River Valley High School
2025 JC1 H2 Biology

Lecture Topic 8: The Structure of Nucleic Acids and Gene Expression – Transcription and Translation

Name: _____ ( ) Class: 25J___ Date: _____

References

Title	Author
Biology (9th edition)	Campbell and Reece
Molecular Biology of the Cell (5th edition)	Alberts, Johnson, Lewis, Raff, Roberts and Walter
Biological Science 1 and 2 (3rd Edition)	Taylor, Green and Stout
Molecular Biology of the Cell (5th edition)	Alberts, Johnson, Lewis, Raff, Roberts and Walter
Principles of Genetics (3rd edition)	Snustad and Simmons
Molecular Cell Biology (6th edition)	Lodish, Berk, Kaiser, Krieger, Scott, Bretscher, Ploegh and Matsudaira
Advanced Biology: Principles and Applications (2nd edition)	Clegg and Mackean

Websites

URL	Description
http://learn.genetics.utah.edu/content/basics/transcribe/	Interactive website on protein synthesis
https://highered.mheducation.com/sites/9834092339/student_view0/chapter15/protein_synthesis.html	Watch the video linked on page 10 and complete the Chapter 15 quiz to reinforce your understanding of the concepts.
http://www.dnaftb.org/	Plenty of animations / video clips for DNA-related mechanisms. Refer mainly to "Molecules of Genetics" tab

H2 Biology Syllabus 9477 (2025)

Candidates should be able to use the knowledge gained in the following section(s) in new situations or to solve related problems.

Related Topics	**Content**
DNA Replication	DNA structure and function

Learning Outcomes

2A. The Structure of Nucleic Acids and Gene Expression

a. describe the structure and roles of DNA and RNA (tRNA, rRNA and mRNA)

c. Describe how the information on DNA is used to synthesise polypeptides (description of the processes of transcription, formation of mRNA from pre-mRNA in eukaryotes and translation is required)

Lecture Outline

I. Central Dogma of Molecular Biology

II. Transcription (Synthesis of RNA)

A. Structure of RNA
B. Overview of Transcription
C. Process of Transcription
D. Features of mRNA

III. Translation (Synthesis of Polypeptides)

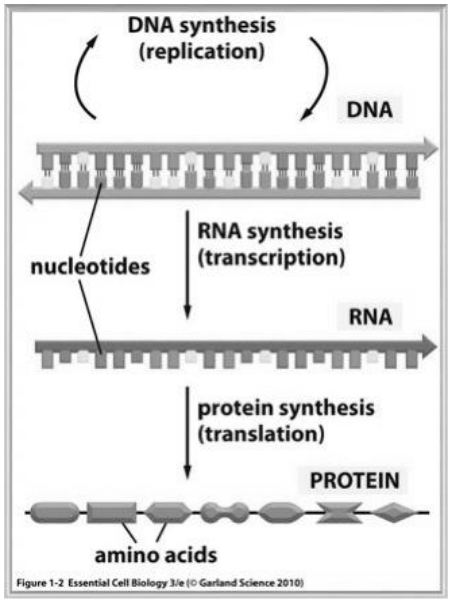
A. Overview of Translation
B. Features of the Genetic code
C. Structure-Function Relationships of tRNA
D. Structure-Function Relationships of ribosome
E. Process of Translation
F. From Polypeptide to Functional Protein

I. Central Dogma of Molecular Biology

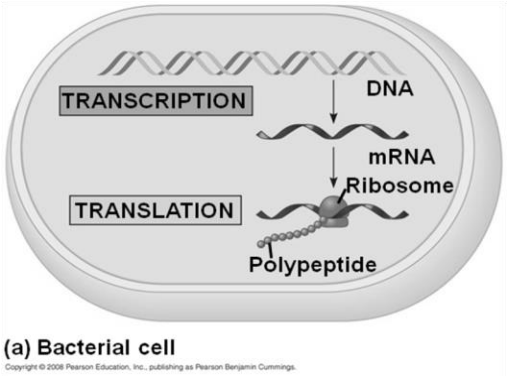
- **Central dogma of molecular biology** – the flow of genetic information in all cells, from DNA to DNA and from DNA to RNA to protein.
- Genetic information is transferred from DNA to DNA during its transmission from generation to generation.
- Genetic information is transferred from DNA to RNA and then to protein during its phenotypic expression in an organism.
  - Information flow is unidirectional.
  - All RNAs are transcribed from DNA by **transcription**. The base sequence of DNA is 'copied' into the messenger molecule (messenger RNA).

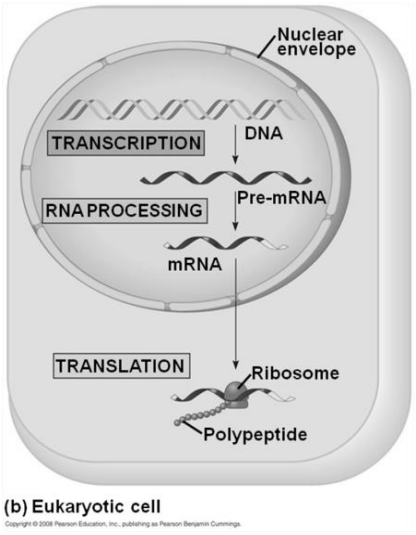
    Location: nucleus (eukaryotes only)
  - All proteins are 'copied' from mRNA by **translation**. Three consecutive mRNA nucleotide bases specify one amino acid in a polypeptide chain using a genetic code that is the same for all organisms.

    Location: cytoplasm

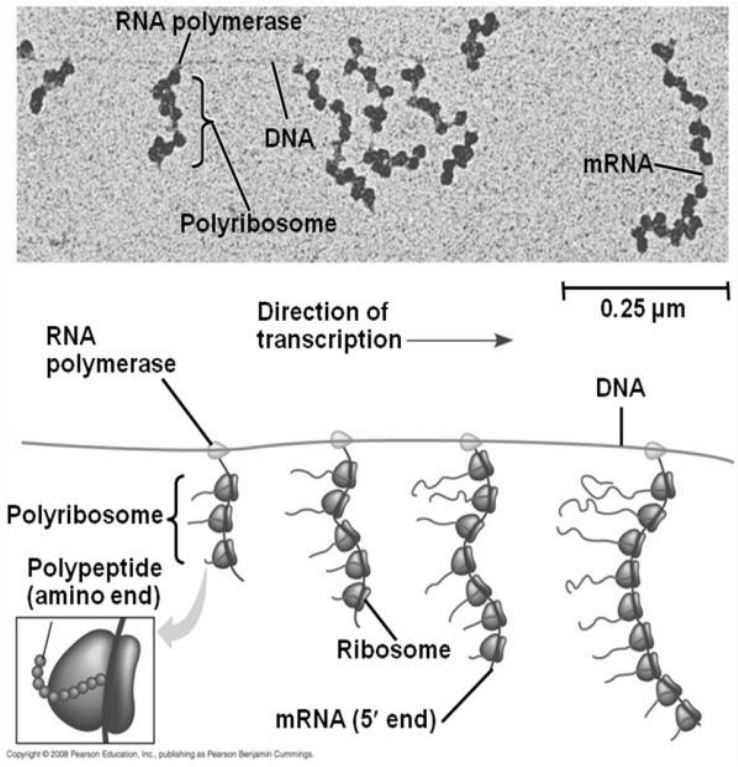


- Key difference in the flow of genetic information between bacteria and eukaryotes:





- In bacteria, the <u>absence of a nuclear membrane</u> allows DNA to share the same space as the protein synthesising machinery in cytoplasm.
  - This allows translation of mRNA to begin while transcription is in progress.
- In eukaryotes, the <u>presence of a nuclear membrane</u> separates DNA in the nucleus from the protein synthesising machinery in the cytoplasm.
  - This causes transcription and translation to take place in different space and at different time.
  - The <u>initial RNA transcripts</u> (**pre-mRNA**) are <u>processed in the nucleus</u> before they are permitted to exit the nucleus as mRNA and be translated into a polypeptide.



