specifies a stop codon, such as Alanine, Methionine, Serine, Stop, etc. These names are positioned aligned with combinations of nucleotide triplets.

Student view

An example path can be followed from the center: start at G, move to C, then U, which leads to the outer segment labeled with the amino acid Alanine. This demonstrates how to decode a nucleotide sequence to find the amino acid it represents.

[Generated by AI]

Try the drag and drop activity to test your understanding of using the genetic code.

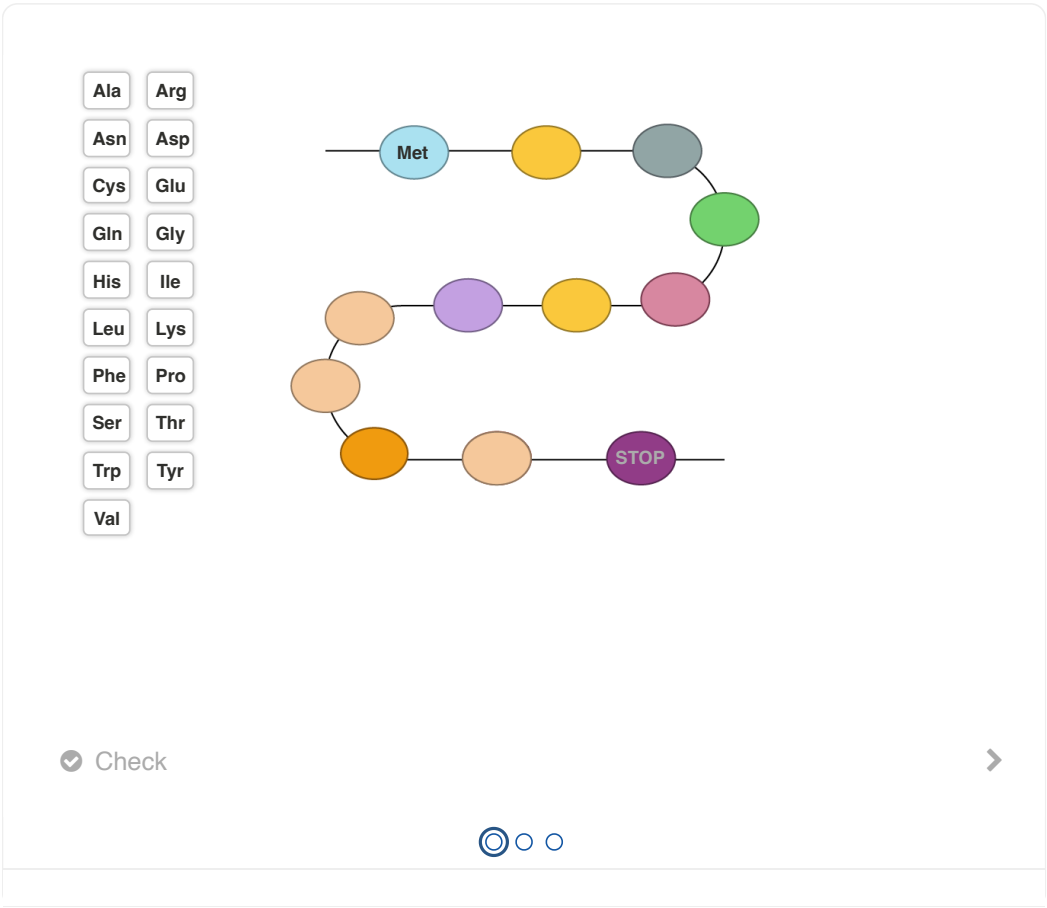
Activity

- **IB learner profile attribute:** Knowledgeable
- **Approaches to learning:** Thinking skills — Applying key ideas and facts in new contexts
- **Time required to complete activity:** 15—20 minutes
- **Activity type:** Individual activity

In **Interactive 1**, build polypeptides using the mRNA base sequences listed below. Do not forget about the start and stop codons — tip: they are marked in bold in the sequences and are in place in the polypeptides. The codon chart is provided above in **Figure 2**.

1. mRNA: **AUG**CCAAGGGUCCACCCCACGGACGACUUUAAU**UAA**CGUAAGCCC
2. mRNA: CG**AUG**GAUUCCCGGCAGGAAAAGGAUCCUCAGGGAACA**UGA**GAGC
3. mRNA: CCAGUA**AUG**GGGCUCAACGAGGGGCUUAAAGACCCUUUUAGC**UAG**

Overview (/study/ap 422- cid- 755105/o



4. **Interactive 1.** Building polypeptides.

5 section questions

D1. Continuity and change: Molecules / D1.2 Protein synthesis

Building polypeptides

D1.2.10: Stepwise movement of the ribosome along mRNA D1.2.11: Mutations that change protein structure

Learning outcomes

By the end of this section you should be able to:

- Describe the elongation process of translation.
- Describe how a point mutation can affect the polypeptide produced.

Student view

Overview (/study/ap 422- cid- 755105/o

During translation, the ribosome brings together the mRNA and the tRNAs to attach the amino acids in the correct sequence to produce a functioning polypeptide. What processes are involved in building the polypeptide?

Similar to transcription, translation can be broken down into three stages: initiation, elongation and termination. In addition, translation includes a separate process of tRNA charging where the amino acids are attached to the correct tRNAs.

Elongation of the polypeptide

Once initiation has occurred and the components are brought together, the elongation process begins; the ribosome begins to move along the mRNA, one codon at a time. As each codon moves into place a new tRNA, carrying the corresponding amino acid, attaches and moves previous tRNA molecules to the next position (**Figure 1**). As new amino acids are delivered, condensation reactions are catalysed and peptide bonds are formed between them.

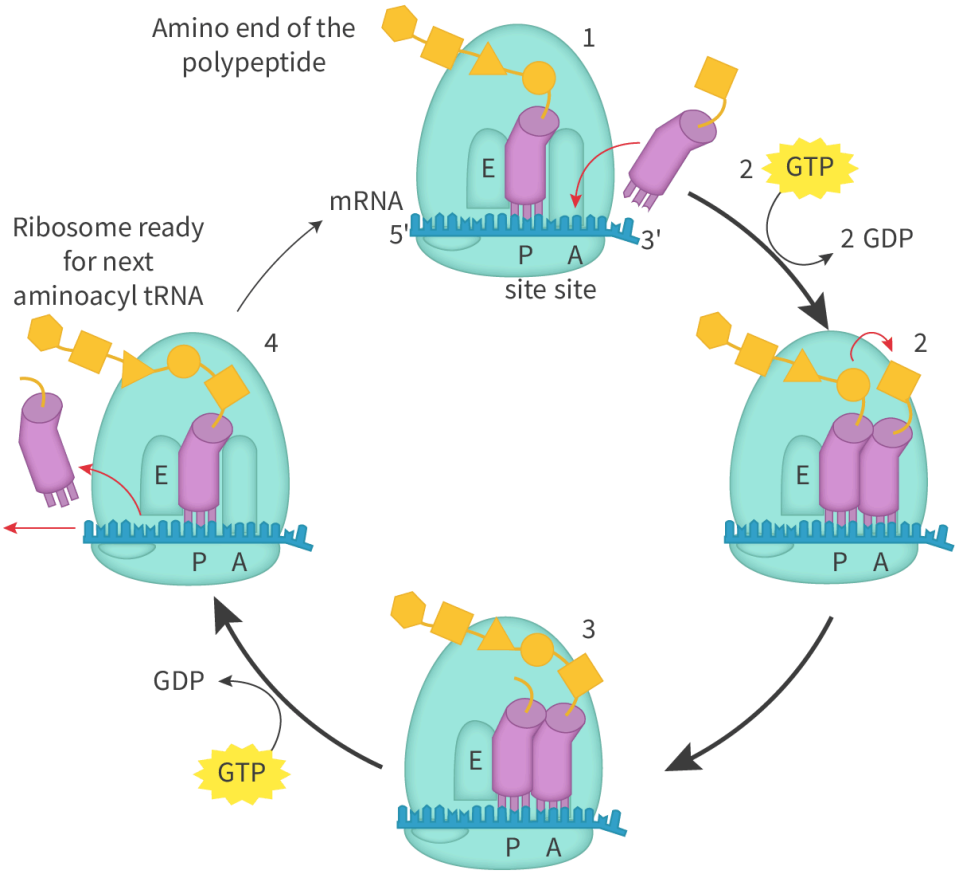


Figure 1. Elongation stage of translation.

