Chapter 17 Warm-Up

1. Explain the contribution that Beadle and Tatum made to understanding the role of DNA.

2. Compare and contrast DNA to RNA.

3. What is the difference between replication, transcription and translation?

Chapter 17 Warm-Up

1. Describe the steps in transcription.

2. Contrast transcription in prokaryotes vs. eukaryotes.

3. How many nucleotides are in an mRNA molecule to code for a protein with 200 amino acids?

Chapter 17 Warm-Up

1. How does mRNA differ from pre-mRNA?

2. What is the difference between introns and exons?

3. Describe how spliceosomes modify mRNA.

Chapter 17 Warm-Up

1. Describe the steps of translation.

1. If the DNA sequence is: 3' T A C G A T C A G 5'
   - the cDNA would be:
   - the mRNA is:
   - the tRNA is:
   - the amino acid sequence is:

2. How does the cell determine the ultimate destination of a polypeptide being synthesized?

Chapter 17 Warm-Up

1. What is a frameshift mutation? How can they impact protein synthesis?

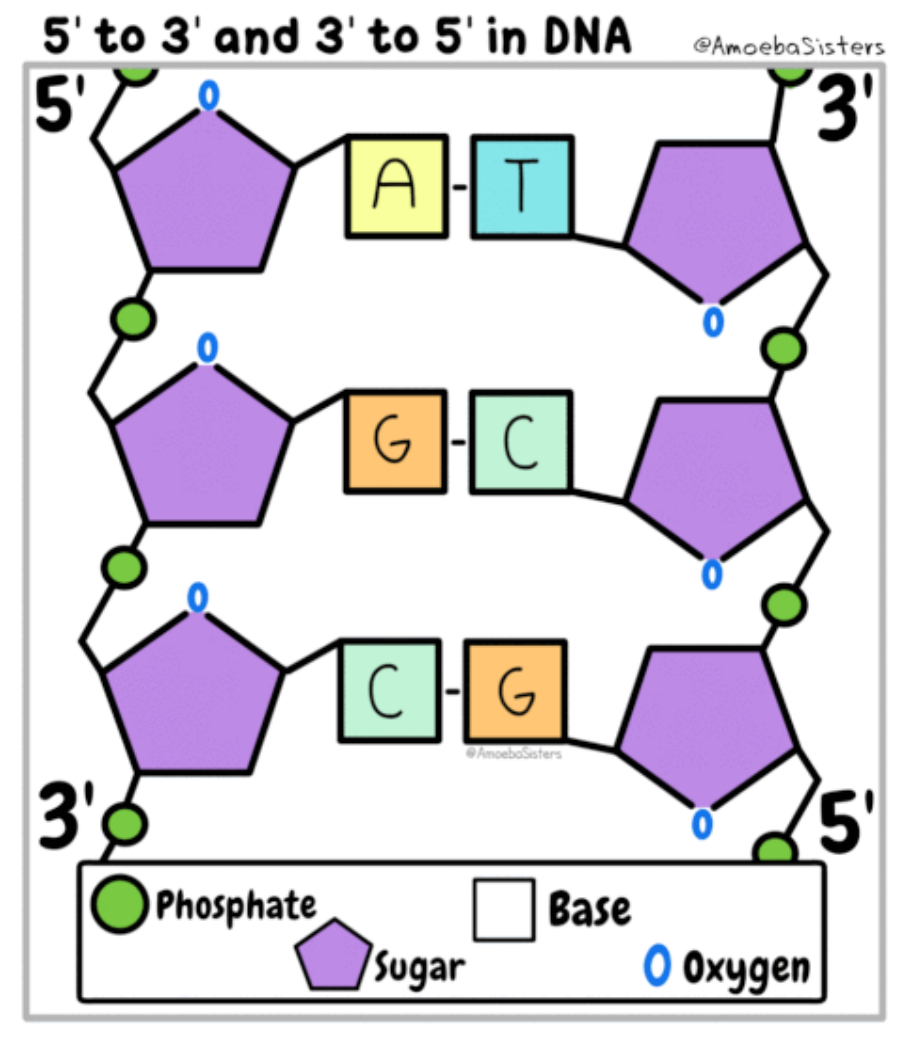
2. Contrast a missense vs. nonsense mutation.

Chapter 17 Warm-Up

Refer to page 327. Fill in the chart comparing prokaryotic and eukaryotic gene expression:

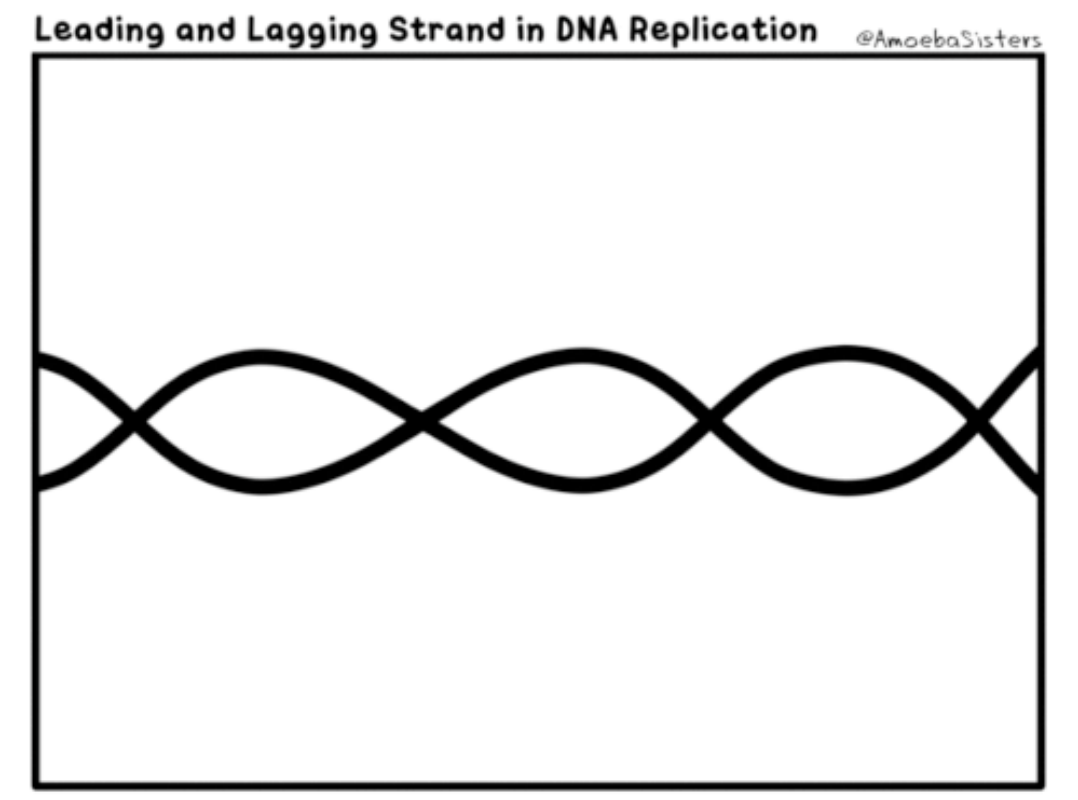
Prokaryotes	Eukaryotes

Review: **Watch this GIF silently**



Tell your neighbor what you think the PURPOSE of this animation is. What is it trying to teach you?

Review: **Watch this GIF silently**



Partner A: Describe how the leading strand is synthesized.

Partner B: Describe how the lagging strand is synthesized.

From Gene to Protein

Chapter 17

What you need to know:

- The key terms: gene expression, transcription, and translation.
- The major events of transcription.
- How eukaryotic cells modify RNA after transcription.
- The steps to translation.
- How point mutations can change the amino acid sequence of a protein.

