Lecture 19

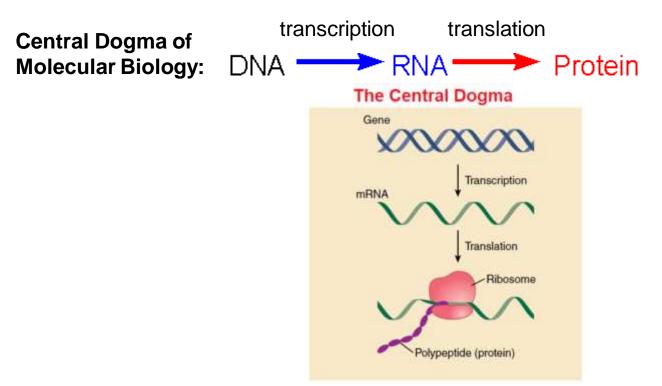
General Biology & Cytology Course 2301130



Faculty of Dentistry, Mutah University Dr. Samer Yousef Alqaraleh

From Gene to Protein (Gene expression)

Overview of gene expression



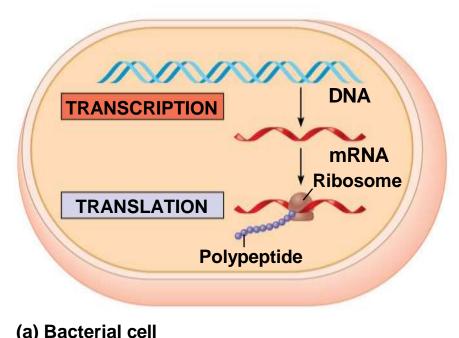
Gene expression: is the process our cells use to convert the instructions in our DNA into a functional product, such as a protein, or non-coding RNA, and ultimately affect a phenotype.

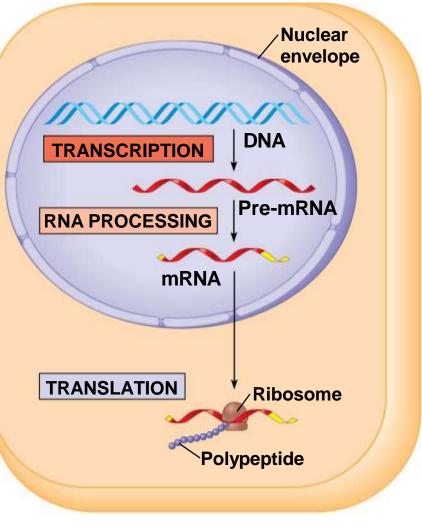
Basic Principles of Transcription and Translation

- RNA is the bridge between genes and the proteins for which they code
- Transcription is the synthesis of RNA under the direction of DNA
- Transcription produces messenger RNA (mRNA)
- Translation is the synthesis of a polypeptide, using information in the mRNA

Where does translation occurs?

- A primary transcript is the initial RNA transcript from any gene prior to processing
- The central dogma is the concept that cells are governed by a cellular chain of command: DNA → RNA → protein

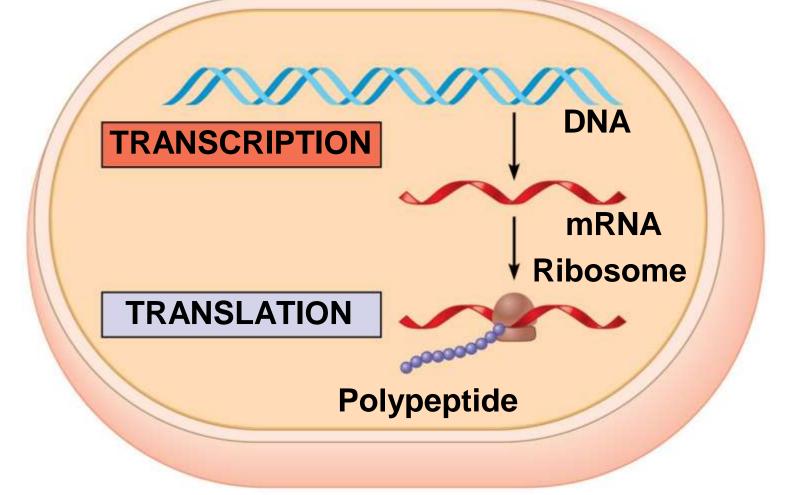




(b) Eukaryotic cell

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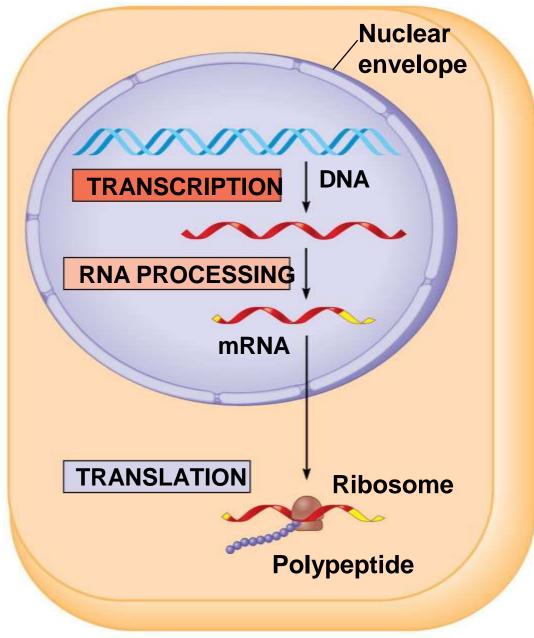
Transcription and Translation in Prokaryotes