<u>Figure showing transcription and translation occurring simultaneously in bacterial cytoplasm</u>

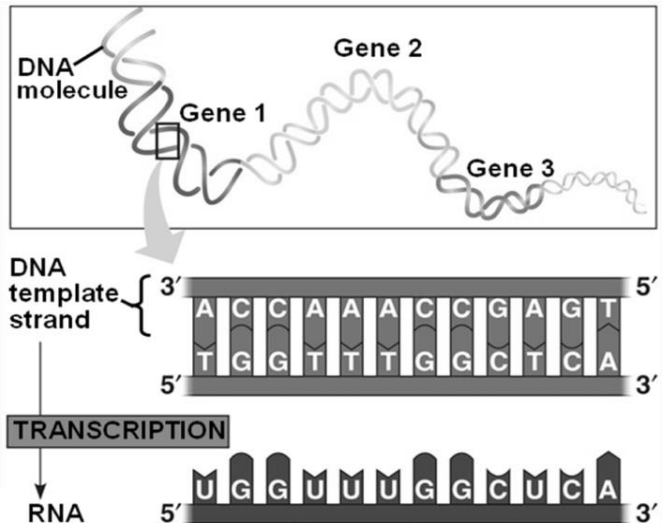
II. Transcription (Synthesis of RNA)

Definition: synthesis of a RNA molecule with a base sequence complementary to a section of DNA, i.e. a **gene**.

A **gene** can be defined as:

a. a segment of DNA with a unique nucleotide/base sequence that encodes information specifying the construction of a particular RNA molecule / polypeptide chain.

b. a unit of inheritance specifying a particular biological function – phenotype. This unit of inheritance is located in a fixed position (called locus) on the chromosome. *(KIV: Inheritance)*



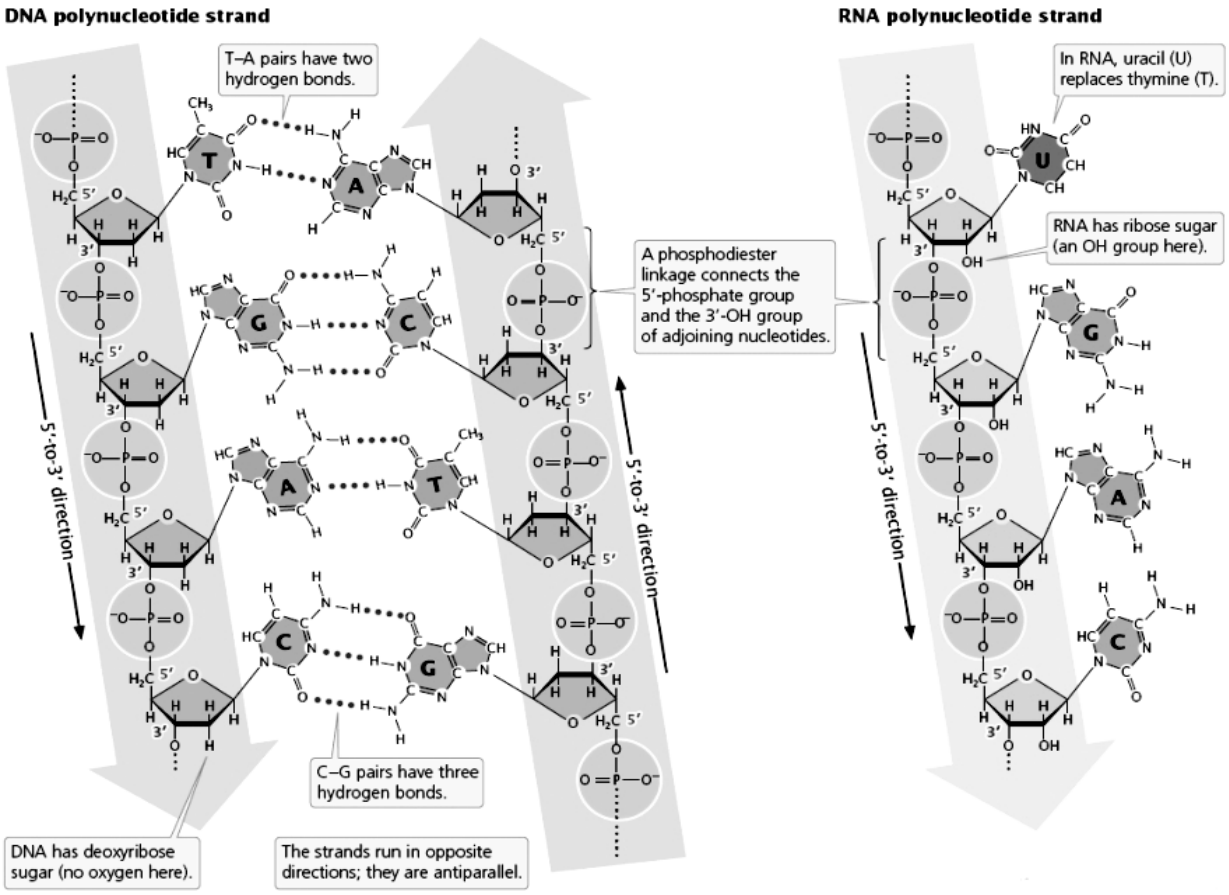
A. Structure of RNA – Intermediaries between DNA and Polypeptide

- Similarities between RNA and DNA:
  1. Presence of phosphoester bonds between monomers
  2. Four different types of nitrogenous bases
- Differences between RNA and DNA:

Parameter	RNA	DNA
Molecular mass	Smaller (20 000 to 2 000 000)	Larger (100 000 to 150 000 000)
Primary structure	1 polynucleotide strand	2 polynucleotide strands
Shape	Variable shapes such as the L-shaped structure of tRNA	Almost always a double helical molecule
Purine / Pyrimidine ratio	A/U ≠ G/C ≠ 1	A/T = G/C = 1
Location	Synthesised in nucleus but found throughout the cell (eukaryotes)	Found almost entirely in the nucleus and in mitochondria and chloroplasts (eukaryotes)
Pentose sugar	Ribose	Deoxyribose
Chemical stability	Less stable – ribose has an additional reactive 2'OH group	More stable – deoxyribose lacks 2'OH group
Nitrogenous bases	Adenine, Guanine, Cytosine, Uracil	Adenine, Guanine, Cytosine, Thymine
Basic forms	Several different kinds and sizes, each with its own function: 1. Messenger RNA (mRNA) 2. Transfer RNA (tRNA) 3. Ribosomal RNA (rRNA) 4. Small nuclear RNA (snRNA)	Only one basic form, but with an almost infinite variety within that form
Amount per cell	Varies from cell to cell (and within a cell according to metabolic activity)	Constant for all cells of a species (except gametes and spores)

- Analysis of the RNA content of cells has shown the existence of three basic types of RNA, all of which are involved in protein synthesis. These are **messenger RNA**, **transfer RNA** and **ribosomal RNA**. All three types are synthesised directly from DNA, which is said to act as template for RNA production, and the amount of RNA in each cell is directly related to the amount of protein synthesis.