Link to Protein Synthesis YouTube Video List: https://bit.ly/2SyMIdd

Concept 17.1: Genes specify proteins via transcription and translation

Amoeba Sisters:

Protein Synthesis & the Lean, Mean, Ribosome Machine

Gene Expression: process by which DNA directs the synthesis of proteins (or RNAs)

- Old idea: *one gene-one enzyme hypothesis*
  - Proposed by Beadle & Tatum – mutant mold experiments
  - Function of a gene = dictate production of specific enzyme

- Newer idea: *one gene-one polypeptide hypothesis*

- Most accurate: *one gene-one RNA molecule (which can be translated into a polypeptide)*

Flow of genetic information

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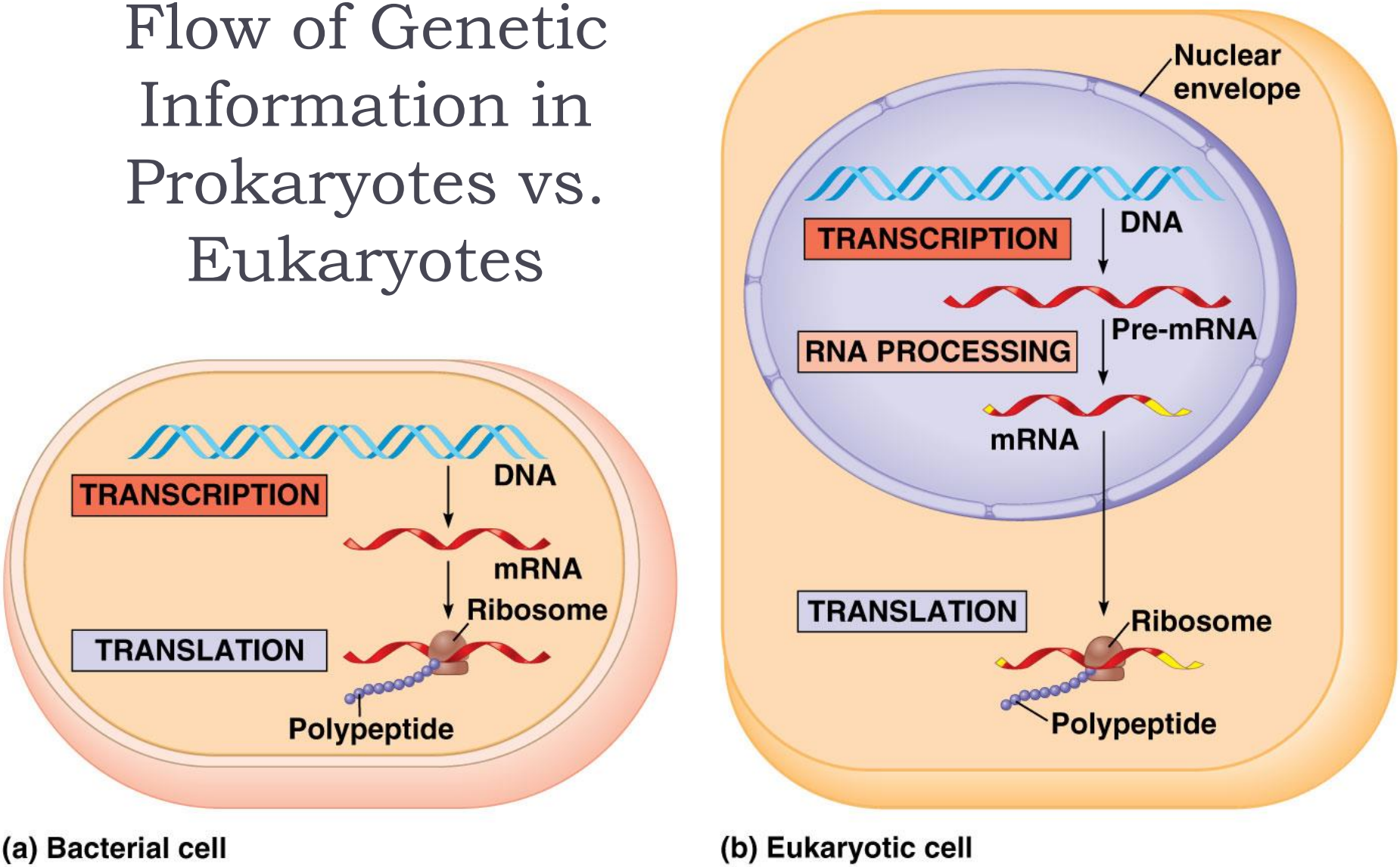
- *CENTRAL DOGMA:* DNA → RNA → protein
  - **Transcription**: DNA → RNA
  - **Translation**: RNA → protein
    - Ribosome = site of translation

Flow of Genetic Information in Prokaryotes vs. Eukaryotes



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one gene = one RNA molecule

DNA

- Nucleic acid composed of nucleotides
- Double-stranded
- Deoxyribose = sugar
- Thymine
- Template for individual

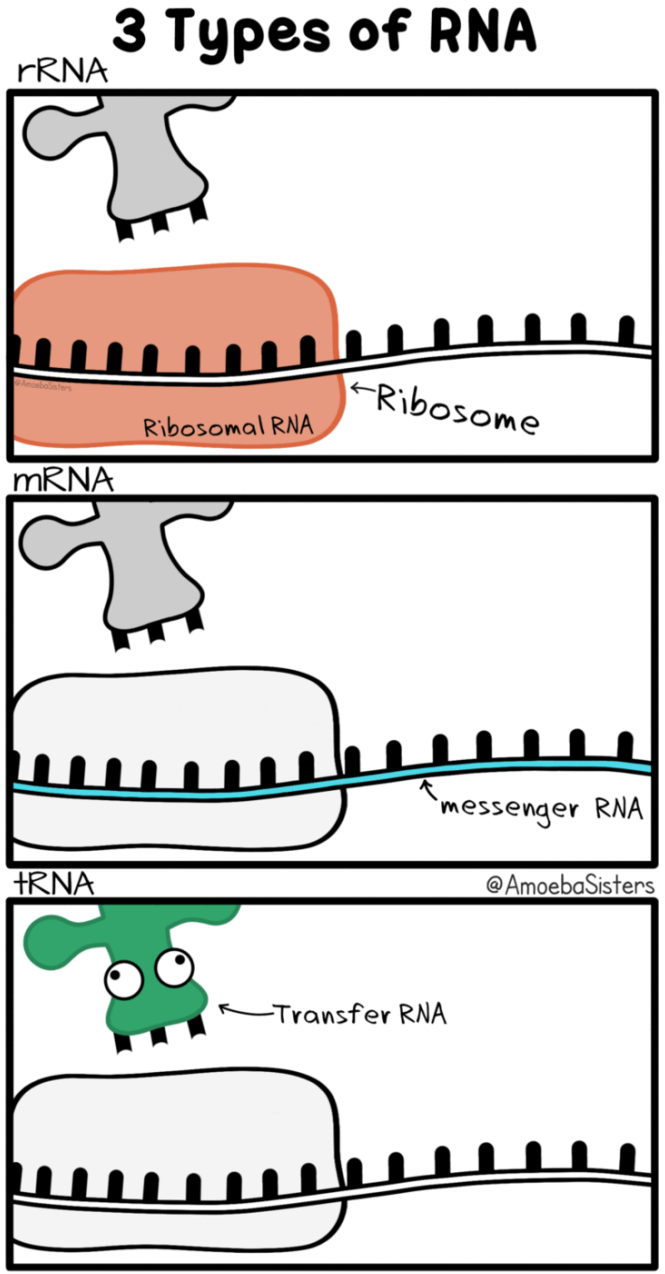
RNA

- Nucleic acid composed of nucleotides
- Single-stranded
- Ribose = sugar
- Uracil
- Many different roles!

Remember RNA?