More information for figure 1

The diagram illustrates the elongation stage of translation in protein synthesis. It shows four main steps in a cyclic sequence.

1. The process begins with the arrival of a tRNA carrying an amino acid matching the mRNA codon at the A site of the ribosome. The mRNA is shown as a blue strand running below the ribosome with labels indicating the 5' to 3' direction.

Student view

Overview (/study/ap 422- cid- 755105/o

2. The second image depicts the elongation factor GTP bound to the tRNA at the A site. A conformational change occurs as GTP is hydrolyzed to GDP, facilitating the movement of the tRNA.

3. The third step shows the tRNA translocation. The ribosome shifts, moving the tRNA carrying the growing polypeptide to the P site and expelling the empty tRNA from the E site.

4. In the final step, the ribosome is shown ready for the next amino-acyl tRNA. The cycle repeats as indicated by the arrows, with the ribosome moving along the mRNA strand one codon at a time, and peptide bonds continuing to form between amino acids, extending the polypeptide chain.

[Generated by AI]

Elongation involves a repeated cycle of events. It begins with a new tRNA coming in and binding to the A site. This tRNA carries a specific amino acid that matches the second codon on the mRNA. The anticodon on this tRNA is complementary to the codon on the mRNA.

Next, a reaction is catalysed by the large subunit of the ribosome, forming a peptide bond between the newly arrived amino acid and the amino acid/polypeptide held by the previous tRNA in the P site.

Once the peptide bond is formed, the ribosome translocates along the mRNA by one codon. The tRNA that was in the P site moves to the E site and exits the ribosome. The tRNA that was in the A site and is carrying the polypeptide is moved to the P site, leaving the A site available for the next tRNA to enter with the next amino acid.

The whole process repeats many times until the polypeptide is complete and the ribosome reaches any of the termination codons, UAG, UAA or UGA, at which point the components disassemble.

Mutations that change protein structure

When a mistake is made synthesising either DNA or RNA, it is known as a mutation. There are many checks and other processes to find and repair most of these errors, but occasionally the errors will escape these measures and a mutation occurs. Mutations are often seen as negative; however, they are naturally occurring and play an important role in introducing genetic variation and therefore are also essential for evolution (see section D1.3.4–7 (/study/app/bio/sid-422-cid-755105/book/causes-and-consequences-of-gene-mutations-id-45759/)).

Student view

Overview (/study/ap 422- cid- 755105/o

There are several types of mutation but here we will focus on only one, called a point mutation (**Figure 2**). In a point mutation, a single nucleotide is changed. It may be deleted, added or replaced with another. This usually happens during DNA replication but can also occur during transcription. If a nucleotide is added (insertion mutation) or deleted (deletion mutation) the effects are quite significant. This is because it causes something known as a frameshift mutation where all of the codons following that mutation are altered as there is a shift in the base sequence.

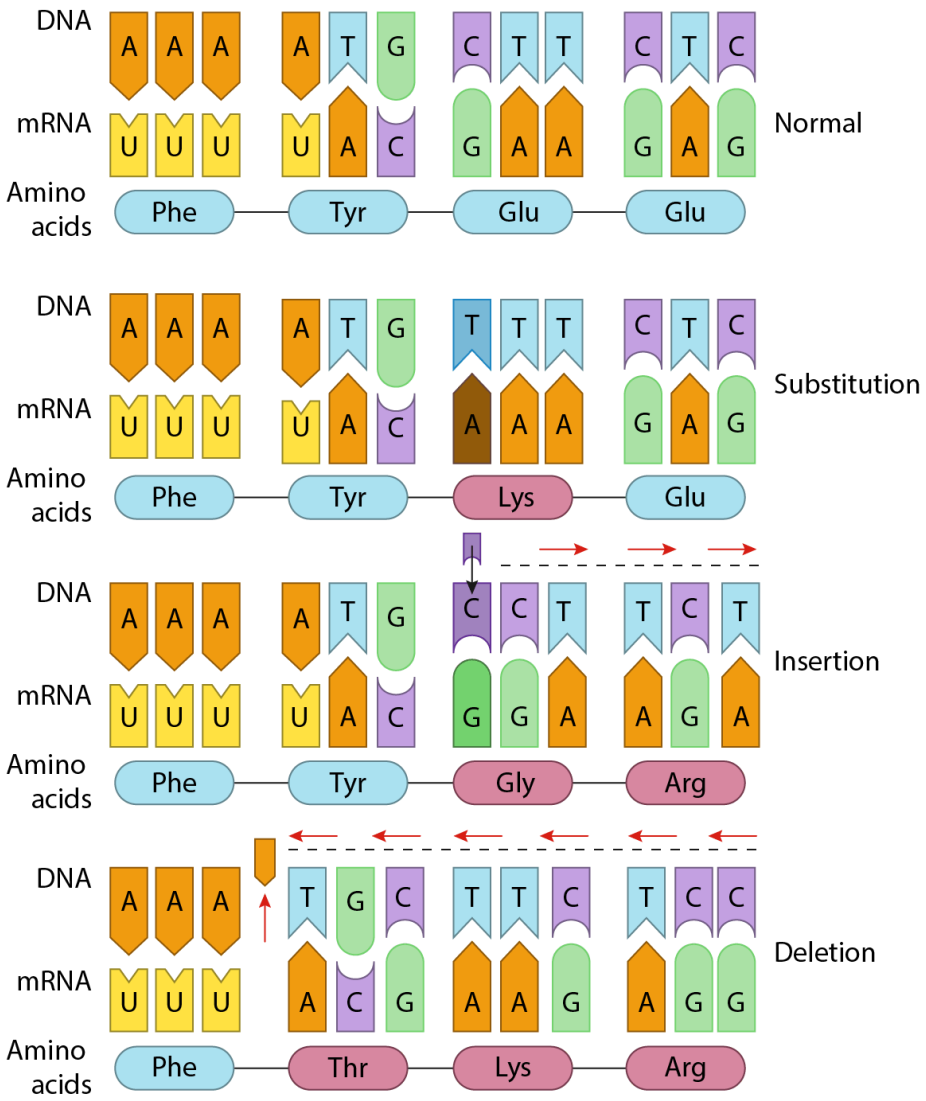


Figure 2. Examples of point mutations.

More information for figure 2

The illustration shows examples of point mutations in DNA and their effects on the corresponding mRNA and amino acids.

1. **Normal:** The DNA sequence consists of paired bases with mRNA and amino acids represented below. The DNA sequence is AAA ATG CTT CTC, the mRNA is UUU UAC GAA GAG, and the resulting amino acids are Phe, Tyr, Glu, and Glu.

Student view

Overview (/study/ap 422- cid- 755105/o

2. **Substitution Mutation:** The DNA segment shows a change in the middle, AAA ATG TTT CTC, corresponding to mRNA UUU UAC AAA GAG, resulting in the amino acids Phe, Tyr, Lys, Glu. The substitution changes a Glutamic (Glu) to Lysine (Lys).

3. **Insertion Mutation:** An additional C nucleotide is inserted in the DNA sequence, altering it to AAA ATG CCT TTC, creating an mRNA sequence of UUU UAC GGA AAG. This results in the amino acids Phe, Tyr, Gly, and Arg. The insertion causes a frameshift with a significant change in the resulting amino acids.

4. **Deletion Mutation:** One nucleotide is deleted, transforming the sequence to AA ATG CTC TCC in DNA, corresponding to mRNA UU UAC GAG AGG, and producing the amino acids Phe, Thr, Lys, Arg. This deletion also results in a frameshift with all subsequent amino acids altered.

[Generated by AI]

The result of a point mutation where a nucleotide is changed (substitution mutation) varies greatly. Due to the degeneracy of the genetic code, sometimes a change in base produces a codon which codes for the same amino acid, and there is therefore, no effect. This is essentially a silent mutation. This is most likely the case if the mutation occurs to the third base in a codon.

For example, CCU, CCA, CCC, and CCG all code for the amino acid proline. If the third base is changed, proline will still be placed correctly in the polypeptide and no change will result from the mutation.

If the point mutation occurs to the first or second base in a codon there is a higher chance that it will lead to the addition of a different amino acid in the sequence for that polypeptide. The outcome of this mutation may be quite significant or it may be quite minimal. If the mutation changed a codon to a stop codon, that would end the polypeptide early and it would be unlikely to function as required. A change to another amino acid would likely lead to an effect on the overall polypeptide.