Type of RNA	**Structure**	**Function(s)**
Messenger RNA (mRNA)	♦ Short, linear, single-stranded RNA corresponding to a gene encoded within DNA. ♦ Has a 5' modified guanine nucleotide and a 3' poly-A-tail. ♦ Is unstable and degraded easily.	Carries information specifying the amino acid sequences of proteins from DNA. Serves as the template in translation by ribosomes
Transfer RNA (tRNA)	♦ Short (70-90 nucleotides), stable RNA with extensive hydrogen bonds with complementary bases (A-U, C-G) to acquire a cloverleaf shape (2D). ♦ Comprises of 3 loops – anticodon loop (binds to mRNA codon), D-loop (activating enzyme site) and T-loop (ribosome recognition site) ♦ And a 3' CCA stem - an amino acid binding site	Carries specific amino acids to mRNA on ribosome for protein synthesis.
Ribosomal RNA (rRNA)	♦ Longer, stable RNA molecules composing 60% of ribosome's mass. ♦ Has varied 3D conformations.	Plays structural and enzymatic roles in ribosomes – the sites of protein synthesis • structural component of ribosome and contribute to the structure of the binding sites for binding of mRNA and rRNA • as ribozyme that catalyses the formation of peptide bond between amino acids



Structural differences between DNA and RNA

B. Overview of Transcription

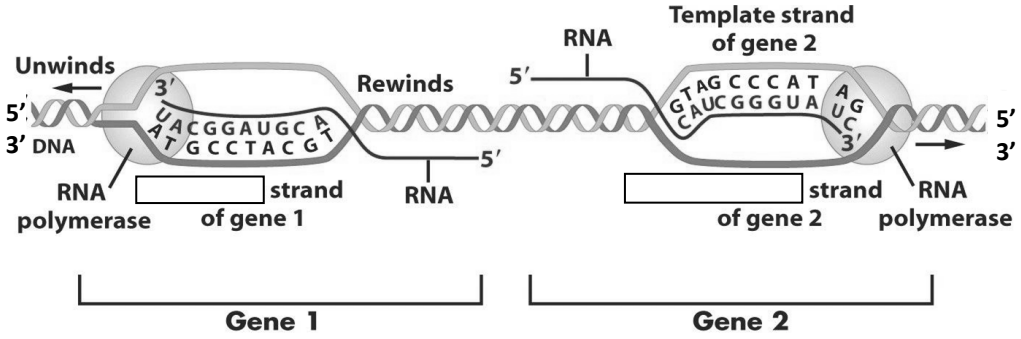
1. Transcription results in the formation of single-stranded RNA molecules. Only one strand of any DNA molecule is transcribed. *Which of the two strands is being used as the template?*

   Template strand

   - sequence on this DNA strand is complementary to that of the RNA
   - serves as the template for synthesis of RNA molecules

   Non-template strand

   - sequence on this DNA strand is the same as that of the RNA, except that the nitrogenous base thymine in DNA is replaced with uracil in RNA



For your information:

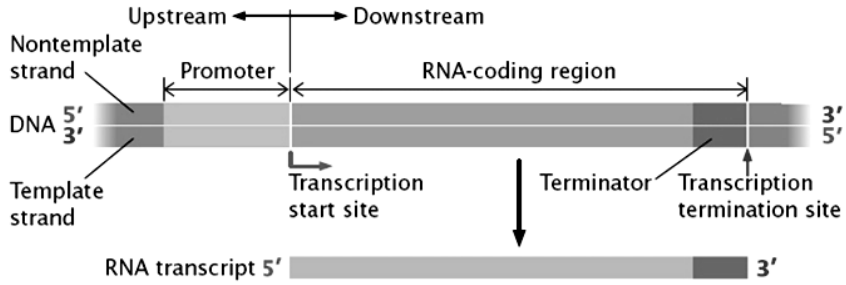
- The template strand is also called the antisense strand or non-coding strand.
- The non-template strand is also known as the sense strand or coding strand because its sequence matches the RNA transcript.

2. Transcription is conservative – the deoxyribonucleotide sequence being transcribed is conserved and is not changed by the process of transcription.
3. Synthesis of the RNA molecule can only be in the 5' to 3' direction.
   It is antiparallel to the template DNA strand, which is read in the 3' to 5' direction.
4. The nucleotide sequence of the RNA chain is determined by the complementary base-pairing between the incoming nucleotides and DNA template.

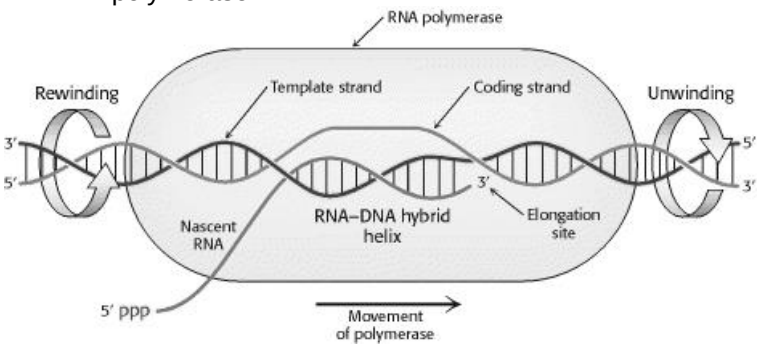
   DNA base sequence: 5' ACTGACTG 3'

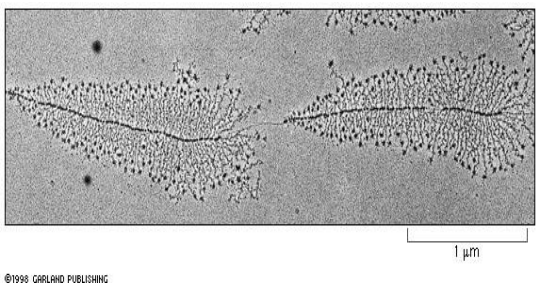
   RNA base sequence: 3' UGACUGAC 5'

5. The segment of the DNA molecule which is transcribed into a single RNA molecule is known as the **transcription unit**, which starts at the **promoter** and ends at the **terminator**.



6. Transcription requires the presence of the enzyme – **RNA polymerase**.
   - A complex molecule composed of several subunits with several functions. For example, **promoter binding**, **template binding**, **nucleotide binding** and **transcription initiation**.
   - Recognises and binds to the promoter in the DNA template.
   - Unwind the DNA helix just upstream of the site for polymerisation to expose a new region of the template strand for complementary base-pairing.
   - Can initiate RNA synthesis without a primer (unlike DNA polymerase).
   - Catalyses the formation of phosphoester bonds that link the ribonucleotides together to form a RNA chain.
   - Transcription of the DNA template continues until the **termination sequence**.
7. A single gene can be transcribed simultaneously by several molecules of RNA polymerase.
   - Unlike a newly formed DNA strand, RNA strand does not remain hydrogen-bonded to the DNA template. It dissociates from the DNA template as it is being synthesised.
   - As soon as the first few bases of a DNA template sequence have been transcribed, they are free to be bound by another RNA polymerase for transcription to form a new RNA strand.
   - This increases the amount of RNA transcribed, thus helping the cell to synthesise the encoded protein in large amounts.
   - The number of simultaneous transcriptions possible depends ultimately on the availability of RNA polymerase.