 In prokaryotes, translation of mRNA can begin before transcription has finished

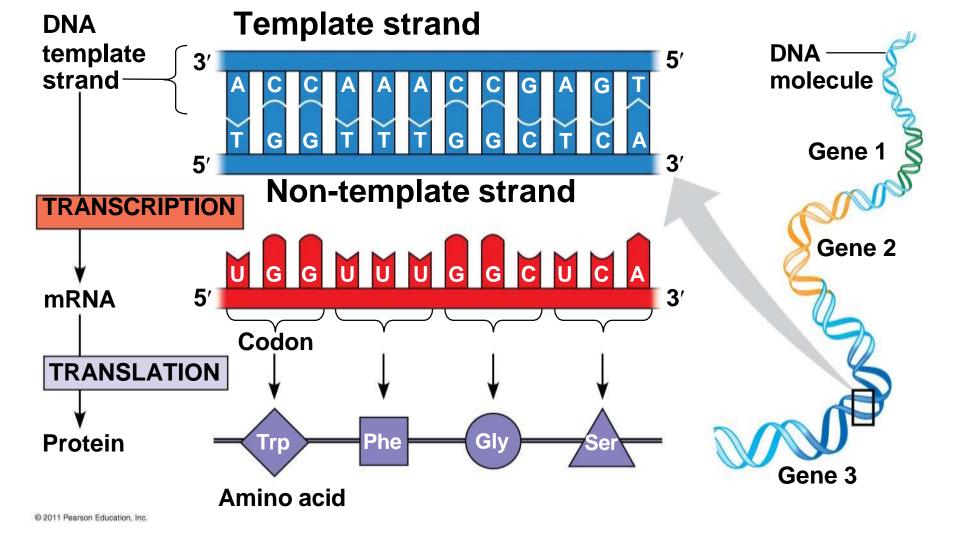
Transcription and Translation in Eukaryotes

- In a eukaryotic cell, the nuclear envelope separates transcription from translation
- Eukaryotic RNA transcripts are modified through RNA processing to yield finished mRNA



The Genetic Code

- The genetic code refers to the code (rules) that governs how a DNA sequence is converted to a protein (amino acid) sequence
- There are 20 amino acids, but only <u>four</u> nucleotide bases in DNA (and RNA)
 - What is the minimum number of nucleotides needed to code for a single amino acid?



 The genetic code is a triplet code where a 3-nucleotide DNA word codes for a 3-nucleotide mRNA word (a codon) which codes for an amino acid

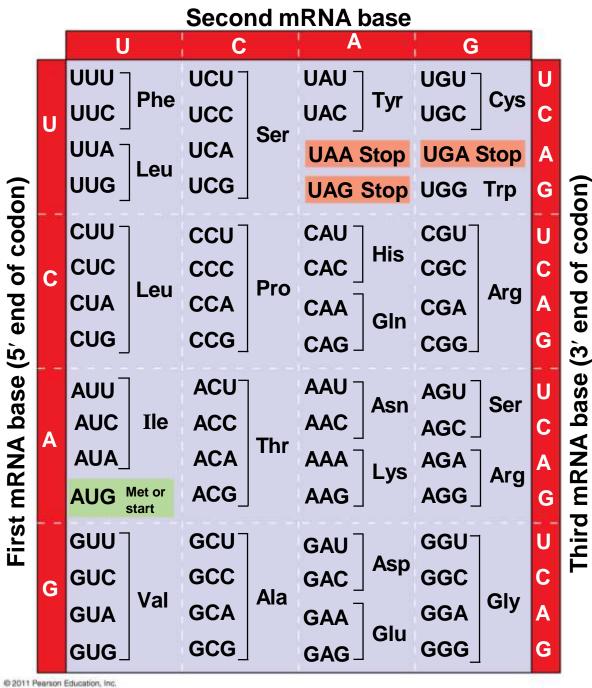
- During transcription, one of the two DNA strands, called the template strand, provides a template for ordering the sequence of complementary nucleotides in an RNA transcript.
- The template strand is always the same strand for a given gene
- During translation, the mRNA base triplets, called codons, are read in the 5' to 3' direction
- Each codon specifies the amino acid (one of 20) to be placed at the corresponding position along a polypeptide

Cracking the Code

- All 64 codons were deciphered by the mid-1960s
- Of the 64 triplets, 61 code for amino acids; 3 triplets are "stop" signals to end translation
- The genetic code is redundant (more than one codon may specify a particular amino acid) but not ambiguous; no codon specifies more than one amino acid
- Codons must be read in the correct reading frame (correct groupings) in order for the specified polypeptide to be produced

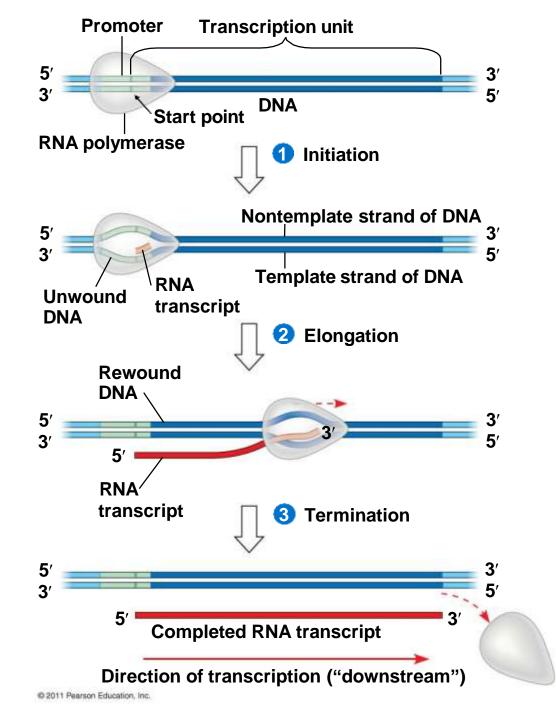
Properties of the Genetic Code

- 64 triplets
 - 61 code for amino acids
 - 3 triplets are "stop" codons
- The genetic code is redundant but not ambiguous