An example of a point mutation that has a significant effect is the mutation that causes sickle cell anaemia. This is a result of a single point mutation in the gene responsible for producing one of the polypeptides in haemoglobin. See subtopic D1.3 (/study/app/bio/sid-422-cid-755105/book/the-big-picture-id-43250/) for the mechanisms involved in mutations.

International Mindedness

Malaria is one of the most widespread and dangerous diseases on Earth. It is thought that up to half of the world's population is at risk. Hundreds of thousands are killed each year by malaria.

Student view

Overview (/study/ap 422- cid- 755105/o

It is thought that sickle cell anaemia evolved in response to malaria as those with the mutated gene for sickle cell, have immunity or resistance to malaria.

Try the activity to help with your understanding of the effects of point mutations.

Activity

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:** Thinking skills — Providing a reasoned argument to support conclusions
- **Time required to complete activity:** 15—20 minutes
- **Activity type:** Individual activity

Your task in this activity is to determine the outcome of a series of point mutations and suggest how they will affect the polypeptide produced.

1. The following is the base sequence of a DNA coding strand.

   ATGTCCGATGGAATACGCAGACTACGGGCACACATATATGCGCCCTAA

   Determine the corresponding mRNA base sequence.

   Using the genetic code lookup table in **Figure 4**, determine the amino acid sequence.

   The following point mutation occurs.

   ATGTCCGATGGAATACGC**T**GACTACGGGCACACATATATGCGCCCTAA

   Determine the new amino acid sequence.

   How has this polypeptide been changed by this point mutation? Is this a significant change?

2. The following is the base sequence of a DNA template strand.

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/the-genetic-code-id-46208/print/) Assign

   TACAAAGCTCCTGACTGACTTGACCTTTGAGCCTTGGGGGAAATGAAT

   Determine the corresponding mRNA base sequence.

   Using the genetic code lookup table in **Figure 4**, determine the amino acid sequence.

   The following point mutation occurs.

   TACAAAGCTCCC**G**ACTGACTTGACCTTTGAGCCTTGGGGGAAATGATT

   Determine the new amino acid sequence.

Student view

Overview (/study/ap 422- cid- 755105/o

How has this polypeptide been changed by this point mutation? Is this a significant change?

3. The following is the base sequence of a mRNA strand.

   AUGCCGCUAAAUUUUCAGCCAAGCAAUGAGGGGCAUUGGCUCUGA

   Using the genetic code lookup table in **Figure 4**, determine the amino acid sequence.

   The following point mutation occurs.

   AUGCCGCUAAAUUUUCAGCCAAGCAAUGAGGGGC**GU**UGGCUCUGA

   Determine the new amino acid sequence.

   How has this polypeptide been changed by this point mutation? Is this a significant change?

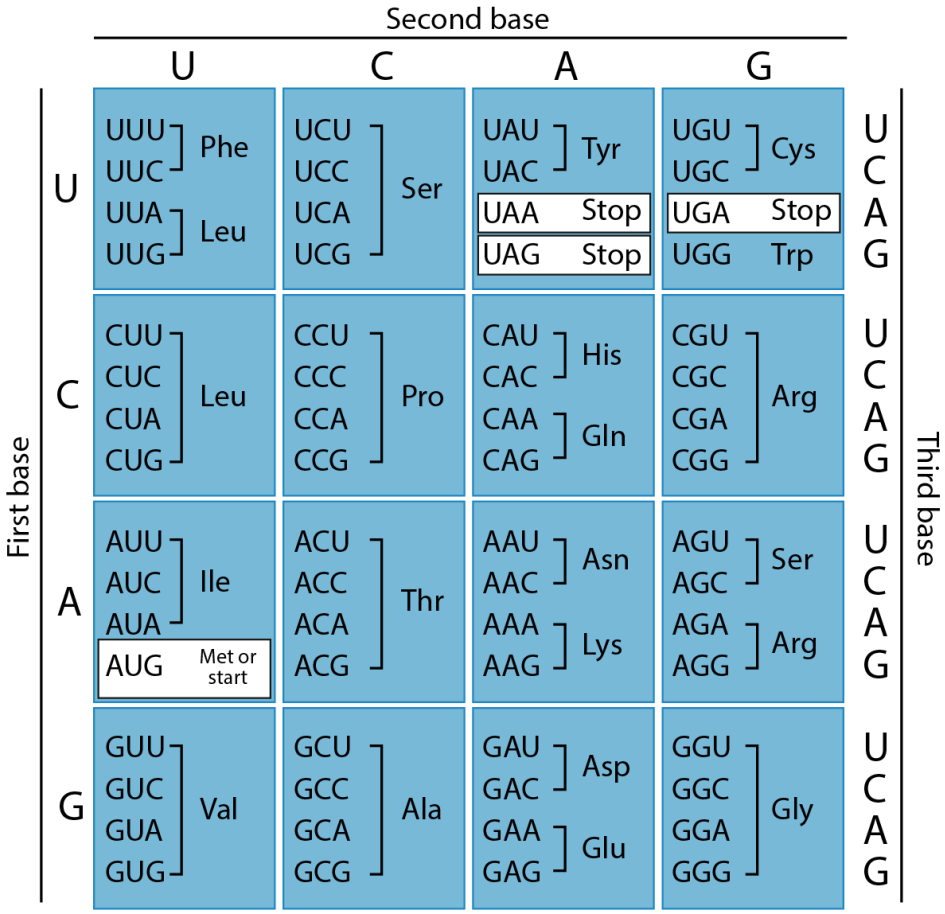


Figure 4. The genetic code.

More information for figure 4

The image is a diagram representing the genetic code in a tabular form. The table has three rows and four columns corresponding to the four RNA bases (U, C, A, G). The first row and column indicate the 'First base' and 'Second base', while the vertical column on the right shows the 'Third base'.

Each box in the grid represents a combination of three bases, forming a codon. For example, under the combination of the first base 'U', second base 'C', and third base 'A or G', the codon represents 'Serine'. Each codon box is divided by square brackets containing three bases (e.g., UUU, UUC) and their corresponding

Student view

Overview (/study/ap 422-cid-755105/o

amino acid abbreviation (e.g., Phe for phenylalanine).

Some codons function as start signals, such as 'AUG', indicated as 'Met or start', while 'UAG', 'UGA', and 'UAA' are indicated as 'Stop' codons that terminate protein synthesis.

The chart is organized to display the specific amino acid or function each codon combination corresponds to within the genetic code, helping understand how sequences of bases are translated into proteins.

[Generated by AI]

4 section questions

Controlling transcription and translation (HL)

D1.2.12: Directionality of transcription and translation (HL) D1.2.13: Initiation of transcription at the promoter (HL)
D1.2.14: Non-coding sequences in DNA (HL)

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Describe the directionality of transcription and translation as 5' to 3'.
- Describe the role of the promoter in transcription and how the binding of transcription factors to the promoter initiates transcription.
- Explain the roles of non-coding regions of DNA.

Building a polypeptide involves the processes of transcription and translation. To ensure that the polypeptide is assembled correctly, what controls these processes?

Directionality of transcription and translation

Just as DNA replication has directionality, so too does transcription and translation. Also, as in DNA replication, the direction remains 5′ to 3′. RNA polymerase builds mRNA molecules in a 5′ to 3′ direction. Again, similar to DNA polymerase, the RNA polymerase,

Student view

Overview (/study/ap 422- cid- 755105/o

being an enzyme, only functions in a very specific way and can only catalyse a very specific reaction. In this case it is the formation of a phosphodiester bond between the 3′ end of one RNA nucleotide and the 5′ end of the next nucleotide.

During translation the mRNA moves through a ribosome in a 5′ to 3′ direction as the codons on it are read to assemble the amino acids in the correct sequence. This is because the mRNA only fits the binding site of the ribosome if it is oriented correctly. If the mRNA was able to attach in either direction and the code was read backwards, the code would be completely different, resulting in a completely different polypeptide.

Initiation of transcription at the promoter

The initiation of transcription is one of the points in gene expression at which control can be exerted. RNA polymerase is not able to bind to DNA at any point and begin producing RNA. On the DNA, just before a gene, is a region of code known as the promoter (**Figure 1**). At the promoter, proteins known as transcription factors can bind. It is the binding of the correct transcription factors in the correct orientation that allows the RNA polymerase to also bind and then begin to transcribe the DNA into RNA. If those transcription factors are missing or something has blocked their ability to bind to the promoter, transcription will not take place and that gene cannot be expressed.