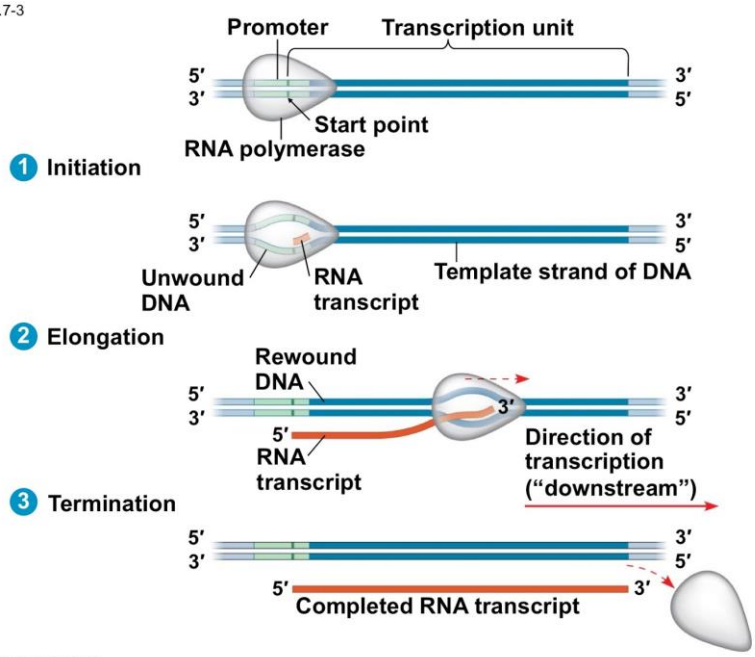


8. **Post-transcriptional modification** is needed for eukaryotic mRNA.
    - In a eukaryotic cell, because of the presence of a nuclear membrane, ribosomes cannot translate the RNA messages as they are being transcribed. These RNA need to be extensively modified / processed before they are transported to cytoplasm.

C. Process of Transcription

- The process of transcription involves three stages:
    1. **Initiation**
    2. **Elongation**
    3. **Termination**

Figure 17.7-3



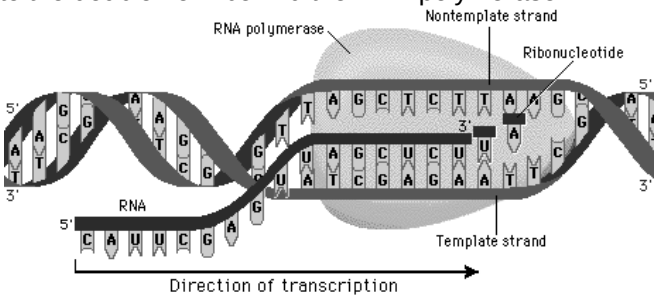
- Note that transcription is the general term for the synthesis of *any* kind of RNA on a DNA template. Here, we are only looking at transcription to form mRNA, which conveys genetic information from DNA to polypeptide.

1. Initiation of Transcription

1. **RNA polymerase** recognises and binds to the **promoter** of the gene on DNA.
    - **Promoter**: region on DNA where RNA polymerase binds and initiates transcription
        - Determines which of the two DNA strands is used as a template
        - Contain the transcription start point / site (i.e. the nucleotide where RNA synthesis actually begins)
        - Certain sections of a promoter are especially important for binding RNA polymerase. For example, the TATA box. *Why TATA box?*
2. RNA polymerase breaks the hydrogen bonds between complementary base-pairs of the DNA double helix.
3. The DNA double helix unwinds and the two DNA strands separates
4. One of the DNA strands acts as a template for the formation of mRNA.

2. Elongation of Transcription

1. Free ribonucleoside triphosphates / ribonucleotides are aligned along the DNA template strand
2. according to complementary base-pairing rule, i.e. A-U, T-A, G-C.
3. RNA polymerase catalyses the linkage of ribonucleotides via phosphoester bond.
4. RNA polymerase catalyses elongation of the RNA in the 5' to 3' direction by adding ribonucleotides to the free 3' OH end of the growing RNA molecule.
5. The separated DNA strands rewind into the double helix behind the RNA polymerase.



3. Termination of Transcription

1. Transcription proceeds until after the RNA polymerase transcribes a **termination sequence** in the DNA.
2. RNA polymerase detaches from the DNA molecule. mRNA is released.

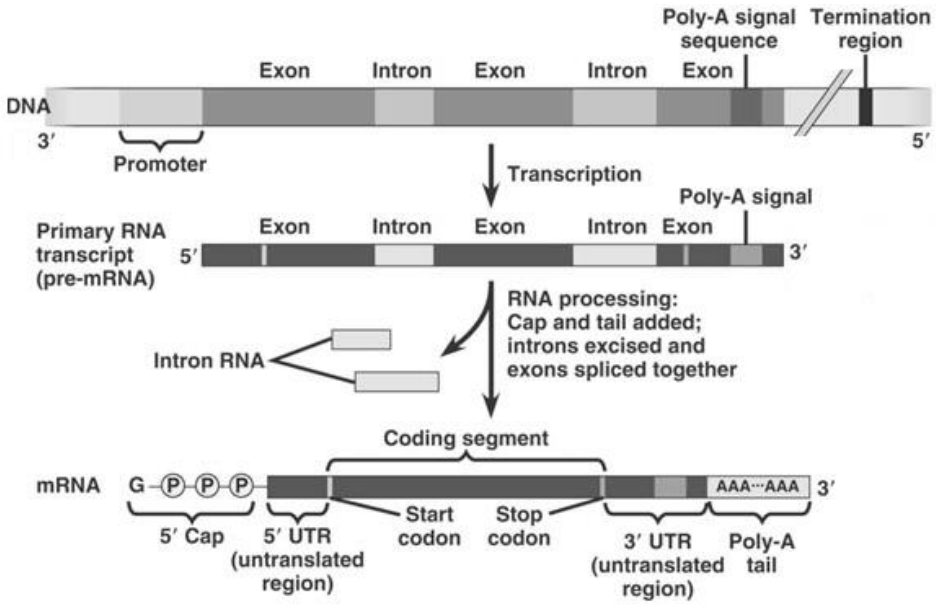
Watch this animation for the transcription process

D. Features of mRNA

- An RNA polynucleotide strand corresponding to a given segment of DNA of an organism, which codes for a polypeptide.
- Relatively unstable – it is continually being synthesised and degraded.
- The minimum length of an mRNA is set by the length of the polypeptide chain for which it codes, i.e. the amount of genetic information it meant to encode.
- There is very little intra-molecular hydrogen bonding in mRNA – the molecule exists as a fairly linear-stranded structure.
- After transcription, enzymes in the eukaryotic nucleus modify the primary transcript in various ways before it leaves the nucleus via the nuclear pore.

Post-transcriptional modifications (only for eukaryotes)

1. Each end of a pre-mRNA molecule is modified in a particular way:
   a. The 5'end is immediately capped off with a modified form of guanine (G) nucleotide. This 5' cap has at least 2 important functions:
      i. Helps protect the mRNA from degradation by hydrolytic enzymes
      ii. After the mRNA reaches the cytoplasm, the 5' cap functions as part of an 'attach here' sign for ribosomes.
   b. At the 3' end, an enzyme makes a poly(A) tail consisting of some 50 to 250 adenine nucleotides
      i. Serves to inhibit degradation and probably helps ribosomes to attach to it
      ii. Facilitate export of mRNA from the nucleus
2. Spliceosome cuts out the introns from the pre-mRNA and joins all the exons together into a continuous coding strand via process called splicing.



III. Translation (Synthesis of Polypeptide)

Definition: process by which the sequence of codons in mRNA is converted into a sequence of amino acids in a polypeptide chain

A. Overview of Translation

1. The genetic information, encoded in mRNA in the form of codons, is decoded into its corresponding sequence of amino acids in a polypeptide.
2. The translation process lines the amino acids in the order defined by the nucleotide sequence. The amino acids are linked together by peptide bonds.

B. Features of the Genetic code

1. **T**: genetic code consists of triplet of bases (codons) on the mRNA. Each codon specifically codes for one amino acid (except for "STOP" codons).
   - Each codon is written as it appears in the mRNA and is read in a 5' to 3' direction.
   - There are 64 (4^3) possible codons, because there are three nucleotides in each codon and there are four possible bases (A, G, C and U) for each nucleotide position.
   - Of the 64 possible codons, 61 code for amino acids and 3 serve as termination signals of polypeptide synthesis.
2. **U**: genetic code is universal, i.e. the same codons code for the same amino acids in all species of organisms.
   - Any particular codon represents the same amino acid in all organisms. For example, lysine is coded for by AAA or AAG in the mRNA of all organisms.
3. **N**: genetic code is non-overlapping. mRNA sequence is read continuously in a series of triplets without skipping any nucleotides
4. **D**: genetic code is degenerate. There are 64 possible codons coding for 20 different amino acids, hence >1 codons may code for the same amino acid.
   - Only 2 amino acids – methionine and tryptophan are coded by a single codon. Most amino acids are coded for by several codons, up to a maximum of six.
   - The codons coding for the same amino acid are similar, particularly in their first two nucleotides. For example glycine:

GGA
GGU
GGG
GGC

5. Start: "START" codon is AUG, which also codes for the amino acid methionine, and initiates synthesis of all polypeptide chains.