In your groups…discuss what you remember about the 3 main types of RNA.

Use the animations to help you.



RNA plays many roles in the cell

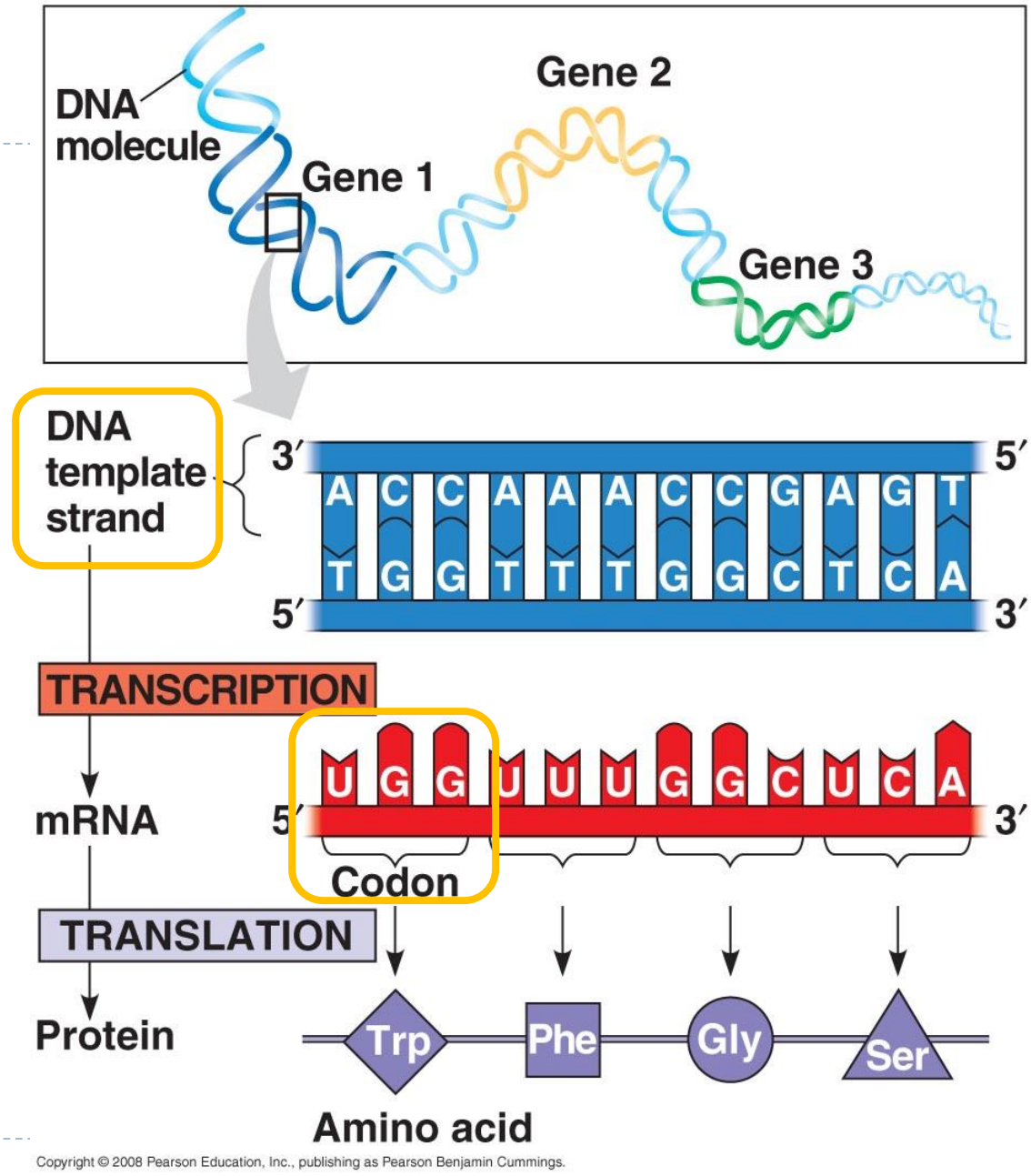
1. pre-mRNA=precursor to mRNA, newly transcribed and *not edited*
2. mRNA= the edited version; carries the code from DNA that specifies amino acids
3. tRNA= carries a specific amino acid to ribosome based on its anticodon to mRNA codon
4. rRNA= makes up 60% of the ribosome; site of protein synthesis
5. snRNA=small nuclear RNA; part of a spliceosome. Has structural and catalytic roles
6. srpRNA=a signal recognition particle that binds to signal peptides
7. RNAi= interference RNA; a regulatory molecule
8. ribozyme= RNA molecule that functions as an enzyme

The Genetic Code

For each gene, one DNA strand is the **template strand**

mRNA (5’ → 3’) complementary to template

mRNA triplets (**codons**) code for amino acids in polypeptide chain



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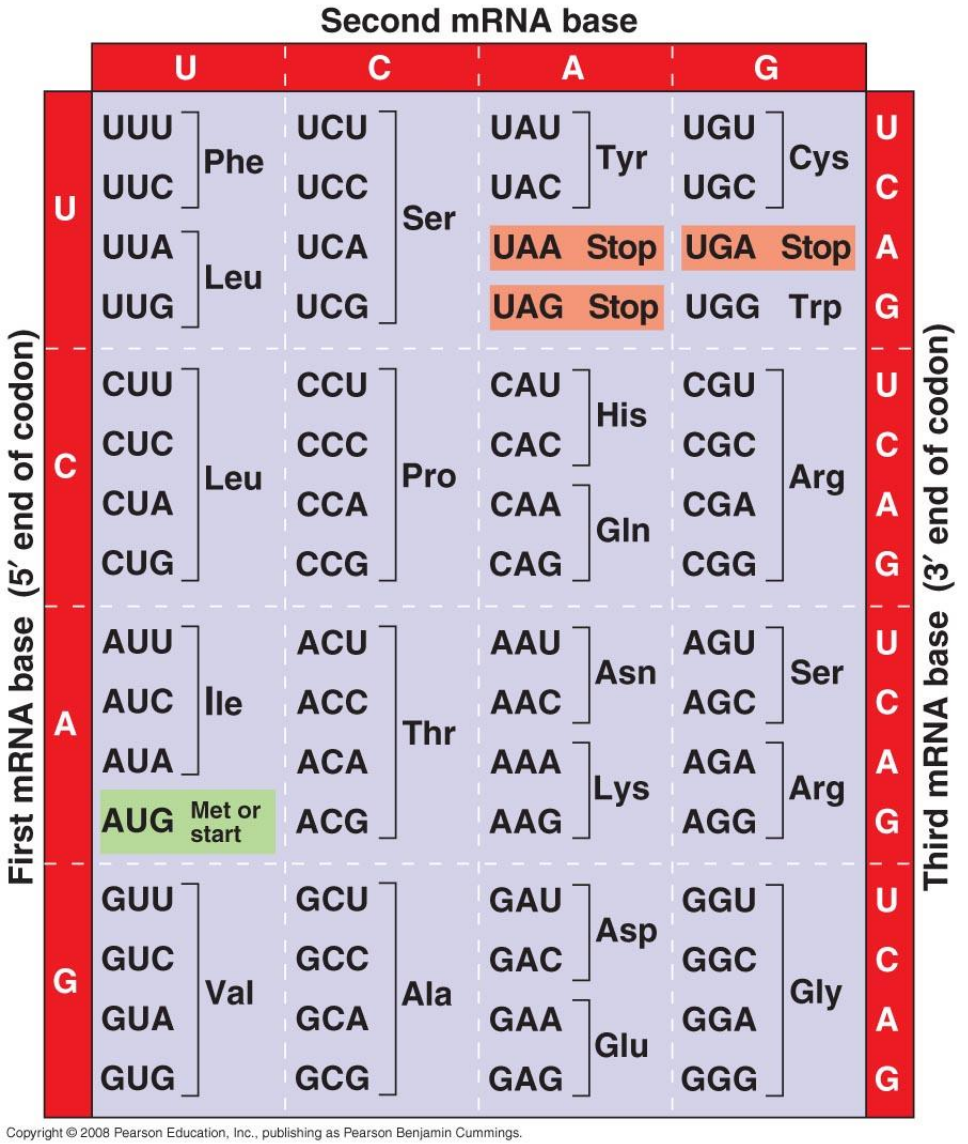
The Genetic Code

64 different codon combinations

Redundancy: 1+ codons code for each of 20 AAs

Reading frame: groups of 3 must be read in correct groupings

This code is universal: all life forms use the same code.