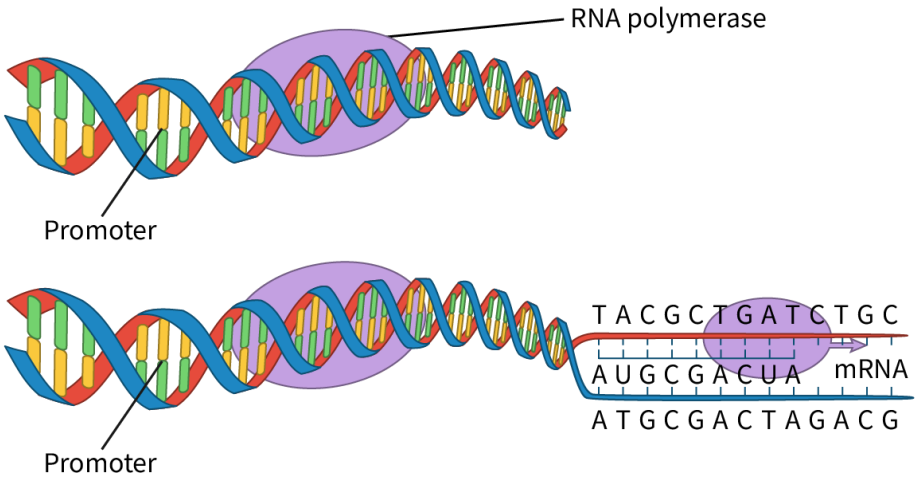


Figure 1. Promoter region of a gene and initiation of transcription.

More information for figure 1

The image is a diagram illustrating the initiation of transcription in a DNA double helix. It shows the promoter region on the DNA highlighted, which is the site where transcription factors and RNA polymerase bind. At the top part of the image, the RNA polymerase is labeled and positioned over the DNA strand near the promoter. Below this, the diagram shows a detail of transcription in progress. The DNA is unwound, showing the sequence of nucleotides. The RNA polymerase is bound to the DNA, and a short sequence of mRNA is being synthesized, shown as a strand of RNA with its complementary bases aligning with the template DNA strand. The text "Promoter," "RNA polymerase," and the corresponding nucleotide sequences such as “TACGCTGATCTGC” are visible, illustrating the process of RNA synthesis from DNA.

[Generated by AI]

Student view

Overview (/study/ap 422-cid-755105/o

Non-coding sequences in DNA do not code for polypeptides

Non-coding DNA accounts for more than 98% of the human genome and is defined as DNA sequences within a genome that do not consist of the information to make a protein. In other words, these DNA bases are never represented within the amino acid sequence of expressed proteins. This does not mean that non-coding DNA does not have a function. DNA is 'expensive' to maintain, so, from an evolutionary viewpoint, it should have a function, but we do not always know what that function is.

The regions of DNA that do not code for proteins include:

- Regulators of gene expression: these are DNA sequences that regulate gene expression in various ways. For instance, promoters are sequences that occur just before genes and act as a binding point for the RNA polymerase enzymes that catalyse the transcription process. Other DNA sequences may act as binding sites for proteins that either increase or decrease the rate of transcription; these are known as enhancers and silencers, respectively.
- Introns: these are DNA base sequences found within eukaryotic genes that get removed at the end of transcription. They do not contribute to the amino acid sequence of the polypeptide made from the gene.
- Telomeres: These are repetitive sequences that protect the ends of the chromosome. Telomeres help ensure that DNA is replicated correctly. With every cell division, short stretches of DNA are lost from the telomeres.
- Genes for tRNAs and rRNAs: These genes code for RNA molecules that do not get translated into proteins, but instead fold to form tRNA molecules that play an important role in translation or the rRNA that forms part of the structure of ribosomes.

Theory of Knowledge

The use of lab animals to understand the nature and process of DNA replication/structure/modification/editing

Do scientists or the cultures in which scientists operate exert a greater influence on what is ethically acceptable in this area of knowledge? Who makes the decision on whether these practices are ethical? Are there exceptions? Are the practices ethical if there is potential to save human lives?

In the activity in the next section, you will use a simulation to explore gene expression.

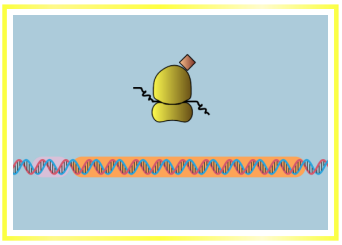
5 section questions

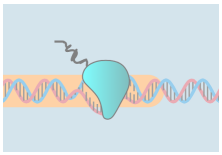
Activity: Gene expression (HL)

Overview (/study/ap 422-cid-755105/o

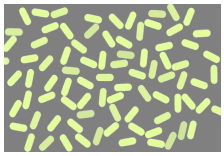
D1.2.12: Directionality of transcription and translation (HL) D1.2.13: Initiation of transcription at the promoter (HL)

D1.2.14: Non-coding sequences in DNA (HL)





mRNA



Multiple Cells

PhET

Activity

Higher level (HL)

- **IB learner profile attribute:** Thinker
- **Approaches to learning:** Thinking skills — Reflecting on the credibility of results
- **Time required to complete activity:** 20—30 minutes
- **Activity type:** Individual activity

For this activity you will be working with the PhET simulation.

Follow the directions and answer the questions.

Start with the first part called ‘Expression’. In this simulation the region of the DNA labelled ‘regulatory region’ is the promoter.

Student view

Overview (/study/ap 422-cid-755105/o

1. Try dragging the RNA polymerase onto the DNA. What happens?
   What else might you have to do to get the RNA polymerase to transcribe the gene?
2. Once you are able to make an mRNA, drag a ribosome to it to produce the protein. Use the mRNA destroyer on the mRNA. Suggest why our cells would have these.
3. What is the role of the negative transcription factor? Suggest why our cells would have these.
4. Produce the first protein.
5. Moving to the next gene, What steps are necessary for successfully producing this protein? How does it differ from the first protein?
6. Complete the first activity by producing each of the three different proteins.
   Move onto the next part of the simulation called 'mRNA' by clicking the second box along the bottom of the window.
7. Using the sliders and observing the simulation, describe the effects of changing each of the three conditions. Which has the greatest impact on the rate of transcription?
8. Check the box at the bottom and introduce the negative transcription factor. How does it interact with the rest of the system? How does changing its concentration and affinity to the DNA affect the rate of transcription?
9. What does the term affinity mean?
10. Summarise the roles and/or functions of each component shown in the first two parts of the simulation.

Modification and splicing (HL)

D1.2.15: Post-transcriptional modification in eukaryotic cells (HL) D1.2.16: Alternative splicing of exons to produce protein variants (HL)

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Explain post-transcriptional modification of mRNA in eukaryotes.
- Describe how alternative splicing can produce variants of a protein.

Student view

In eukaryotes, the mRNA that is produced needs to be prepared for translation. This process is called post-transcriptional modification of mRNA. Why is this necessary?

Overview (/study/ap 422-cid-755105/o

Post-transcriptional modification in eukaryotic cells

Eukaryotic genes include introns and exons. Introns are DNA sequences that contain no coding information but sometimes contain controlling sequences that regulate transcription of the gene. Exons are the DNA sequences that code for a polypeptide.

Figure 1 shows the steps involved in modifying RNA so that it will be used in translation; these steps are:

- transcription (synthesis of pre-mRNA)
- addition of a 5' cap and a poly-A tail (which protect the mRNA molecule from degradation)
- splicing, which involves removing (excising) the introns and joining (ligating) the exons to form mature mRNA.

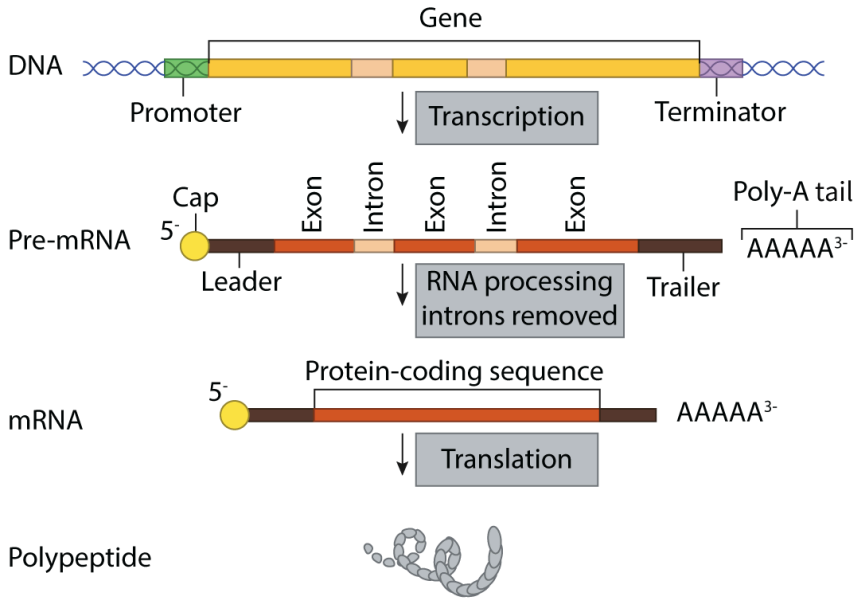


Figure 1. Post-transcriptional modification of mRNA.