Transcription is the DNA-directed synthesis of RNA

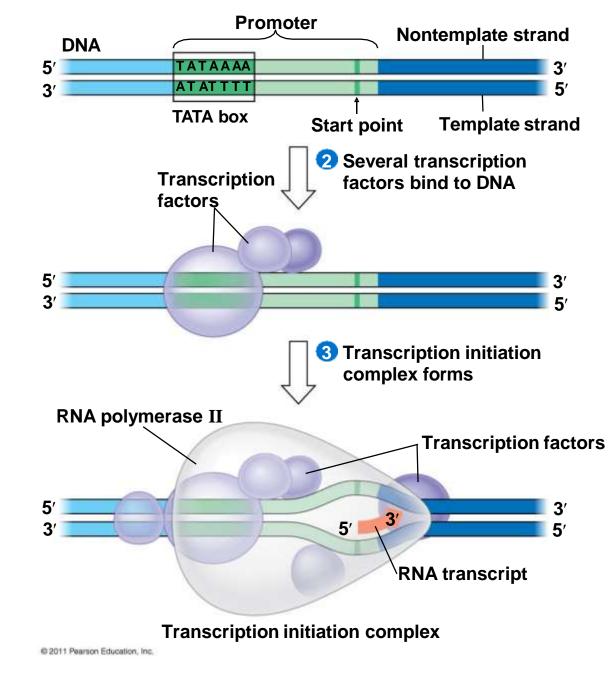
- Transcription consists of three steps
 - Initiation
 - The DNA sequence where RNA polymerase attaches is called the **promoter**
 - Elongation
 - RNA polymerase pries the DNA strands apart and hooks together the RNA nucleotides
 - The RNA is complementary to the DNA template strand, but uracil replaces thymine
 - Termination
 - in bacteria, the sequence signaling the end of transcription is called the **terminator**



RNA Polymerase Binding and Initiation of Transcription

- Promoters signal the transcriptional start point and usually extend several dozen nucleotide pairs upstream of the start point
- **Transcription factors** mediate the binding of RNA polymerase and the initiation of transcription
- The completed assembly of transcription factors and RNA polymerase II bound to a promoter is called a transcription initiation complex
- A promoter called a **TATA box** is crucial in forming the initiation complex in eukaryotes

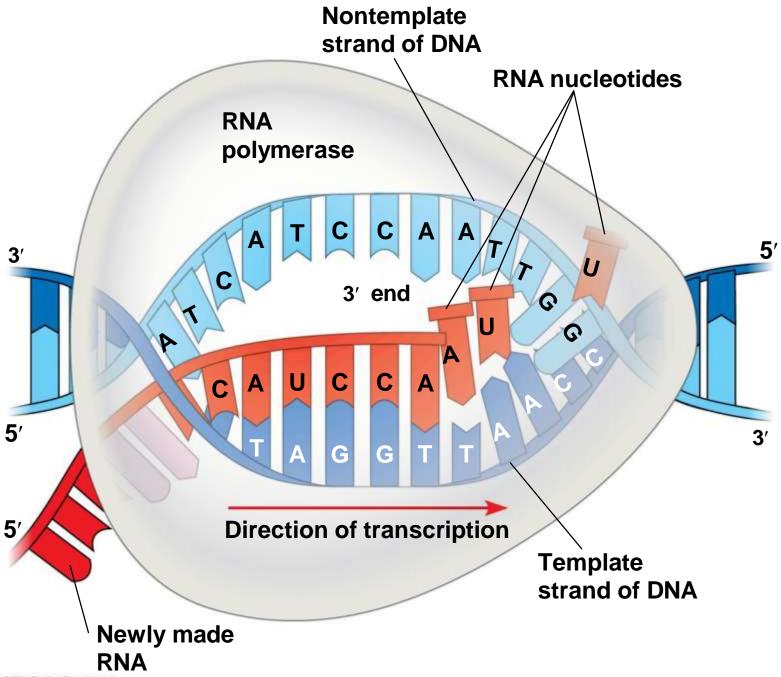




 Transcription in eukaryotes

Elongation of the RNA Strand

- As RNA polymerase moves along the DNA, it untwists the double helix, 10 to 20 bases at a time
- Transcription progresses at a rate of 40 nucleotides per second in eukaryotes
- A gene can be transcribed simultaneously by several RNA polymerases
- Nucleotides are added to the 3' end of the growing RNA molecule



Termination of Transcription

- The mechanisms of termination are different in bacteria and eukaryotes
- In bacteria, the polymerase stops transcription after reaching a *terminator* sequence and the mRNA can be translated without further modification
- In eukaryotes, RNA polymerase II transcribes the polyadenylation signal sequence (AAUAAA); the RNA transcript is released 10–35 nucleotides past this polyadenylation sequence