6. End: "STOP" codons are UGA, UAA and UAG, which do not code for amino acids. They signal the termination of translation.

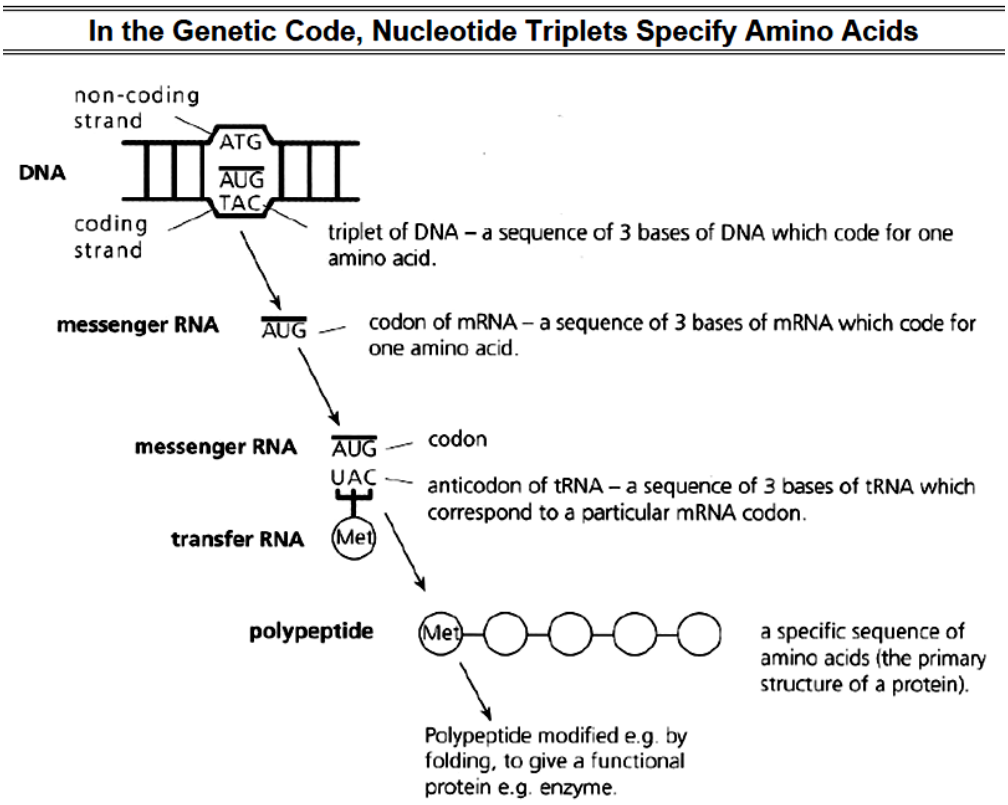


Table 9.7 The 20 amino acids found in proteins and the genetic code

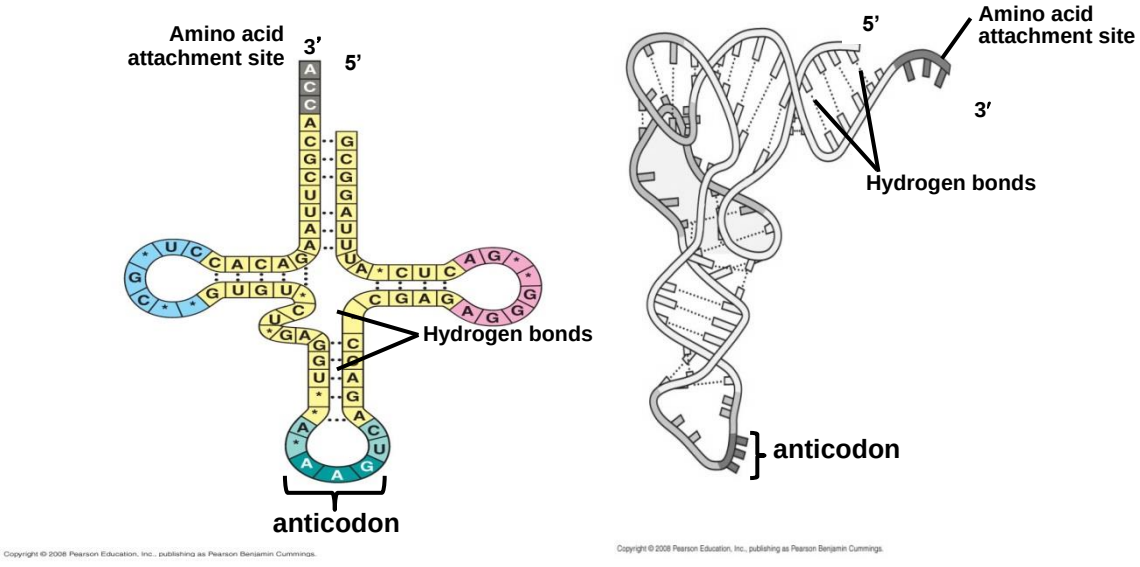
Amino acid	Abbreviation
alanine	Ala
arginine	Arg
asparagine	Asn
aspartic acid	Asp
cysteine	Cys
glutamine	Gln
glutamic acid	Glu
glycine	Gly
histidine	His
isoleucine	Ile
leucine	Leu
lysine	Lys
methionine	Met
phenylalanine	Phe
proline	Pro
serine	Ser
threonine	Thr
tryptophan	Trp
tyrosine	Tyr
valine	Val

The genetic code (the code is given here in terms of the mRNA codons)

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

C. Structure - Function Relationships of tRNA

- The codons in mRNA do not directly recognise the amino acids they specify i.e. the nucleotide triplets do not directly bind to the amino acids.
- The translation of mRNA into polypeptide depends on adaptor molecules that can recognise and bind both to the codon and to the amino acid. These adaptors consist of a set of small RNA molecules known as **transfer RNA** (tRNAs).
- Each of the 20 amino acids found in the cell has at least 1 corresponding tRNA molecule.
- tRNAs are relatively small molecules compared to the other RNA species, having an average of 80 nucleotides per molecule. They constitute about 15% of the total cellular RNA.
- tRNAs acquire a characteristic cloverleaf shape structure at the two dimensional structure. Nucleotide bases in certain regions of the tRNA strand form hydrogen bonds with complementary bases in the other regions.
- There are three loops – the **T loop**, the **anticodon loop** and the **D loop**.
    - **Anticodon loop**: a specialised base triplet that binds to a specific mRNA codon via complementary base-pairing.
    - **Ribosome recognition site (T loop)**: makes specific base pairing with rRNA of ribosome
    - **Activating enzyme site (D loop)**: site for enzyme (amino-acyl tRNA synthetase) that attaches tRNA with its specific amino acid
- The last three nucleotides (**CCA**) at the 3' end of all tRNAs are added on after the transcription of the tRNAs.
    - 3' CCA end is the attachment site for an amino acid.
- The tRNA twists and folds into a compact three-dimensional structure that is roughly L-shaped.
    - The anticodon loop extends from one end of the L-shaped tRNA and 3' CCA end protrudes from the other end of the L.
    - This conformation helps to reduce steric hindrance in the process of translation.