More information for figure 1

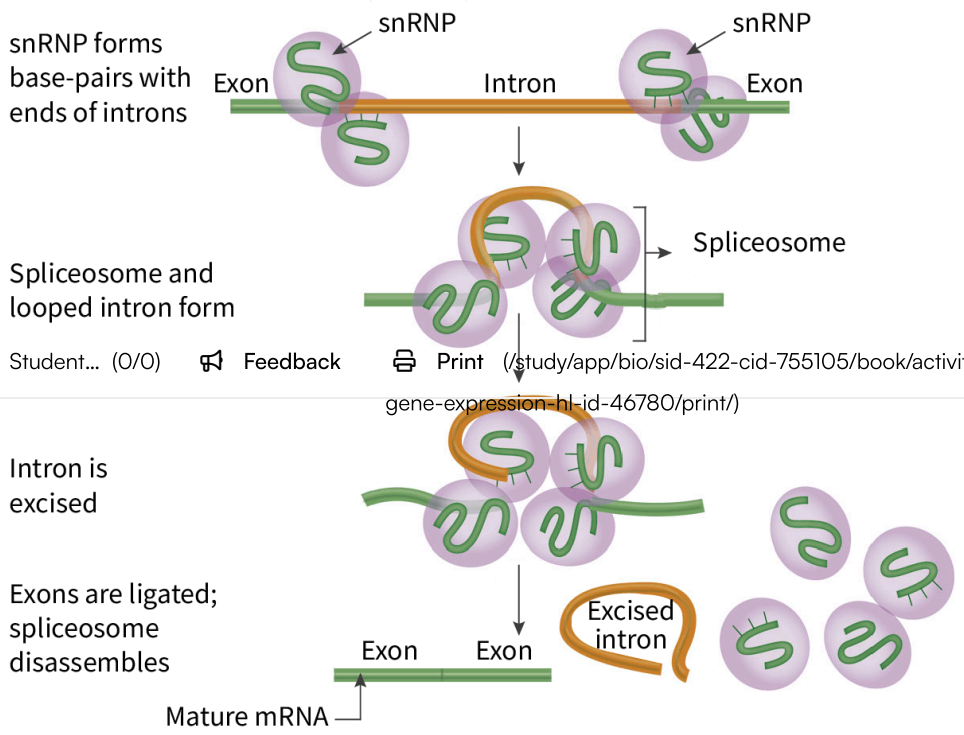
This diagram depicts the process of post-transcriptional modification of mRNA. At the top, a DNA segment is shown with labeled areas: Promoter, Gene, and Terminator. The gene contains alternating exons and introns. Below, pre-mRNA is illustrated as it undergoes transcription, resulting in mRNA that includes a 5' cap and a Poly-A tail. The pre-mRNA's intron structure is also shown. The diagram shows RNA processing where introns are removed, leading to the formation of mRNA with a protein-coding sequence, and a Poly-A tail labeled 'AAAAA3' at its end. At the bottom, a polypeptide is represented, indicating the result of translation.

[Generated by AI]

The splicing of the introns is a complicated process, involving what is known as a spliceosome (**Figure 2**).

Student view

Overview (/study/ap 422- cid- 755105/o



Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/activity-gene-expression-hl-id-46780/print/) Assign

Figure 2. Spliceosome removing introns and joining exons to form mature mRNA.

More information for figure 2

The diagram illustrates the process of mRNA splicing, highlighting the role of the spliceosome. It is divided into several stages:

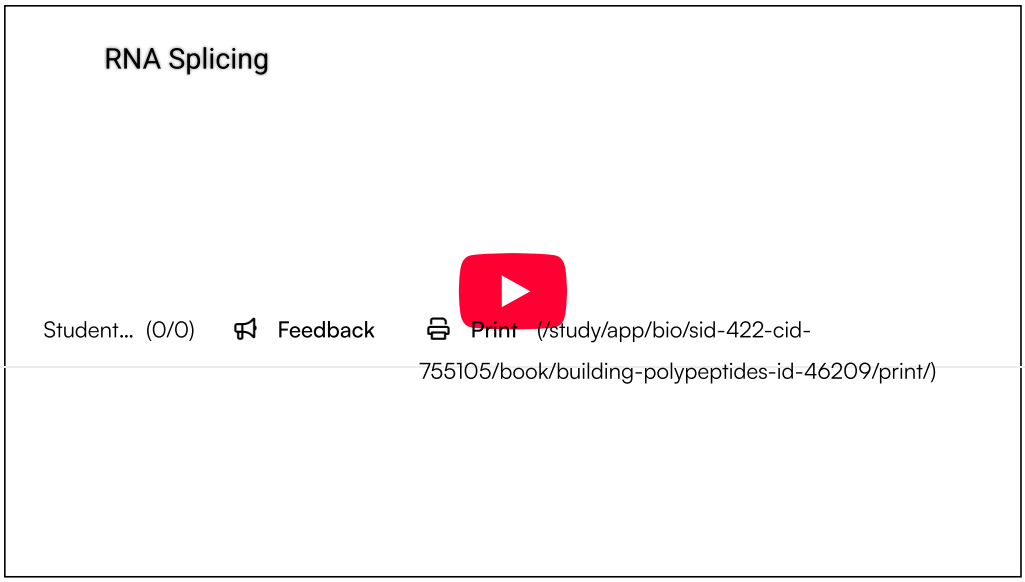
1. At the top, the diagram shows snRNPs forming base-pairs with the ends of an intron. Exons are represented as green strands flanking the orange intron sequence.
2. Moving down, the spliceosome is formed by a cluster of snRNPs around the intron, causing it to loop. An arrow labeled "Spliceosome" points to this structure.
3. Further down, the intron is excised, marked by a looped intron being cut and separated from the exon sequence.
4. At the bottom, exons are ligated together forming mature mRNA, shown as a continuous green strand with the excised intron depicted separately as an orange loop with the label "Excised intron."

Text on the diagram explains each step, including: "snRNP forms base-pairs with ends of introns," "Spliceosome and looped intron form," "Intron is excised," and "Exons are ligated; spliceosome disassembles," culminating in "Mature mRNA."

[Generated by AI]

The process of mRNA splicing is summarised in **Video 1.**

Student view



Video 1. mRNA splicing.

Alternative splicing

Sometimes a gene can be spliced in multiple ways by combining different exons and omitting others. This results in different versions of proteins which will often function differently. This is known as alternative splicing. **Figure 3** outlines a generic example of this.

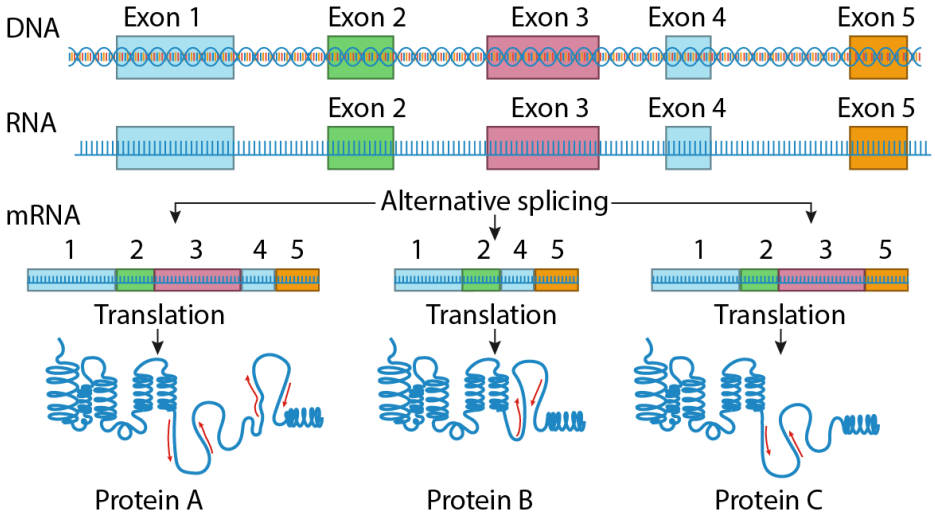


Figure 3. Alternative splicing.