Eukaryotic cells modify RNA after transcription

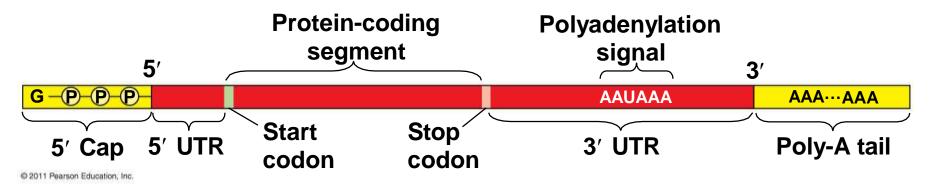
- Enzymes in the eukaryotic nucleus modify premRNA (RNA processing) before the genetic messages are dispatched to the cytoplasm
- RNA processing including:
- 1. Capping: both ends of the primary transcript are usually altered
- 2. Polyadenylation
- 3. Splicing: Some interior parts of the molecule are cut out, and the other parts spliced together

Alteration of mRNA Ends

- Each end of a pre-mRNA molecule is modified in a particular way
 - The 5' end receives a modified nucleotide
 5' cap (7-Methyl guanosin) to be functional in protein synthesis
 - 2. The 3' end gets a poly-A tail
- These modifications share several functions
 - They seem to facilitate the export of mRNA
 - They protect mRNA from hydrolytic enzymes
 - They help ribosomes attach to the 5' end of the mRNA

mRNA in Eukaryotes

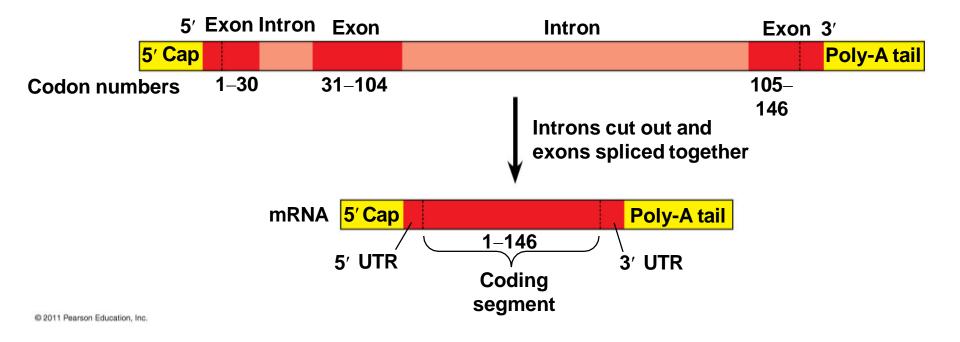
- Note that pre-mRNA (shown on subsequent slides)
 - does not contain the 5' Cap or Poly-A tail
 - does contain introns which are spliced out or removed
- mRNA has the following form:



3. Split Genes and RNA Splicing

- Most eukaryotic genes and their RNA transcripts have long noncoding stretches of nucleotides that lie between coding regions
- These noncoding regions are called intervening sequences, or introns
- The other regions are called exons because they are eventually expressed, usually translated into amino acid sequences
- RNA splicing removes introns and joins exons, creating an mRNA molecule with a continuous coding sequence

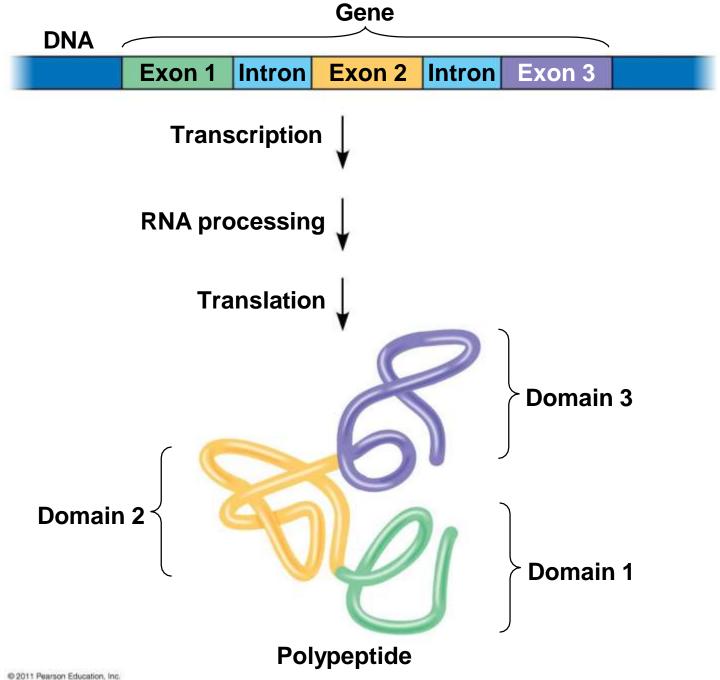
Pre-mRNA following addition of 5' Cap and Poly-A tail:



The Functional and Evolutionary Importance of Introns

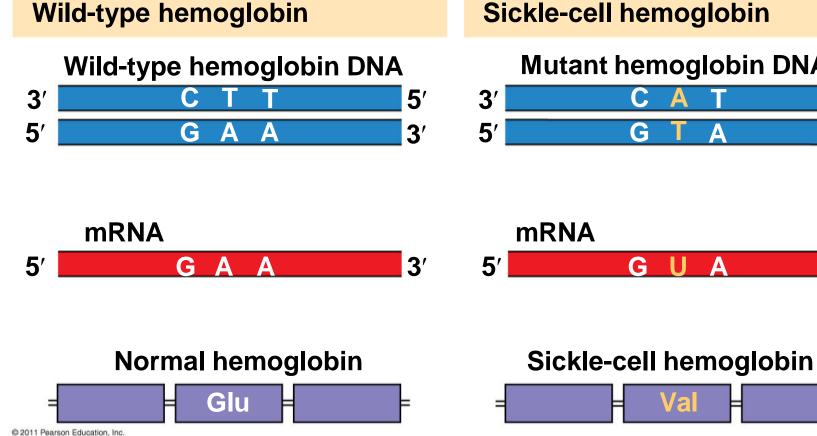
- Some introns contain sequences that may regulate gene expression
- Some genes can encode more than one kind of polypeptide, depending on which segments are treated as exons during splicing
- This is called **alternative RNA splicing**
 - approximately 95% of genes with multiple exons are alternatively spliced!
 - the number of different proteins an organism can produce is much greater than its number of genes