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Re-Read, Review, & Reflect

1. Re-read your notes.
2. Talk to a neighbor to fill in any missing information.
3. Highlight key ideas

4. Tell your neighbor 2 facts about the information presented.
5. Ask your neighbor 1 lingering question.

Concept 17.2: Transcription is the DNA-directed synthesis of RNA

Transcription

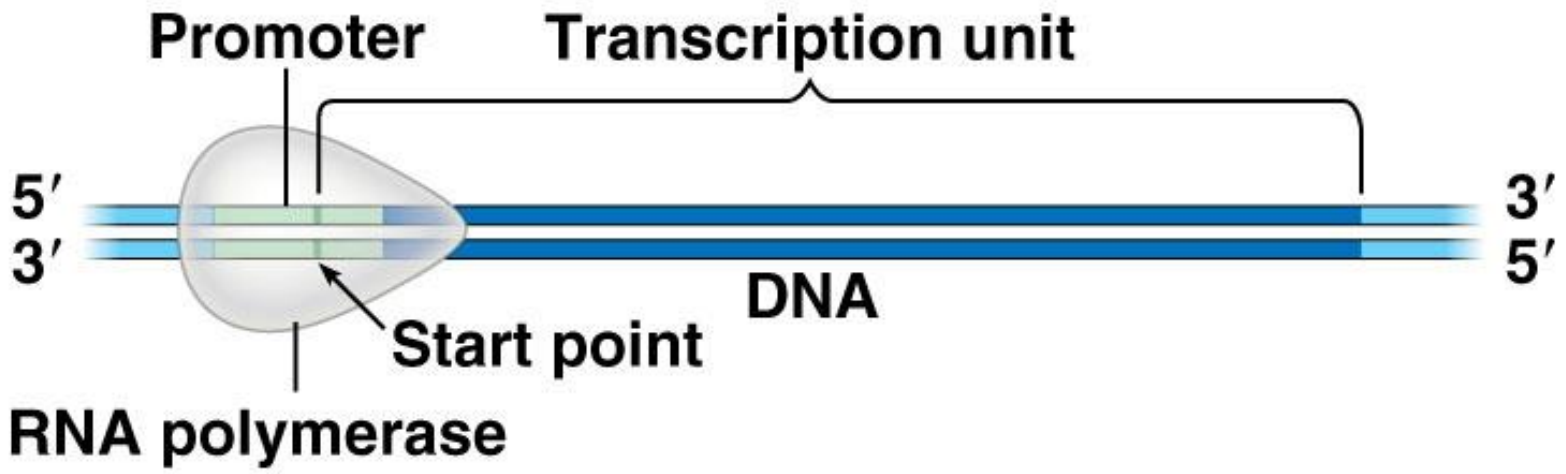
Transcription unit: stretch of DNA that codes for a polypeptide or RNA (eg. tRNA, rRNA)

RNA polymerase:

- Separates DNA strands and transcribes mRNA
- mRNA elongates/grows in 5' → 3' direction
- **Uracil (U)** replaces thymine (T) when pairing to adenine (A)
- Attaches to **promoter** (start of gene) and stops at **terminator** (end of gene)

1. Initiation

Bacteria: RNA polymerase binds ***directly*** to **promoter** in DNA

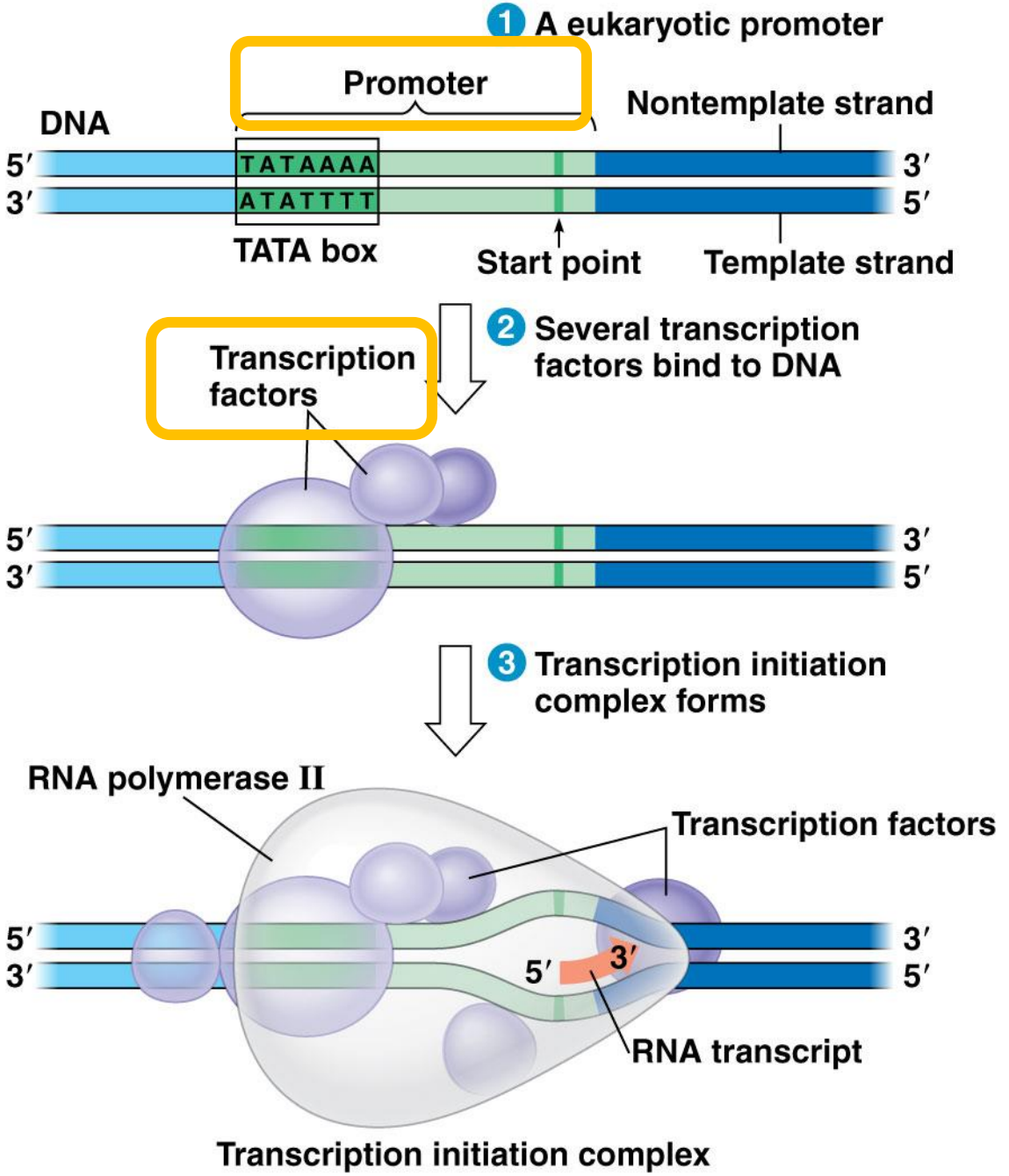


1. Initiation

Eukaryotes:

TATA box = DNA sequence (TATAAAA) *upstream* from **promoter**

Transcription factors must recognize TATA box before RNA polymerase can bind to DNA promoter



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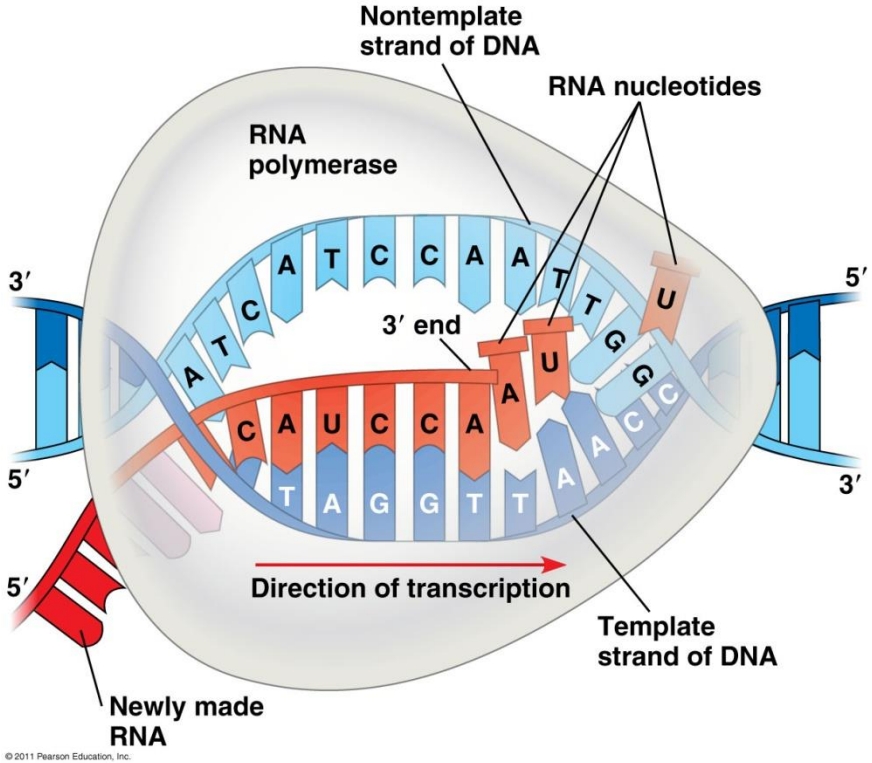
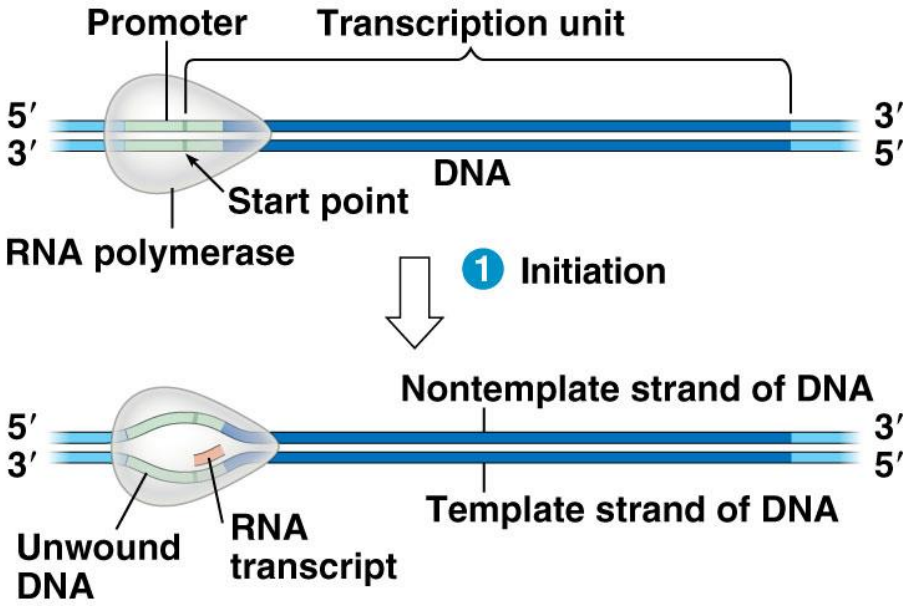
2. Elongation





- **RNA polymerase** adds RNA nucleotides to the 3’ end of the growing chain (A-U, G-C)

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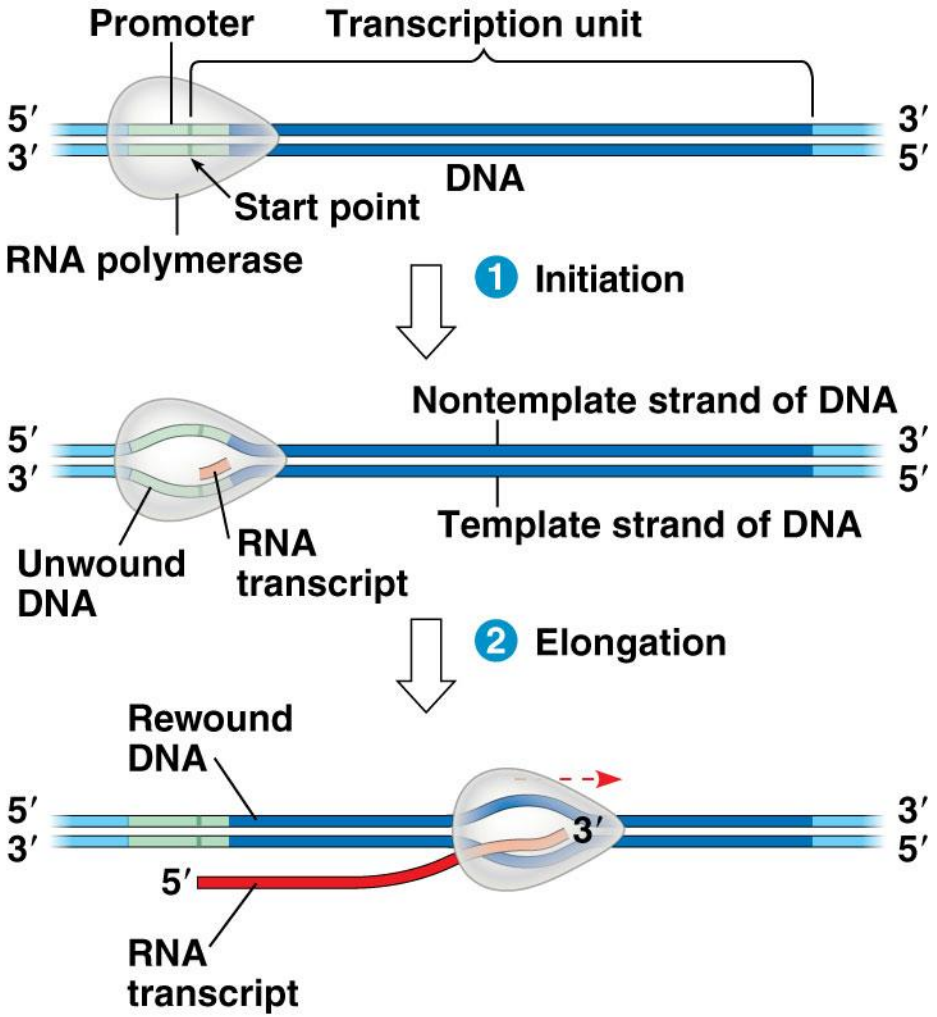
2. Elongation