More information for figure 3

The diagram illustrates alternative splicing, showing the stages from DNA to RNA to mRNA, and the resulting proteins. At the top, the DNA sequence is depicted with five exons labeled 1 through 5. Below, RNA is shown with the same exons lined up. The mRNA section provides three different combinations through alternative splicing:

1. First combination includes all exons (1, 2, 3, 4, 5) leading to Protein A.
2. Second combination skips exon 3, using exons 1, 2, 4, 5, resulting in Protein B.
3. Third combination omits exons 4, using exons 1, 2, 3, 5, creating Protein C.

Overview (/study/ap 422-cid-755105/o

The diagram shows the translation process of mRNA into proteins, each with different configurations symbolized by different shapes and colors, indicating that each splicing variation results in proteins with varying structures and functions. The sequence of exons demonstrates how different proteins are formed from the same initial genetic material, emphasizing diversity in protein function due to alternative splicing.

[Generated by AI]

A more specific example of this is the alternative splicing of one of the genes responsible for the production of troponin (troponin T), a protein involved in muscle contraction. In a developing foetus the troponin T gene in cardiac muscle cells is spliced in one way. This gives the troponin a higher sensitivity to Ca^{2+} and greater tolerance to acidosis, which is when the blood's pH gets too low. Several weeks after the birth of the baby, its cardiac muscle cells begin to splice the troponin T gene in a different way and the troponin loses its higher sensitivity to Ca^{2+} and its tolerance to acidosis.

Nature of Science

Aspect: Observations

Scientists observed that the human body was capable of making many more proteins than there were genes in our DNA. This could not fully be explained until alternative splicing was discovered. It now appears that the vast majority of human genes undergo alternative splicing. Humans have over 20 000 protein-coding genes yet we have identified almost 100 000 proteins produced by human cells.

Try the activity to delve deeper into the process of alternative splicing.

Activity

- **IB learner profile attribute:** Communicator
- **Approaches to learning:** Communication skills — Practising active listening skills; Using digital media for communicating information
- **Time required to complete activity:** 45 minutes
- **Activity type:** Pair/group activity

In pairs or groups of three, conduct further research into alternative splicing in humans and prepare a presentation.

Your presentation should include details on the following:

Student view

Overview (/study/ap 422- cid- 755105/o

- a summary of what alternative splicing is
- at least three examples of human genes that exhibit alternative splicing
- the significance of alternative splicing to the human proteome
- any current interesting research happening in relation to alternative splicing.

The desired outcomes of this activity are to provide you with an opportunity to conduct some research, collaborate in a pair or group and extend your knowledge of alternative splicing beyond the curriculum.

5 section questions

D1. Continuity and change: Molecules / D1.2 Protein synthesis

Making use of proteins (HL)

D1.2.17: Initiation of translation (HL) D1.2.18: Modification of polypeptides into their functional state (HL)

D1.2.19: Recycling of amino acids by proteasomes (HL)

Higher level (HL)

Learning outcomes

By the end of this section you should be able to:

- Describe the initiation stage of translation.
- Describe the modification of polypeptides to their functional state using pre-proinsulin to insulin as an example.
- Describe the recycling of amino acids by proteasomes.

Translation consists of three distinct stages: initiation, elongation and termination. What are the signals that initiate translation? And how is the supply of amino acids necessary to create polypeptides maintained?

Initiation of translation

Translation starts when mature mRNA binds to a small ribosomal subunit at the mRNA binding site. All mRNA have an initiation (start) codon, AUG, which can be linked to the initiator tRNA (**Figure 1**). This specific tRNA always carries methionine. Thus, all proteins start with this amino acid.

Student view

Overview (/study/ap 422- cid- 755105/o

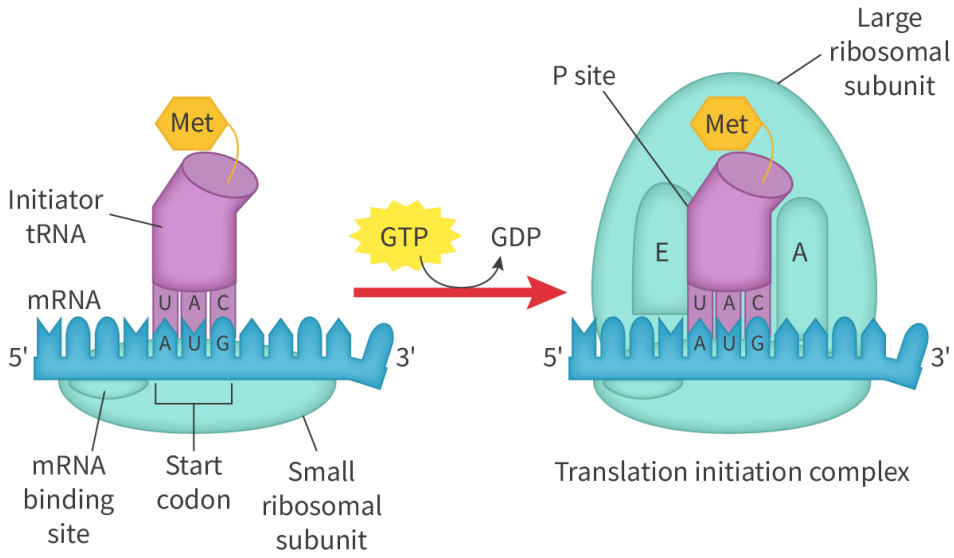


Figure 1. Initiation of translation.

More information for figure 1

The diagram visually explains the initiation of translation. On the left, it shows a small ribosomal subunit with an mRNA binding site labeled 5' to 3'. The mRNA strand with a start codon AUG is aligned below this site. An initiator tRNA molecule, labeled with a hexagon and the word 'Met' for methionine, is positioned above, with its anticodon UAC matching the mRNA start codon. Arrows indicate the conversion of GTP to GDP.

On the right, the diagram depicts the translation initiation complex formed by the union of the large and small ribosomal subunits, with binding sites labeled E, P, and A. The initiator tRNA occupies the P site and is still paired with the start codon AUG. The labeled site positions indicate the spatial arrangement crucial for the process. The diagram captures each component's role and positioning during the translation initiation process, providing a visual representation of molecular biology concepts.

[Generated by AI]

At initiation, the 5′ terminal of the mRNA binds to the small ribosomal subunit. The ribosome then moves along the mRNA until it finds the start codon AUG. Next, the anticodon of the initiator tRNA, carrying the amino acid methionine, binds to the codon of the mRNA. Finally, the large ribosomal subunit joins to complete the assembly of the translation complex. Now that each component is in its correct location, the process of translation can start.

In **Figure 1** you see the labels E and A on the large ribosomal subunit. The space filled by the initiator tRNA is called the P site. A, P and E stand for Aminoacyl-tRNA binding site, Peptidyl-tRNA binding and Exit, respectively. The A site is where the incoming tRNA with its attached amino acid binds, while the P site is where tRNA from the A site moves after its amino acid forms a peptide bond with the growing polypeptide chain. Therefore the P site is where the tRNA holding the growing polypeptide chain is found. As the name suggests, the E site is where the tRNA moves after transferring its amino acid to the growing polypeptide chain, ready to exit the ribosome.

Student view

Overview (/study/ap 422-cid-755105/o

Modification of polypeptides into their functional state

After a polypeptide is synthesised at a ribosome by translation, it is often still not in its final functional state. This requires further modification of the polypeptide. When polypeptides are synthesised by ribosomes on the rough endoplasmic reticulum, they are packaged in vesicles which carry them to the Golgi apparatus. It is in the Golgi apparatus where many of these modifications are carried out.

An example of post-translational modification is the production of insulin. Insulin is a peptide-based hormone produced in the beta cells of the pancreas.

When the insulin gene is translated, the product is pre-proinsulin (**Figure 2**). This is a polypeptide 110 amino acids in length. It is composed of four main sections: a signal peptide (28 amino acids), an A chain (21 amino acids), a B chain (30 amino acids) and a C-peptide (31 amino acids). Once the pre-proinsulin enters the rough endoplasmic reticulum, the signal peptide is removed. The remaining polypeptide is now called proinsulin. Disulfide bridges form between the A chain and the B chain. The proinsulin is packaged into vesicles that move to the Golgi apparatus where the C-peptide is removed and mature insulin remains.