- Proteins often have a modular architecture consisting of discrete regions called **domains**
- In many cases, different exons code for the different domains in a protein
- Exon shuffling may result in the evolution of new proteins



Mutations of one or a few nucleotides can affect protein structure and function

- Mutations are changes in the genetic material of a cell or virus
- **Point mutations** are chemical changes in just one base pair of a gene
- The change of a single nucleotide in a DNA template strand can lead to the production of an abnormal protein



Sickle-cell hemoglobin

Mutant hemoglobin DNA



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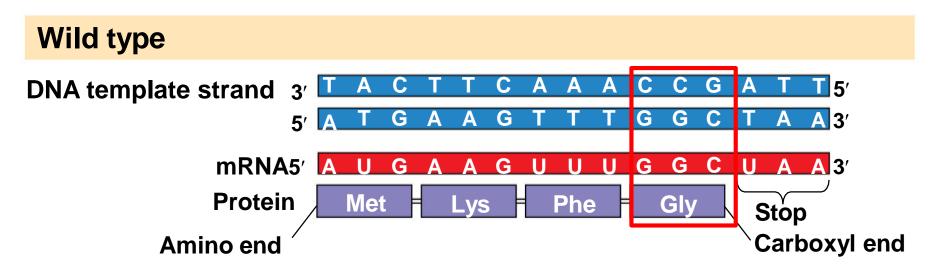
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Types of Small-Scale Mutations

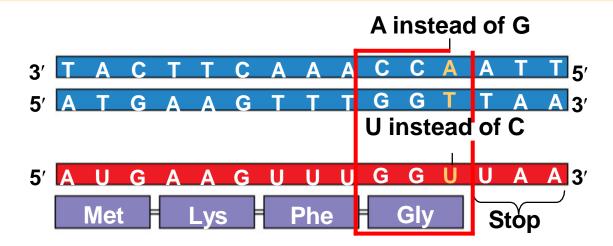
- Point mutations within a gene can be divided into two general categories
 - Nucleotide-pair substitutions
 - Nucleotide-pair insertions or deletions

Nucleotide-Pair Substitutions

- A nucleotide-pair substitution replaces one nucleotide and its partner with another pair of nucleotides
- Silent mutations have no effect on the amino acid produced by a codon because of redundancy in the genetic code
- Missense mutations still code for an amino acid, but not the correct amino acid
- Nonsense mutations change an amino acid codon into a stop codon, nearly always leading to a nonfunctional protein