As RNA polymerase moves, it untwists DNA, then rewinds it after mRNA is made



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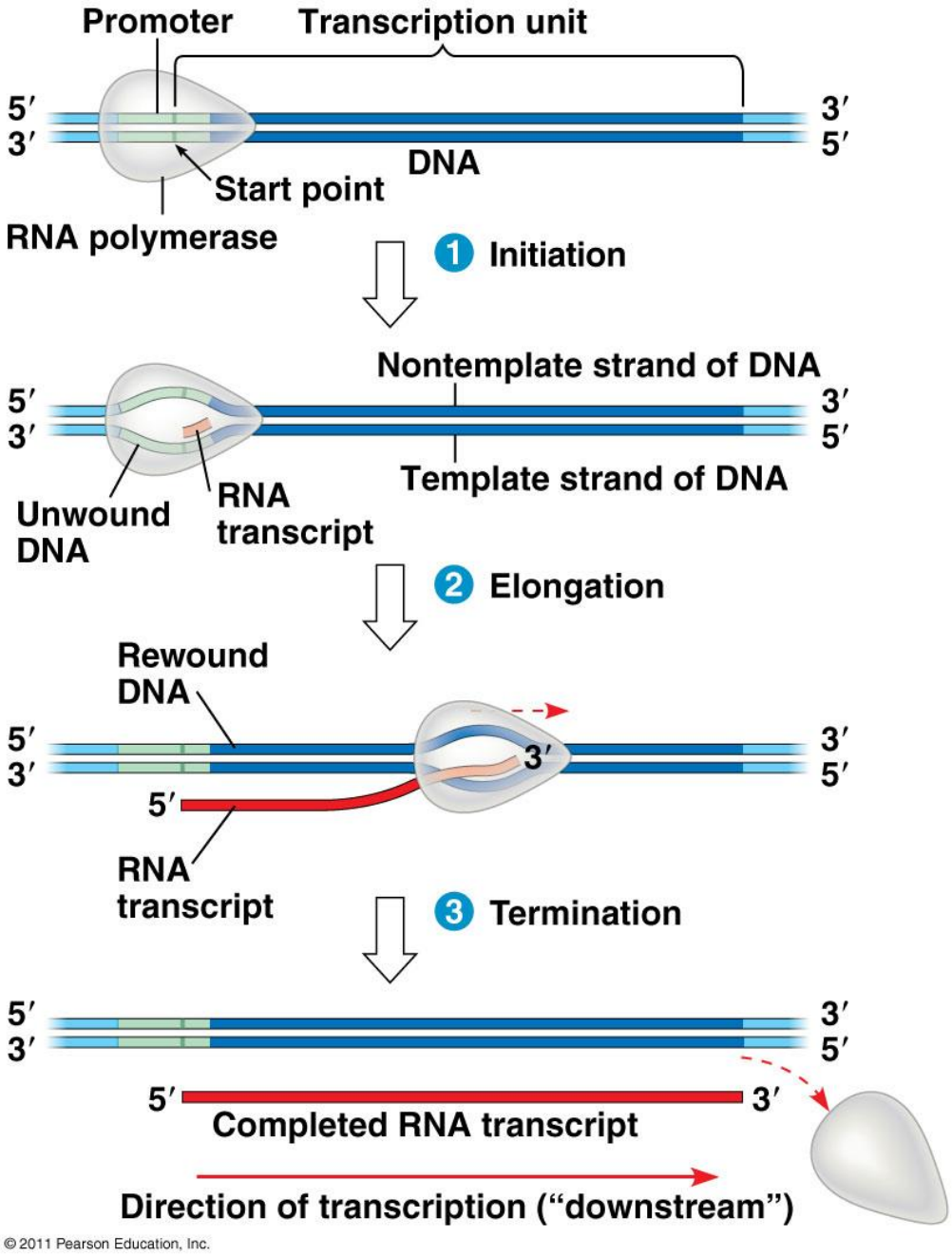
3. Termination

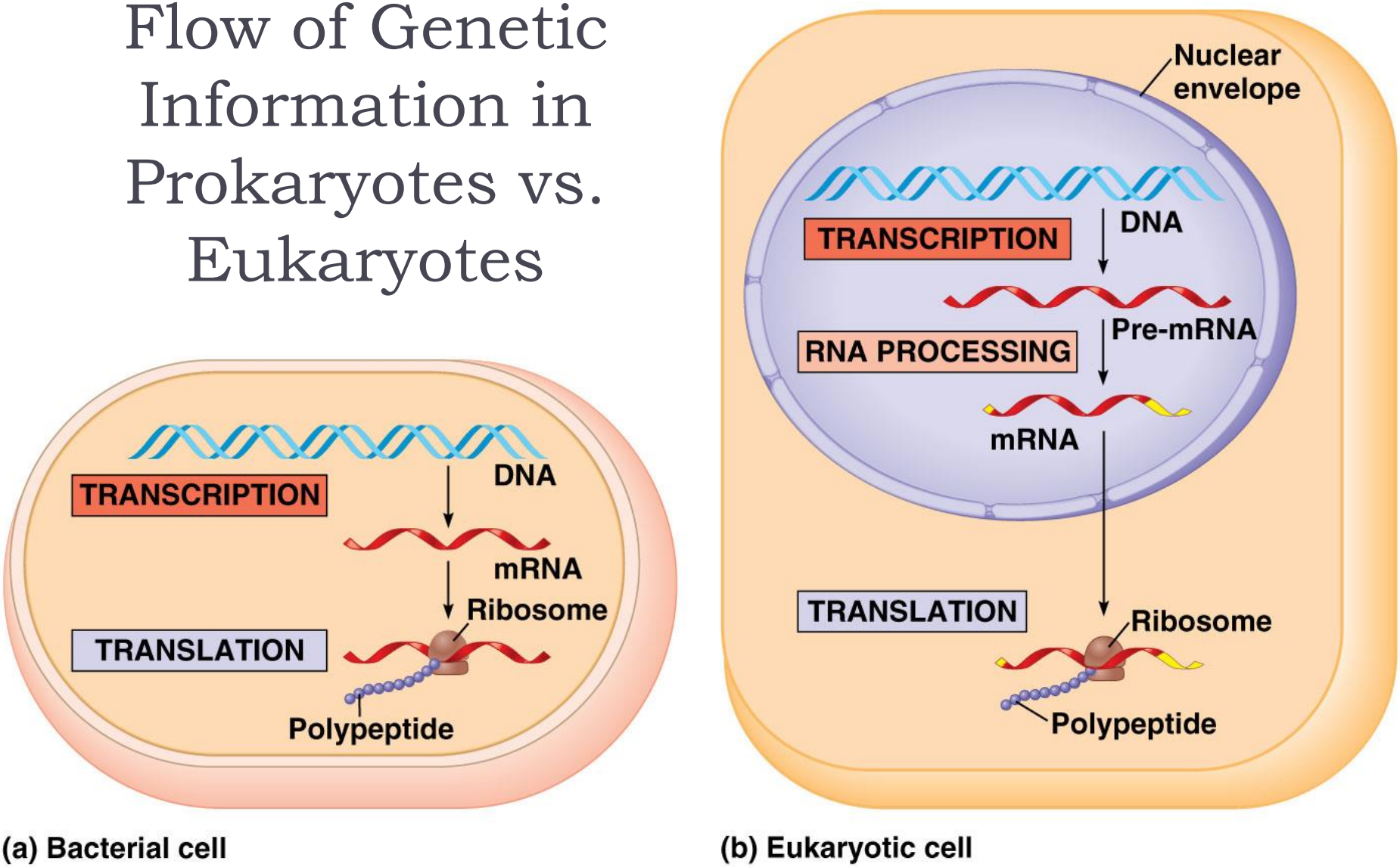
RNA polymerase transcribes a **terminator** sequence in DNA, then mRNA and polymerase detach.

It is now called **pre-mRNA** for eukaryotes.