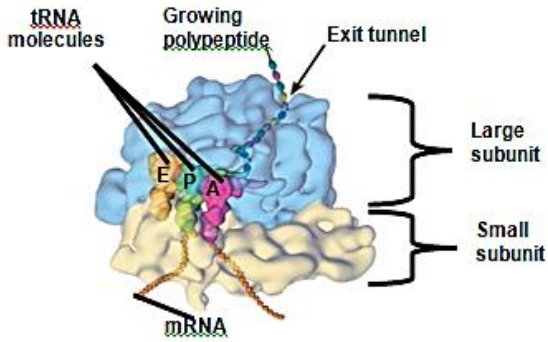


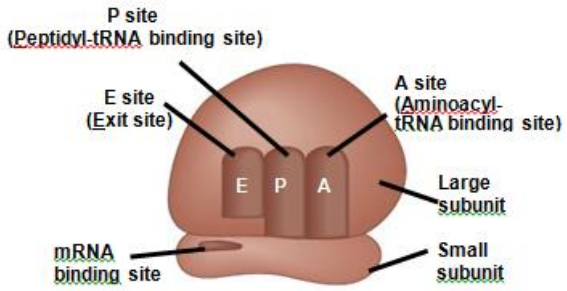
(a) Two-dimensional structure **(b) Three-dimensional structure**

D. Structure - Function Relationships of Ribosome

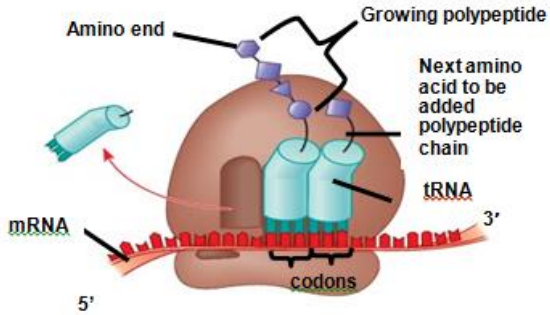
- Ribosomes are the sites for polypeptide synthesis. Its composition is about 60% rRNA and 40% proteins.
  - Ribosomal RNA was the first RNA to be identified, and it makes up approximately 80% of the total cellular RNA.
  - It is synthesised by genes present on the DNA of several chromosomes found at the nucleolus.
  - Following transcription, the primary RNA transcripts are immediately processed to yield shorter strands of rRNA that complexes with ribosomal proteins to assemble the ribosome.

- The structure of the ribosome reflects its function of bringing together mRNAs with tRNAs carrying amino acids (a.k.a. aminoacyl tRNAs).
- A ribosome is made up of two subunits – the large and small subunit.
  - Small subunit has a binding site for mRNA.
  - Large subunit has three binding sites for tRNA.
    i. **Peptidyl-tRNA** site (**P** site) holds the tRNA carrying the growing polypeptide chain
    ii. **Aminoacyl-tRNA** site (**A** site) holds the tRNA carrying the next amino acid to be added to the chain
    iii. **Exit** site (**E** site) allows the discharged tRNA to leave the ribosome.
- In doing so, the ribosome holds the tRNA and mRNA close together and positions the new amino acid for addition to the carboxyl end of the growing polypeptide. It then catalyses the formation of the new peptide bond.
- A single ribosome can synthesise an average sized polypeptide of about 300 amino acids in about 15s.
- Typically, however, a single mRNA is used to make many copies of a polypeptide simultaneously, because a number of ribosomes work on translating the message at the same time.
- These ribosomes are seen as clusters known as **polyribosomes**, which could be bound to the endoplasmic reticulum of plant and animal cells. When ribosomes appear in such aggregates, they are held together by strands of mRNA.

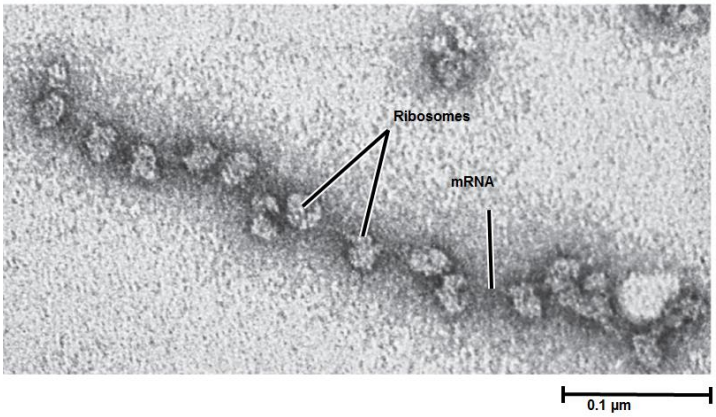


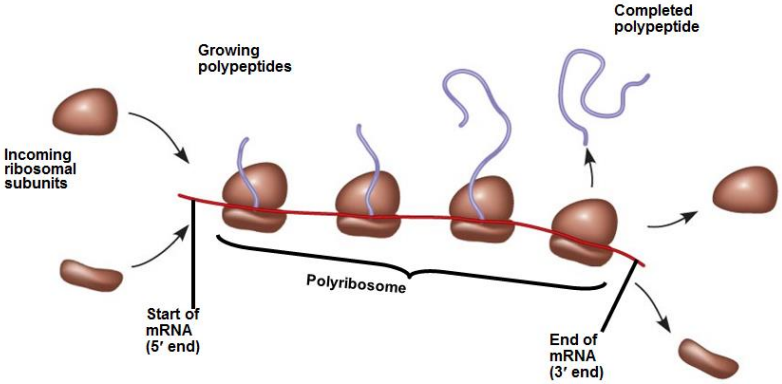


(b) Schematic model showing binding sites



(c) Schematic model with mRNA and tRNA





E. Process of Translation

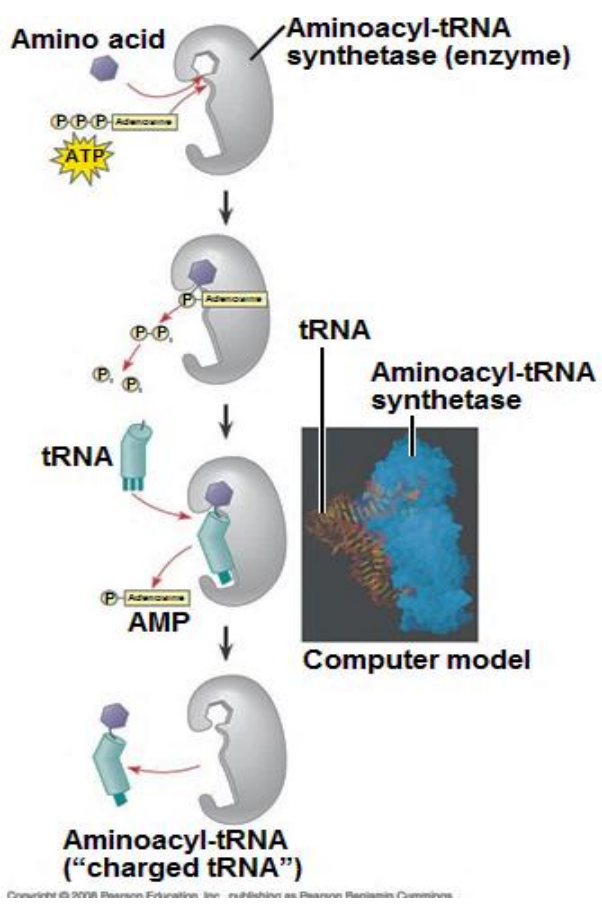
The process of translation requires four steps:

1. **Amino acid activation**
2. **Initiation**
3. **Elongation**
4. **Termination**