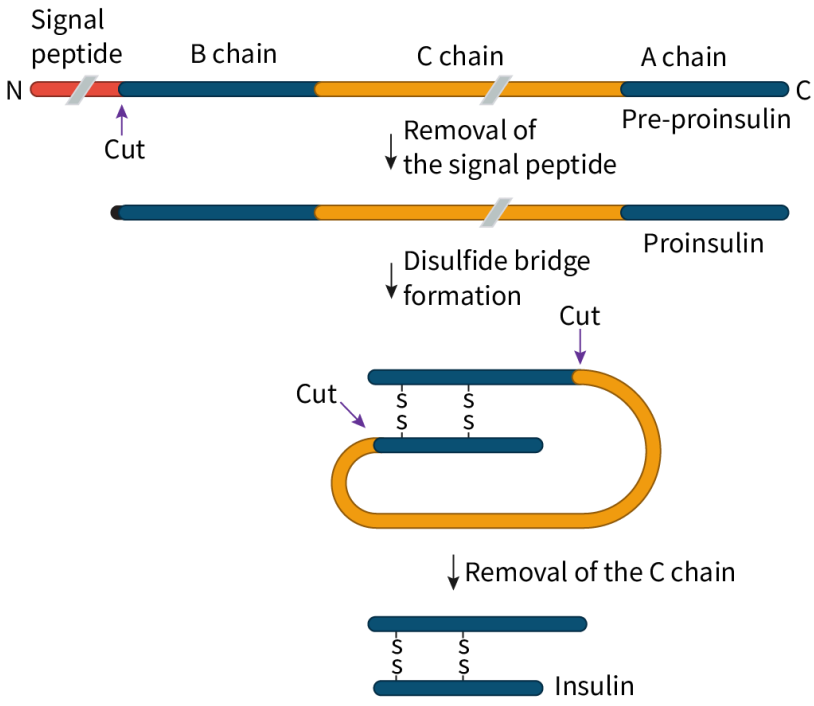


Figure 2. Post-translational modification of pre-proinsulin to insulin.

More information for figure 2

The diagram illustrates the process of transforming pre-proinsulin into insulin through post-translational modification. It begins at the top with a linear representation of pre-proinsulin, showing segments labeled: signal peptide, B chain, C chain, and A chain. An arrow labeled "Cut" points to the removal of the signal peptide, converting pre-proinsulin to proinsulin. Beneath, proinsulin is depicted without the signal peptide, and arrows indicate the formation of disulfide bridges between the A and B chains. The next step shows the proinsulin forming

Student view

Overview (/study/ap 422- cid- 755105/o

a loop to connect the A and B chains, with the C chain labelled. Another "Cut" marks the removal of the C peptide, resulting in the final insulin structure at the bottom, where only the A and B chains remain linked by disulfide bridges.

[Generated by AI]

Creativity, activity, service

Strand: Service
Learning outcome: Demonstrate engagement with issues of global significance

Diabetes is a disease in which the body does not produce enough insulin or respond normally to insulin. This disease affects many millions around the world. Depending on the type of diabetes, some people with the disease have to inject insulin several times a day.

You might consider a CAS project where you raise awareness of the disease and how to care for someone with the disease. You might also consider ways to raise money for those people who struggle to afford safe and effective insulin injections.

Recycling of amino acids by proteasomes

For our cells and our body as a whole to function normally, our proteome must be functional. The proteome is the total of all proteins made and used by the body. Our body's cells are constantly producing proteins to maintain our proteome and need a large supply of amino acids to do this. Many of these are supplied by our diet; however, there is also another source. All of the proteins in our body and in our cells that are unneeded, or damaged can be broken down and recycled for their amino acids. This is carried out by a protein complex called a proteasome. Its job is to hydrolyse proteins by breaking the peptide bonds between amino acids. This allows cells to not only maintain a supply of amino acids, but also assists in maintaining correct concentrations of proteins and getting rid of any that are non-functional, keeping our proteome healthy and complete.

Try the drag and drop activity to help with your understanding of initiation and elongation in translation.

Activity

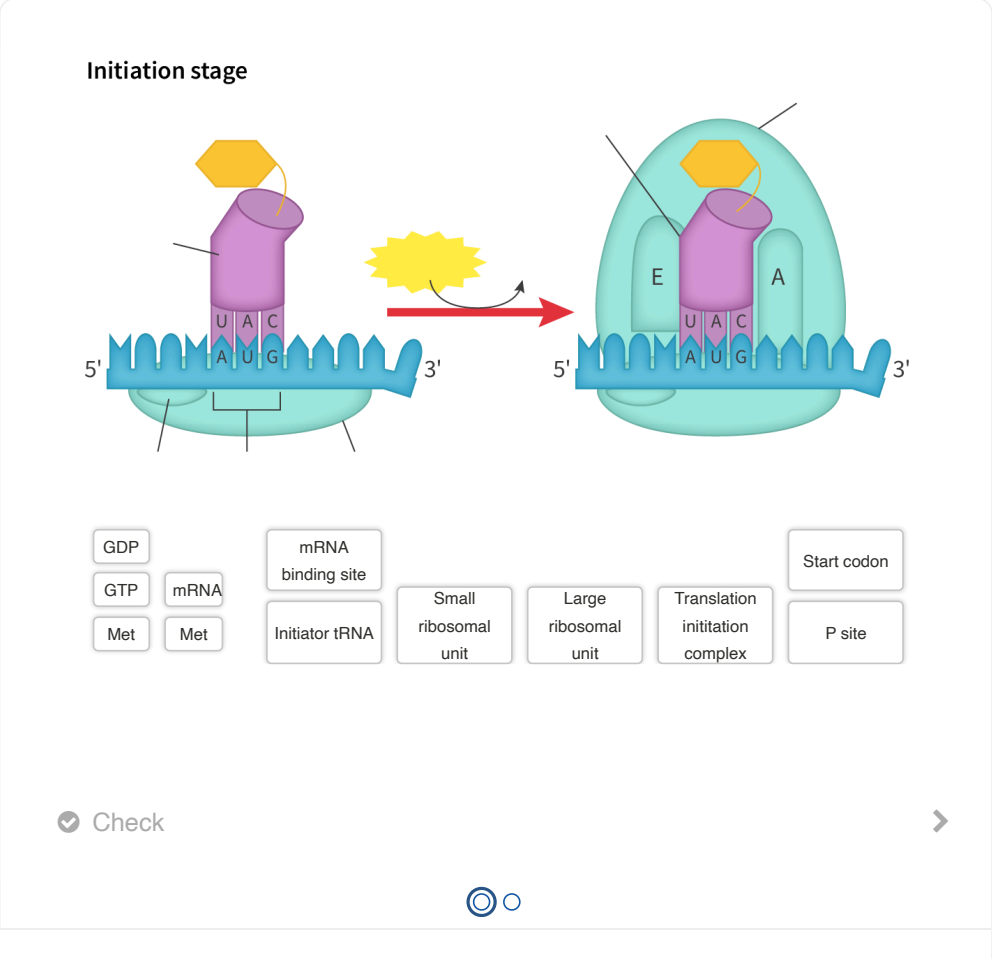
- **IB learner profile attribute:** Knowledgeable

Student view

Overview (/study/ap 422-cid-755105/o

- **Approaches to learning:** Thinking skills — Applying key ideas and facts in new contexts
- **Time required to complete activity:** 15 minutes
- **Activity type:** Individual activity

Drag and drop the labels in **Interactive 1** to review the initiation and elongation stages of translation.



Interactive 1. The initiation and elongation stages of translation.

5 section questions

D1. Continuity and change: Molecules / D1.2 Protein synthesis

Summary and key terms

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/modification-and-splicing-hl-id-44426/print/) Assign

- The first step in protein synthesis is transcription. In transcription RNA polymerase moves along an DNA strand, unzipping it and building a molecule of mRNA. Key to transcription, as

Student view

in DNA replication, is complementary base pairing where the bases A and T always pair and form hydrogen bonds with each other and bases C and G do the same. If an RNA molecule is involved the base U replaces T and pairs with A. DNA must remain stable and unchanged as a result of transcription so that it can be used repeatedly throughout the life of the cell.