Prokaryotes = mRNA ready for use



Flow of Genetic Information in Prokaryotes vs. Eukaryotes



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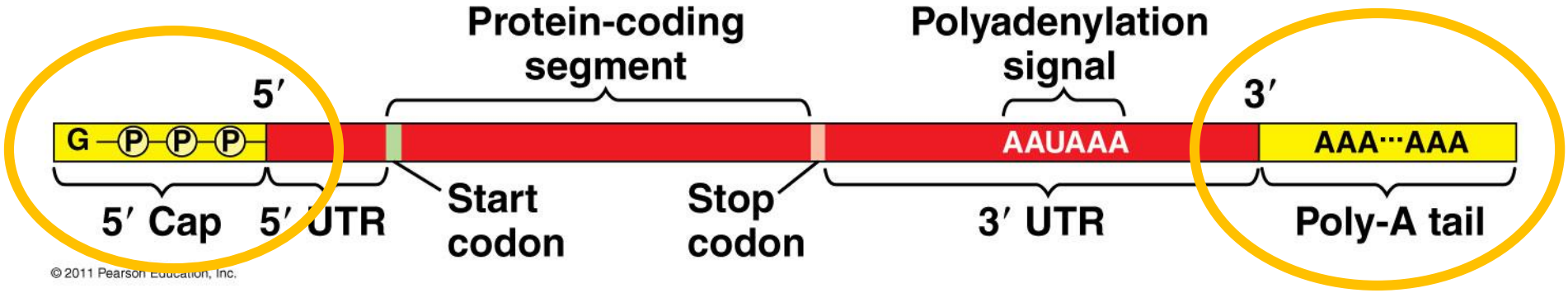
DNALC Video: Transcription

http://www.youtube.com/watch?v=SMtWvDbfHLo

Concept 17.3: Eukaryotic cells modify RNA after transcription

Additions to pre-mRNA:

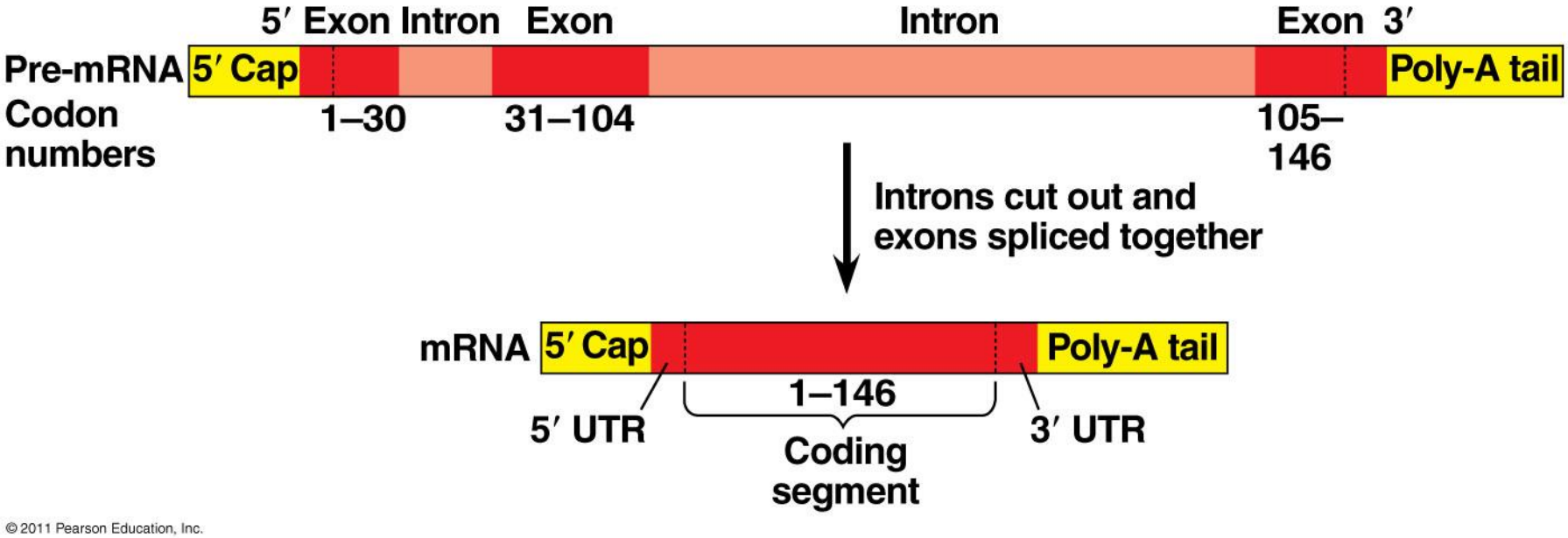
- **5' cap** (modified guanine) and 3' **poly-A tail** (50-520 A's) are added



- Help export from nucleus, protect from enzyme degradation, attach to ribosomes

This is also called RNA processing

RNA Splicing



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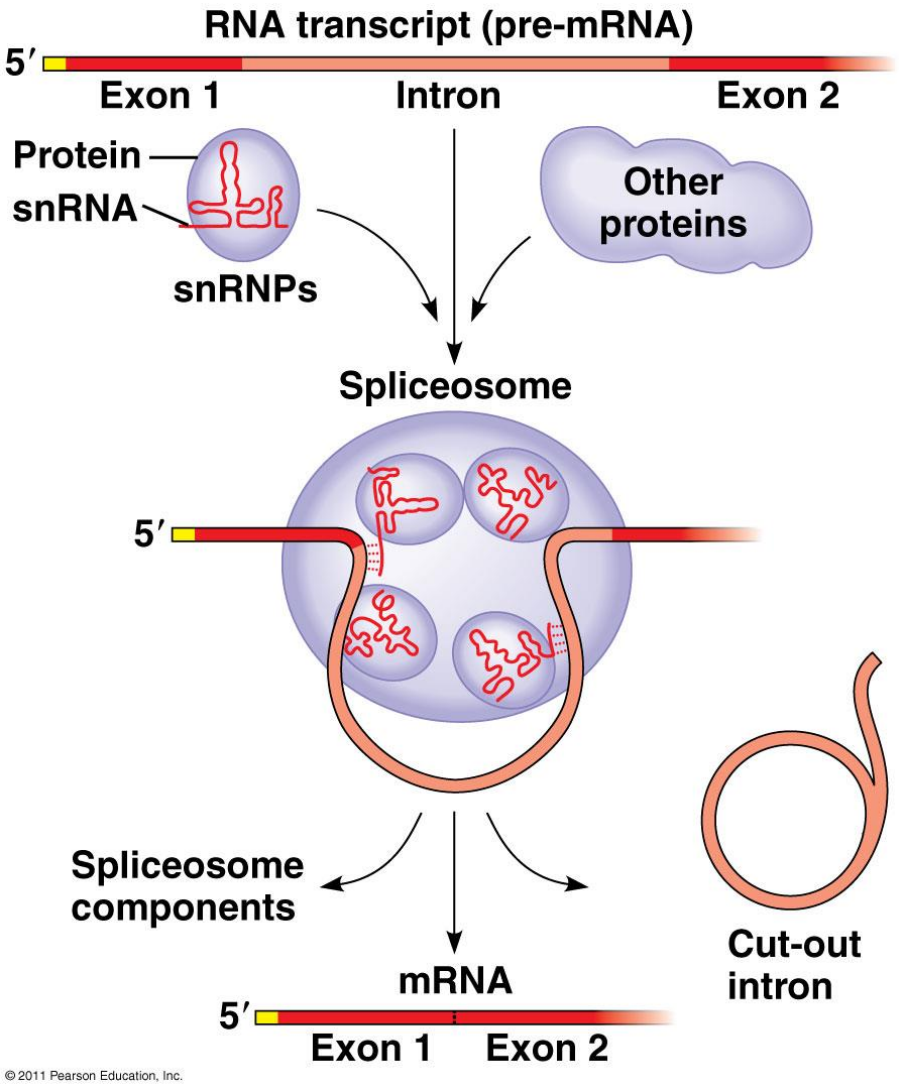
- Pre-mRNA has **introns** (noncoding sequences) and **exons** (codes for amino acids)
- **Splicing** = introns cut out, exons joined together