Watch this animation for the translation process

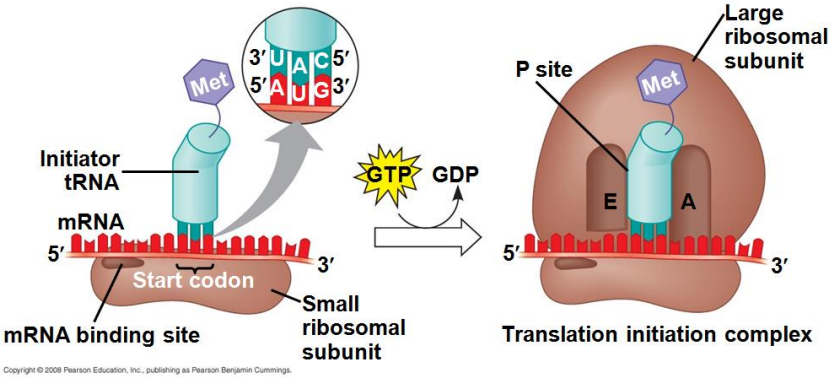
1. Amino acid activation

1. An amino acid is attached to each tRNA molecule at its 3' CCA end forming **aminoacyl-tRNA complex**.
2. tRNA molecules bind to their specific amino acid as determined by their anticodon**.**
3. This reaction is catalysed by the enzyme **aminoacyl-tRNA synthetase**.
   - There are about 20 of these enzymes in the cell – one enzyme for each type of amino acid.
   - Specificity is due to the active site of each type of aminoacyl-tRNA synthetase fits only a specific combination of amino acid and tRNA.
   - The synthetase catalyses the covalent attachment of the amino acid to its tRNA in a process driven by hydrolysis of ATP.



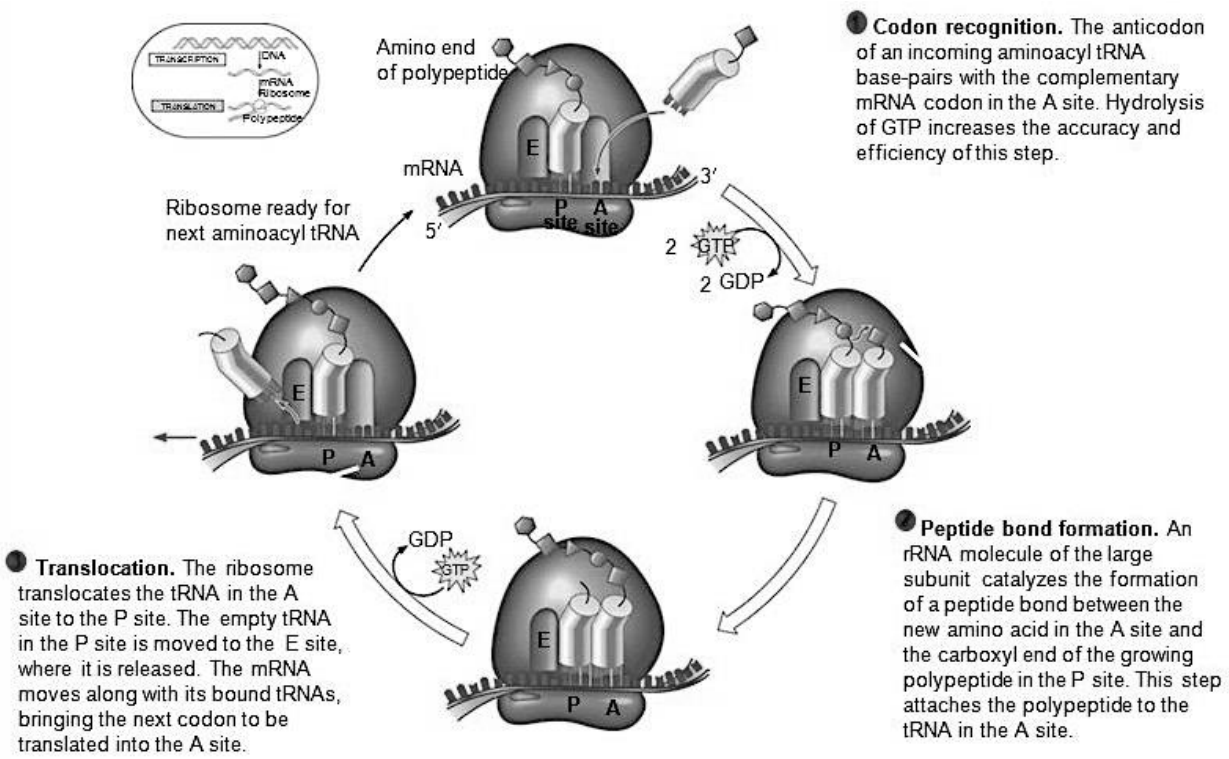
2. Initiation of polypeptide formation

1. mRNA molecule binds to a small ribosomal subunit.
    - Initiation begins when the **5' cap** of the mRNA fits into a special binding site (mRNA binding site) on the small ribosomal subunit.
    - The small ribosomal subunit translocates downstream in search of the **AUG start codon**, where translation of the coding region of the mRNA must begin.
2. The anticodon of the **initiator tRNA** (initiator tRNA already has a methionine attached to it) binds to the start codon on the mRNA.
3. The large ribosomal subunit then binds to the small ribosomal subunit, forming the **initiation complex.**



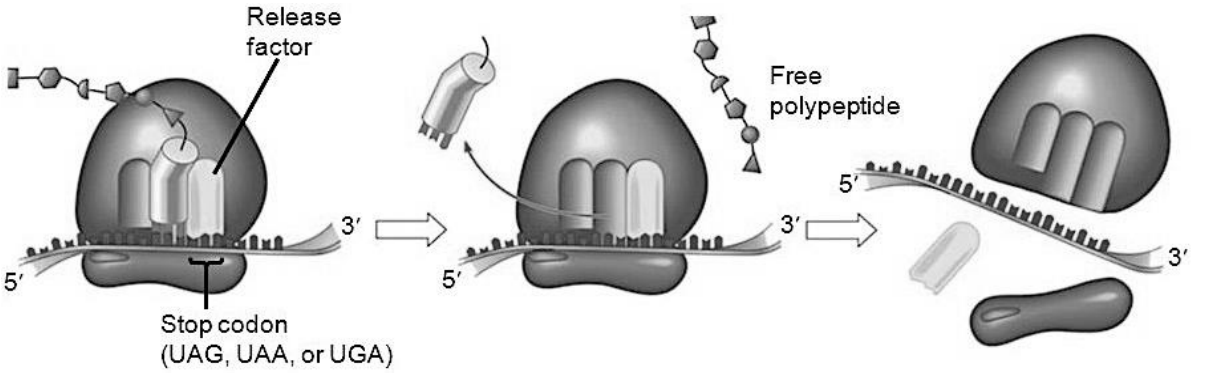
3. Elongation of polypeptide

1. Anticodon of an incoming tRNA molecule carrying its amino acid pairs with the mRNA codon in the aminoacyl-tRNA site (**A** site) of the ribosome.
    - An elongation factor ushers the tRNA into the A site. This step involves the hydrolysis of two molecules of GTP.
2. **Ribozyme / peptidyl transferase** catalyses the peptide bond formation between the amino acid carried by the tRNA in the **A** site with the amino acid/polypeptide bound to tRNA in peptidyl-tRNA site (**P** site).
    - In this step, the polypeptide separates from the tRNA to which it was attached, and the amino acid at its carboxyl end bonds to the amino acid carried by the tRNA in the **A** site.
3. The ribosome translocates (moves) the tRNA in the **A** site, with its attached polypeptide, to the **P** site, taking the mRNA along with it.
4. The tRNA that was in **P** site moves to exit site (**E** site) and from there, leaves the ribosome.
    - In translocation, the ribosome shifts the mRNA by one codon.
    - The translocation step requires energy, which is provided by hydrolysis of a GTP molecule.
5. The mRNA is moved through the ribosome from the 5' to 3' direction (only) on the mRNA.
6. Elongation cycle is repeated until ribosome reaches a stop codon.