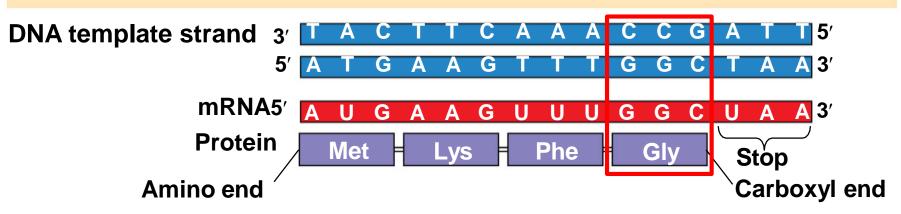


(a) Nucleotide-pair substitution: silent

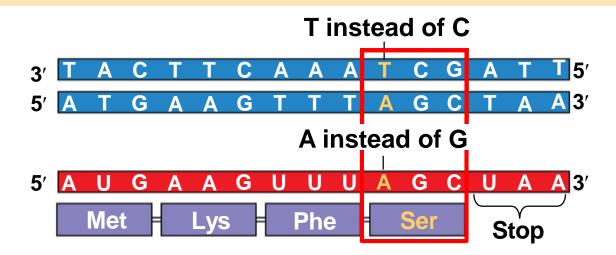


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Wild type

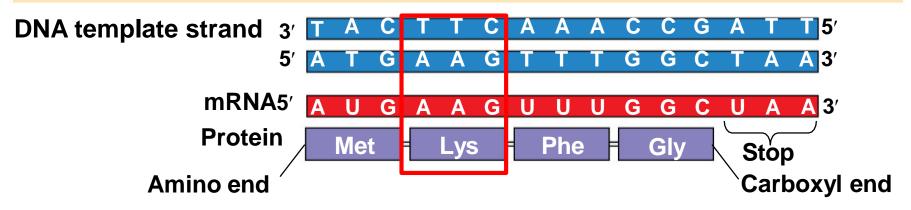


(a) Nucleotide-pair substitution: missense

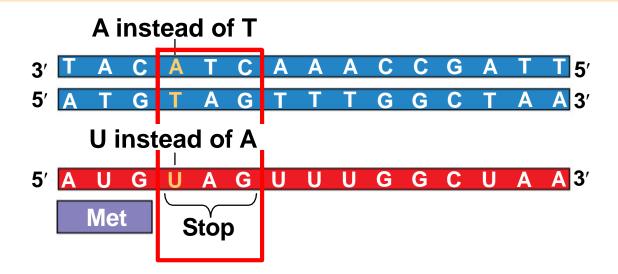


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Wild type



(a) Nucleotide-pair substitution: nonsense

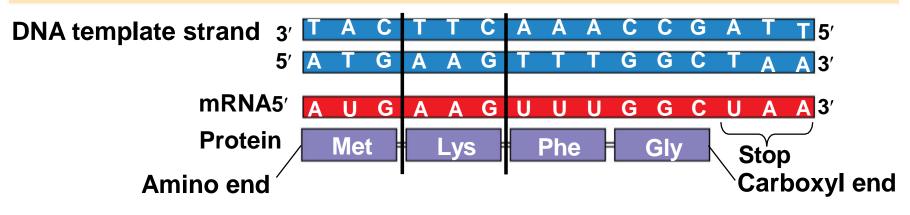


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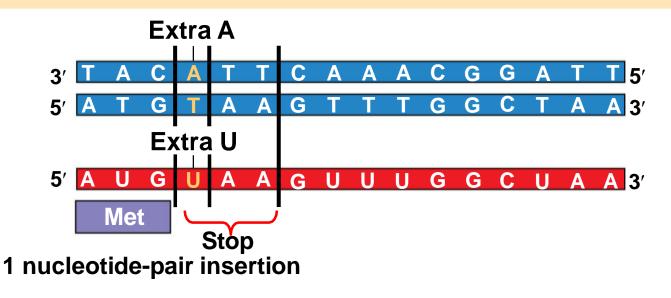
Insertions and Deletions

- **Insertions** and **deletions** are additions or losses of one or more nucleotide pairs in a gene
- These mutations often have a disastrous effect on the resulting protein more often than substitutions do
- Insertion or deletion of nucleotides may alter the reading frame, producing a **frameshift mutation**

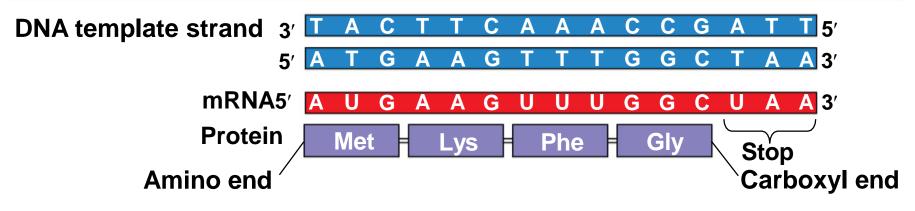
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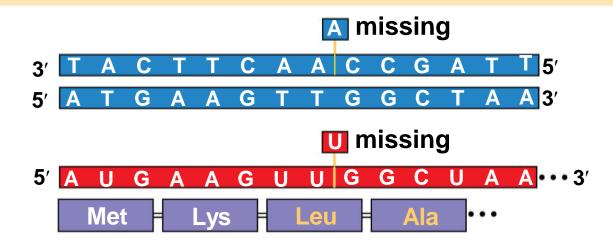
(b) Nucleotide-pair insertion or deletion: frameshift causing immediate nonsense



Wild type

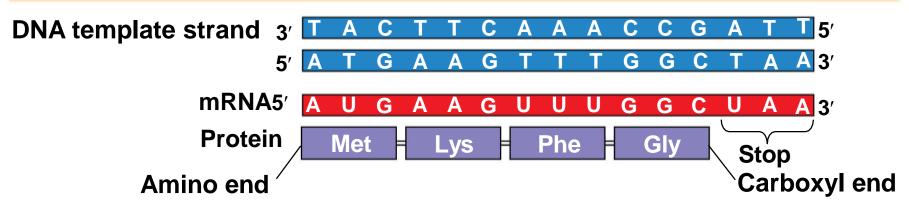


(b) Nucleotide-pair insertion or deletion: frameshift causing extensive missense

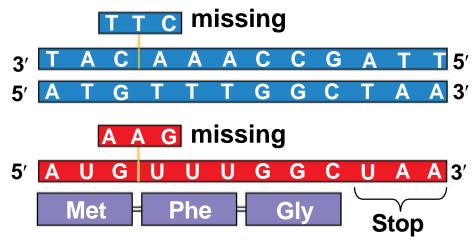


1 nucleotide-pair deletion

Wild type



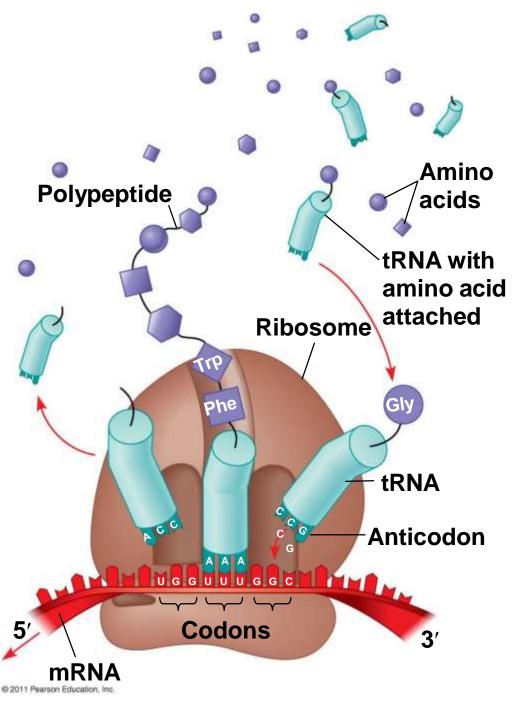
(b) Nucleotide-pair insertion or deletion: no frameshift, but one amino acid missing