- Whether or not a gene is transcribed is one of the main ways that gene expression can be controlled within a cell. Following transcription, the mRNA is then used to carry out translation, where at a ribosome, the code on the mRNA is used to synthesise a polypeptide. The mRNA binds to the ribosome, as do tRNA molecules carrying amino acids. This assembly of components carries out translation.
- The genetic code consists of triplets of bases on the mRNA known as codons. These are complementary to anticodons on the tRNAs, which allows for accurate placement of amino acids in the required sequence, matching the original code on the DNA. The genetic code consists of the 64 possible combinations of the four RNA bases arranged in triplets and the amino acids each codon codes for. As there are only 20 amino acids coded for by 64 codons, the genetic code is degenerate. It is also universal and works the same in almost all living organisms.
- The main stage of translation at which the polypeptide is produced is known as elongation. The ribosome moves along the mRNA one codon at a time. At each codon a new tRNA, carrying the corresponding amino acid, enters the ribosome and binds. Peptide bonds are formed between the growing chain of amino acids.
- Point mutations are errors in DNA or RNA where one base is replaced with another. This can have a range of effects from none to a potentially fatal error in the polypeptide produced.

Higher level (HL)

- Transcription and translation both only occur in the 5' to 3' direction. The directionality of these processes, along with DNA replication helps to ensure the correct placement of nucleotides and amino acids during these processes.
- A region on DNA just before a gene is known as a promoter. This is a non-coding region of DNA that is responsible for control of the transcription of that gene. Proteins known as transcription factors can bind with the promoter, which allows for the RNA polymerase to bind and transcribe the gene. Without the correct transcription factors in place, the RNA polymerase cannot carry out its job. There are many other examples of non-coding regions of our DNA including telomeres, introns and the genes for the production of tRNA and rRNA.
- Following transcription in eukaryotes, post-transcriptional modification occurs. In this process the pre-mRNA is spliced, removing sections known as introns, leaving only the coding exons which are bonded together. The result of this is a molecule of mature mRNA. Alternative splicing is when different combinations of exons can be spliced together to produce different versions of polypeptides which give different functions. Alternative splicing allows the more than 20 000 genes in the human genome to produce many more proteins, possibly close to 100 000 in total.
- The initiation stage of translation involves the assembly of the key components. The mRNA binds to the small subunit of the ribosome. The anticodon of the initiator tRNA, carrying the

Overview (/study/ap 422- cid- 755105/o

first amino acid methionine, bonds with the start codon AUG on the mRNA. Finally the large subunit of the ribosome moves into place.

- Post-translational modification also happens to many polypeptides. For example, the polypeptide pre-proinsulin is produced by translation. It then has a signal peptide removed in the endoplasmic reticulum and its C-peptide removed by the Golgi apparatus leaving mature insulin made of an A chain and B chain connected by disulfide bridges.
- The recycling of proteins is an important process. Damaged and unneeded proteins are broken down by complexes known as proteasomes, providing the cell with a supply of amino acids.

Key terms

Review these key terms. Do you know them all? Fill in as many gaps as you can using the terms in this list.

1. The production of from DNA is known as . This is carried out by the enzyme . It builds the mRNA on the strand of DNA using .
2. is the synthesis of polypeptides using the code on . This occurs at the and also involves , which carry to be used to build the polypeptide.
3. During translation the of the mRNA is complementary to the on the tRNA. The genetic code is as there is often more than one codon for each amino acid.
4. The stage of translation where the polypeptide is being built is known as .
5. Changes to DNA or RNA when one base is substituted for another are known as . These can be due to the degeneracy of the genetic code or they can cause severe consequences.

amino acids | transcription | mRNA | point mutations | mRNA | silent mutations | degenerate | complementary base pairing | codon | template | tRNA | RNA polymerase | Translation | anticodon | ribosomes | elongation

Check

Student view

Overview (/study/ap 422-cid-755105/o

Interactive 1. Gene Expression.

Higher level (HL)

Key terms

Review these key terms. Do you know them all? Fill in as many gaps as you can using the terms in this list.

1. As in DNA replication, transcription and translation have as they both occur in the 5′ to 3′ direction.
2. The region before a gene that controls the expression of that gene is known as a . Proteins known as bind to this region and help determine whether or not a gene is expressed by controlling the binding and activity of RNA polymerase.
3. After transcription mRNA is modified in a process known as . The are removed and the of the mRNA are stuck together. allows for the production of several polypeptides from each gene making the proteome of humans much larger than the genome.
4. Polypeptides can also be modified after translation. is produced following the modification of pre-proinsulin and proinsulin.
5. work in our cells to break down and recycle damaged or unwanted proteins, providing a source of amino acids.

introns | exons | directionality | Proteasomes | transcription factors | Alternative splicing | splicing | Insulin | promoter

Check

Interactive 2. Control and Processing of Gene Expression.

Student view

Overview (/study/app/bio/sid-422-cid-755105/o

D1. Continuity and change: Molecules / D1.2 Protein synthesis

Checklist

What you should know

After studying this subtopic you should be able to:

- Describe transcription as the synthesis of RNA using DNA as a template.
- Describe the use of hydrogen bonding and complementary base pairing in transcription and the replacement of thymine with uracil in RNA.
- Describe how DNA is used as a template for transcription, remains stable and unchanged.
- Explain the use of transcription and its control of gene expression.
- Describe translation as the use of the mRNA produced in transcription to synthesise polypeptides.
- Describe the roles of mRNA, ribosomes and tRNA in translation.
- Describe complementary base pairing between the codons on mRNA and the anticodons on tRNA.
- Explain the main features of degeneracy and universality of the genetic code.
- Deduce the sequence of amino acids from an mRNA strand using a table of mRNA codons.
- Describe the elongation process of translation.
- Describe how a point mutation can affect the polypeptide produced.

Higher level (HL)

- Describe the directionality of transcription and translation as 5' to 3'.
- Describe the role of the promoter in transcription and how the binding of transcription factors to the promoter initiate transcription.
- Explain the roles of non-coding regions of DNA.
- Explain post-transcriptional modification of mRNA in eukaryotes.
- Describe how alternative splicing can produce variants of a protein.
- Describe the initiation stage of translation.
- Describe the modification of polypeptides to their functional state using pre-proinsulin to insulin as an example.
- Describe the recycling of amino acids by proteasomes.

Student view

Investigation

- **IB learner profile attribute:** Inquirer
- **Approaches to learning:**
  - Research skills – Evaluating information sources for accuracy, bias, credibility and relevance
  - Communication skills – Clearly communicating complex ideas in response to open-ended questions
- **Time required to complete activity:** 45–60 minutes
- **Activity type:** Individual activity

Your task

Genetic diseases and disorders affect a large proportion of the human population. Some of these can cause fairly minor symptoms, while others have the potential to greatly impact a person's life and can lead to early death.

Your task is to research a genetic disease or disorder to learn more about how the proteins produced can cause or affect various conditions/ailments. You will share your findings with your class. The following website is a good start for your research. https://www.omim.org (https://www.omim.org)

In your research and when you present, try to answer the following questions:

1. Which gene is affected?
2. Which protein has been altered or changed by the mutation?
3. What is the role or function of the healthy version of the protein?
4. What kind of mutation occurred? If more than one is possible, focus on one.
5. What is the effect of the mutation on the function of the protein?
6. What are the symptoms of the disease/disorder?
7. Are there any treatments, cures or protein therapies?

Reflection

Teacher instructions

The goal of this section is to encourage students to reflect on their learning and conceptual understanding of the subject at the end of this subtopic. It asks them to go back to the guiding questions posed at the start of the subtopic and assess how confident they now are in answering them. What have they learned, and what outstanding questions do they have? Are they able to see the bigger picture and the connections between the different topics?

Students can submit their reflections to you by clicking on 'Submit'. You will then see their answers in the 'Insights' part of the Kognity platform.

Reflection

Now that you've completed this subtopic, let's come back to the guiding question introduced in The big picture (/study/app/bio/sid-422-cid-755105/book/big-picture-id-43547/).

- How does a cell produce a sequence of amino acids from a sequence of DNA bases?
- How is the reliability of protein synthesis ensured?

With these questions in mind, take a moment to reflect on your learning so far and type your reflections into the space provided.

You can use the following questions to guide you:

- What main points have you learned from this subtopic?
- Is anything unclear? What questions do you still have?
- How confident do you feel in answering the guiding questions?
- What connections do you see between this subtopic and other parts of the course?

⚠ Once you submit your response, you won't be able to edit it.

Overview (/study/ap 422- cid- 755105/o

0/2000

Submit

Section Student... (0/0) Feedback Print (/study/app/bio/sid-422-cid-755105/book/summary-and-key-terms-id-46590/print/) Assign

Rate subtopic D1.2 Protein synthesis

Help us improve the content and user experience.

Student view