4. Termination of polypeptide formation

1. **Release factor** binds directly to the stop codon in the **A** site.
2. Release factor causes addition of a water molecule.
3. This reaction hydrolyses the completed polypeptide from the tRNA and freeing the polypeptide from the ribosome.
4. Translational complex disassembled.
5. Polypeptide chain folds into its unique 3-dimensional conformation.



Types of ribosomes

1. **Free Ribosomes**
   - Free ribosomes are suspended in the cytoplasm.
   - They mostly synthesise proteins that stay in the cytoplasm and exert their effects in the cytoplasm.
2. **Bound / Fixed Ribosomes**
   - Bound ribosomes are attached to the cytoplasmic side of the endoplasmic reticulum (ER).
   - They synthesise proteins of the **endomembrane** system (i.e. the nuclear envelope, E.R., Golgi apparatus, lysosomes, vacuoles, and cell surface membrane) as well as proteins **secreted** from the cell.
   - The polypeptides of proteins destined for the endomembrane system or for secretion are marked by a signal peptide, which targets the polypeptides to the **ER**.
   - The signal peptide, a sequence of about 20 amino acids at or near the **N-terminal** of the polypeptide, is recognised as it emerges from the ribosome by a protein-RNA complex called a signal-recognition particle (SRP).
   - The SRP functions as an adaptor that brings the ribosome to a receptor protein built into the ER membrane.
   - Polypeptide synthesis continues there, and the **growing polypeptide moves across the ER membrane** into the cisternal space via a protein pore.

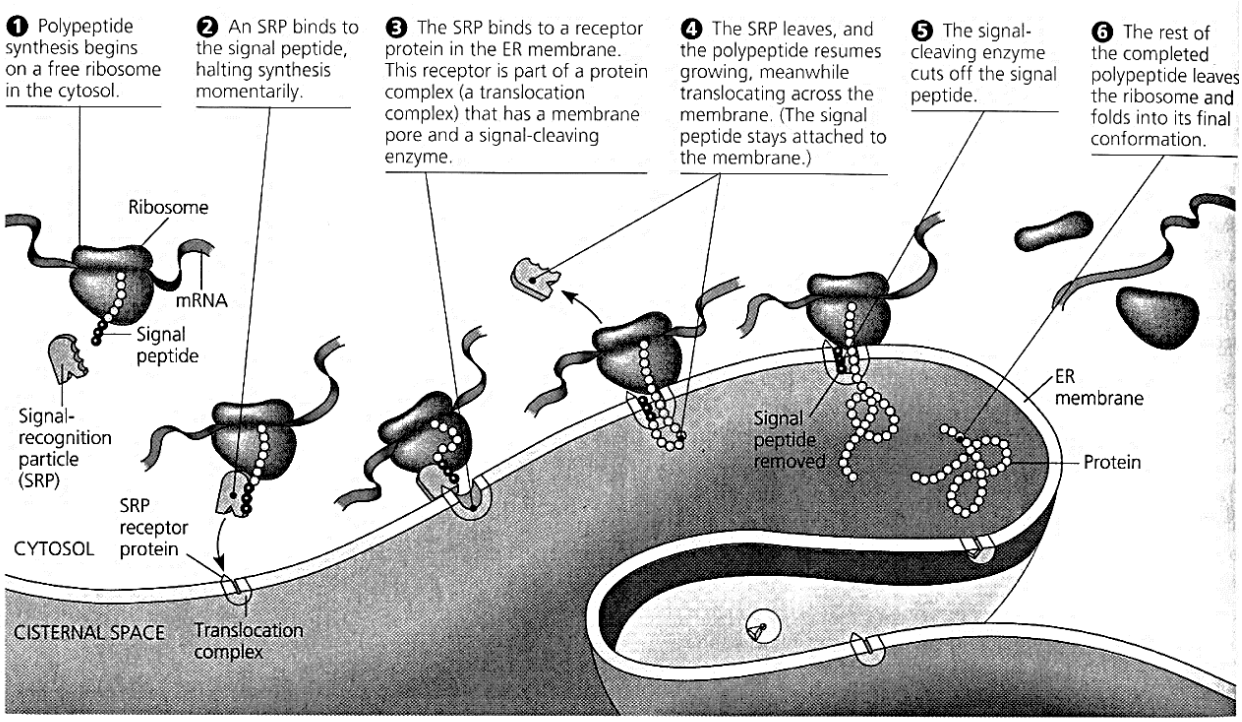


FIGURE 17.21 The signal mechanism for targeting proteins to the ER. A polypeptide destined for the endomembrane system or for secretion from the cell begins with a signal peptide, a series of amino acids that targets it for the ER. This figure shows the synthesis of a secretory protein and its simultaneous import into the ER. In the ER and then in the Golgi, the protein is further processed. Finally, a transport vesicle conveys it to the plasma membrane for release from the cell (see FIGURE 8.8).

F. From Polypeptide to Functional Protein

Post-translational Modification

The process of gene expression is not over when the genetic code has been used to create the sequence of amino acids that constitutes a protein. To be able to perform its designate cellular function, the new polypeptide chain:

1. May be divided into several pieces.
2. May have a major portion of the polypeptide removed. For example, proteolytic cleavage in insulin.
3. Needs to fold into its unique three dimensional conformation.
4. Joins correctly with the other protein subunits which it functions.
5. Binds any small molecule that is required for its activity.
6. Is appropriately modified by protein kinases or other protein modifying organelles. Phosphate groups (via phosphorylation) and sugar groups (via glycosylation) may be added.

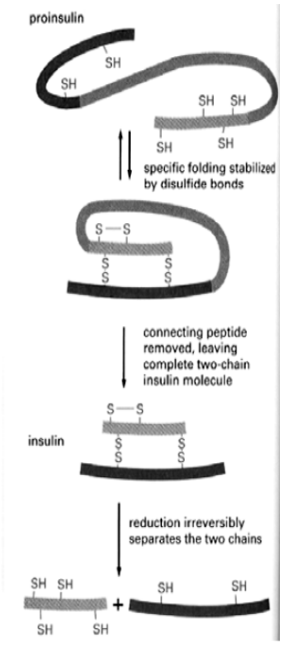
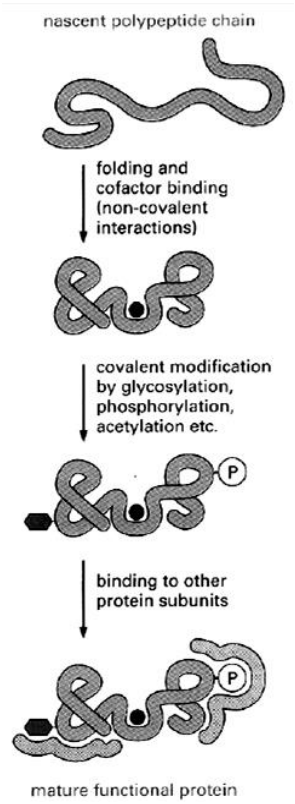


Figure 3–36 Proteolytic cleavage in insulin assembly. The polypeptide hormone insulin cannot spontaneously re-form efficiently if its disulfide bonds are disrupted. It is synthesized as a larger protein *(proinsulin)* that is cleaved by a proteolytic enzyme after the protein chain has folded into a specific shape. Excision of part of the proinsulin polypeptide chain removes some of the information needed for the protein to fold spontaneously into its normal conformation once it has been denatured and its two polypeptide chains separated.



Summary of protein synthesis in an eukaryotic cell