3 nucleotide-pair deletion

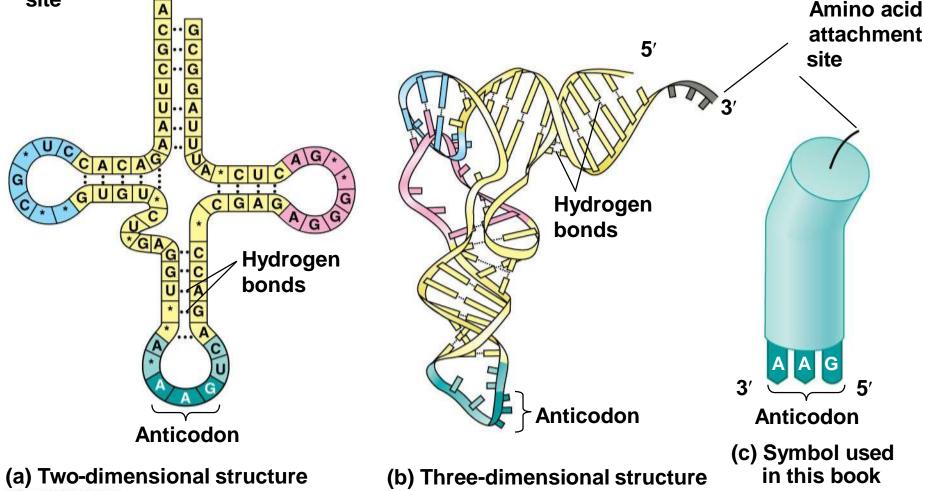
Translation

- A cell translates a mRNA message into protein with the help of transfer RNA (tRNA)
- tRNA transfer amino acids to the growing polypeptide in a ribosome
- Translation is a complex process in terms of its biochemistry and mechanics



tRNA structure

- Each carries a specific amino acid on one end
- Each has an anticodon on the other end; the anticodon base-pairs with a complementary codon on mRNA



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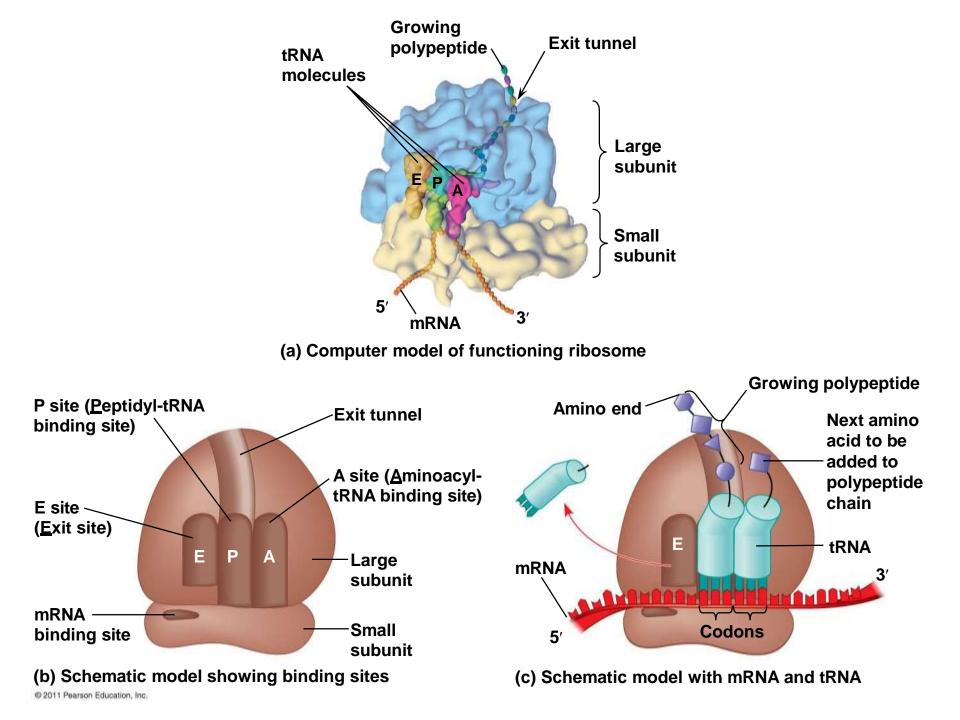
Amino acid

attachment

site

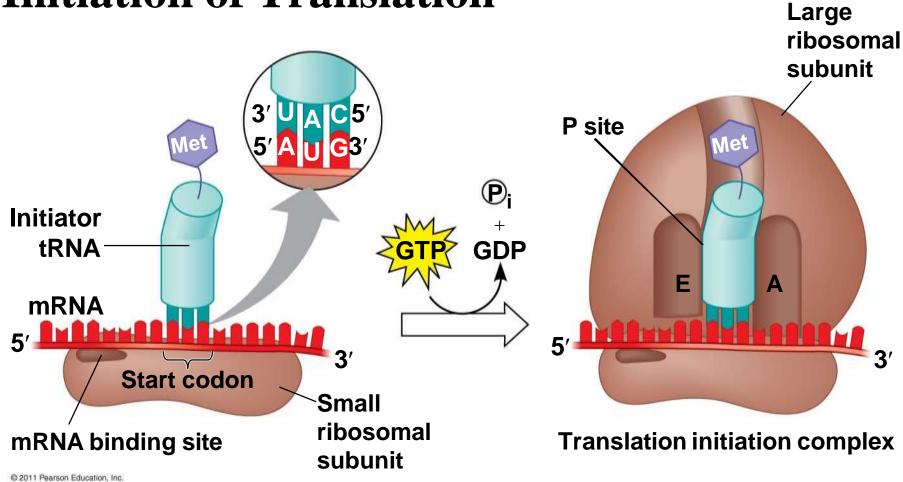
Ribosomes

- Ribosomes facilitate specific coupling of tRNA anticodons with mRNA codons in protein synthesis
- The two ribosomal subunits (large and small) are made of proteins and ribosomal RNA (rRNA)
- Bacterial and eukaryotic ribosomes are somewhat similar but have significant differences: some antibiotic drugs specifically target bacterial ribosomes without harming eukaryotic ribosomes



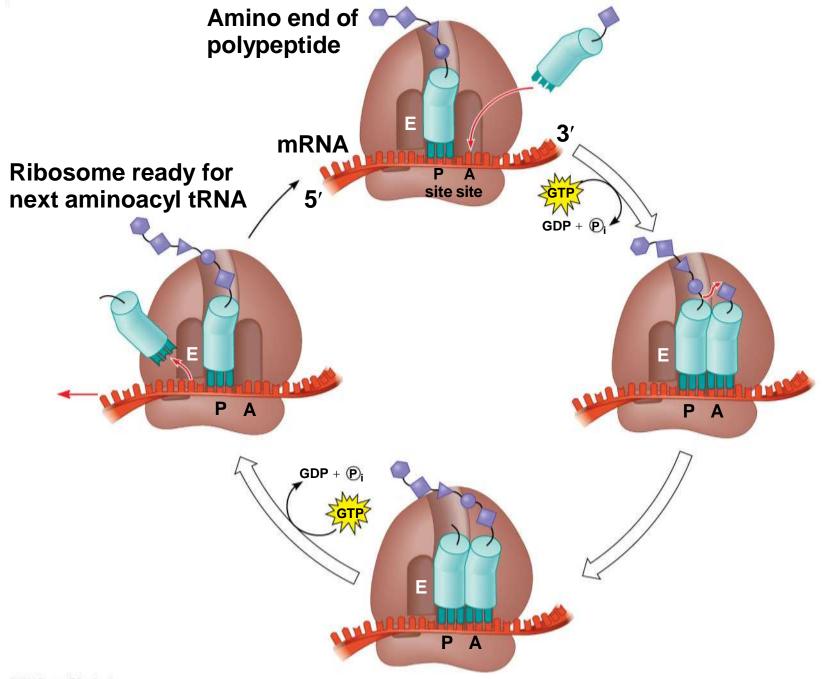
- A ribosome has three binding sites for tRNA
 - The **P site** holds the tRNA that carries the growing <u>polypeptide</u> chain
 - The A site holds the tRNA that carries the next amino acid to be <u>added</u> to the chain
 - The **E site** is the <u>exit</u> site, where discharged tRNAs leave the ribosome
 - As with transcription, there are three steps to translation
 - Initiation
 - Elongation
 - Termination

Initiation of Translation



Elongation of the Polypeptide Chain

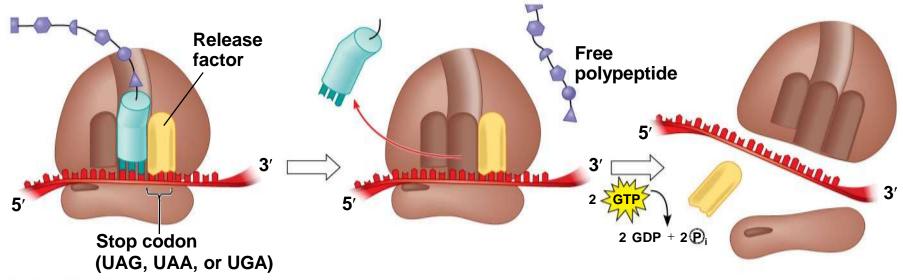
- During the elongation stage, amino acids are added one by one to the preceding amino acid at the C-terminus of the growing chain
- Each addition involves proteins called elongation factors and occurs in three steps:
- 1. codon recognition,
- 2. peptide bond formation,
- 3. and translocation
- Translation proceeds along the mRNA in a 5 to 3 direction



Termination of Translation

- Termination occurs when a stop codon in the mRNA reaches the A site of the ribosome
- The A site accepts a protein called a release factor
- The release factor causes the addition of a water molecule instead of an amino acid
- This reaction releases the polypeptide, and the translation assembly then comes apart

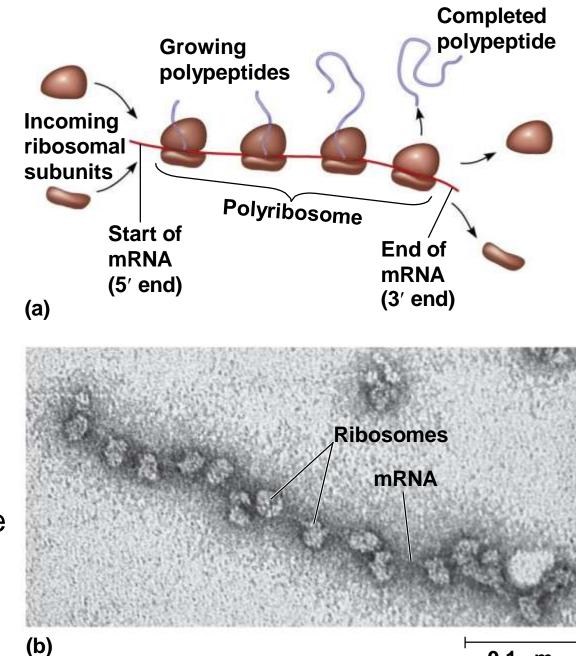
Termination of Translation



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Polyribosomes

- A number of ribosomes can translate a single mRNA simultaneously, forming a polyribosome (or polysome)
- Polyribosomes enable a cell to make many copies of a polypeptide very quickly



What is a gene?

- a region of DNA that can be expressed to produce a final functional product, either
 - a polypeptide or
 - an RNA molecule