RNA Splicing

- **s**mall **n**uclear **r**ibo**n**ucleo**p**roteins = snRNPs
  - snRNP = snRNA + protein
  - Pronounced "snurps"
  - Recognize splice sites
- snRNPs join with other proteins to form a spliceosome

Spliceosomes catalyze the process of removing introns and joining exons

Ribozyme = RNA acts as enzyme



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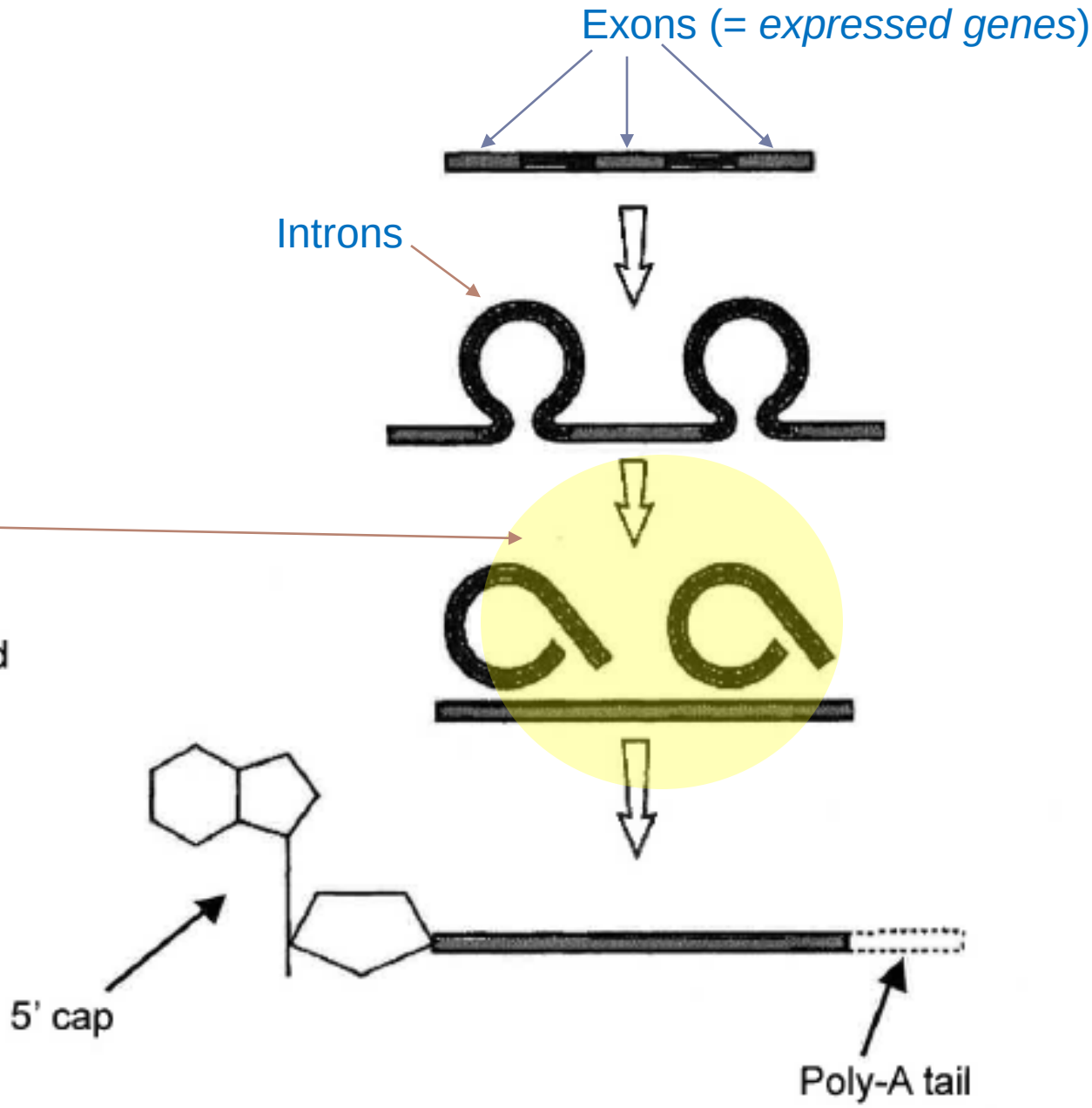
RNA Processing

- occurs in eukaryotic cells
- **Introns** removed
- Exons linked
- 5' cap added
- Poly-A tail added

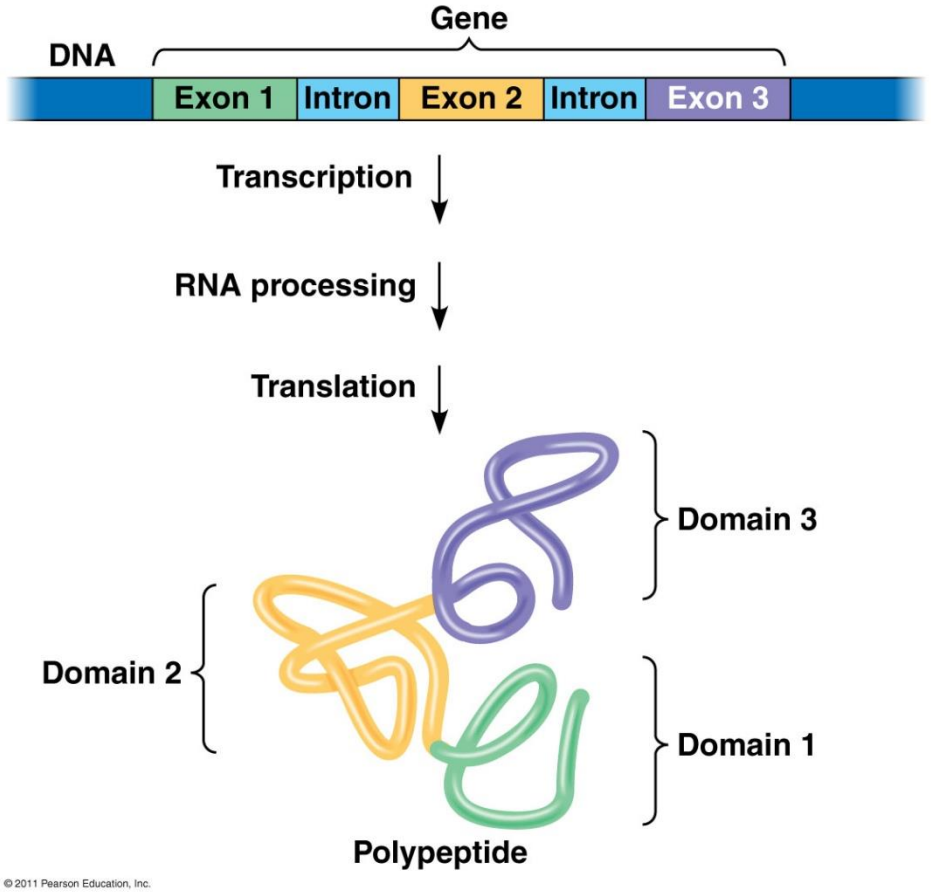
Spliceosome

- Cut out introns
- Slice exons together
- consist of protein and snRNPs



Why have introns?

- Some regulate gene activity
- **Alternative RNA Splicing**: produce different combinations of exons
  - One gene can make more than one polypeptide!
  - 20,000 genes → 100,000 polypeptides



Re-Read, Review, & Reflect

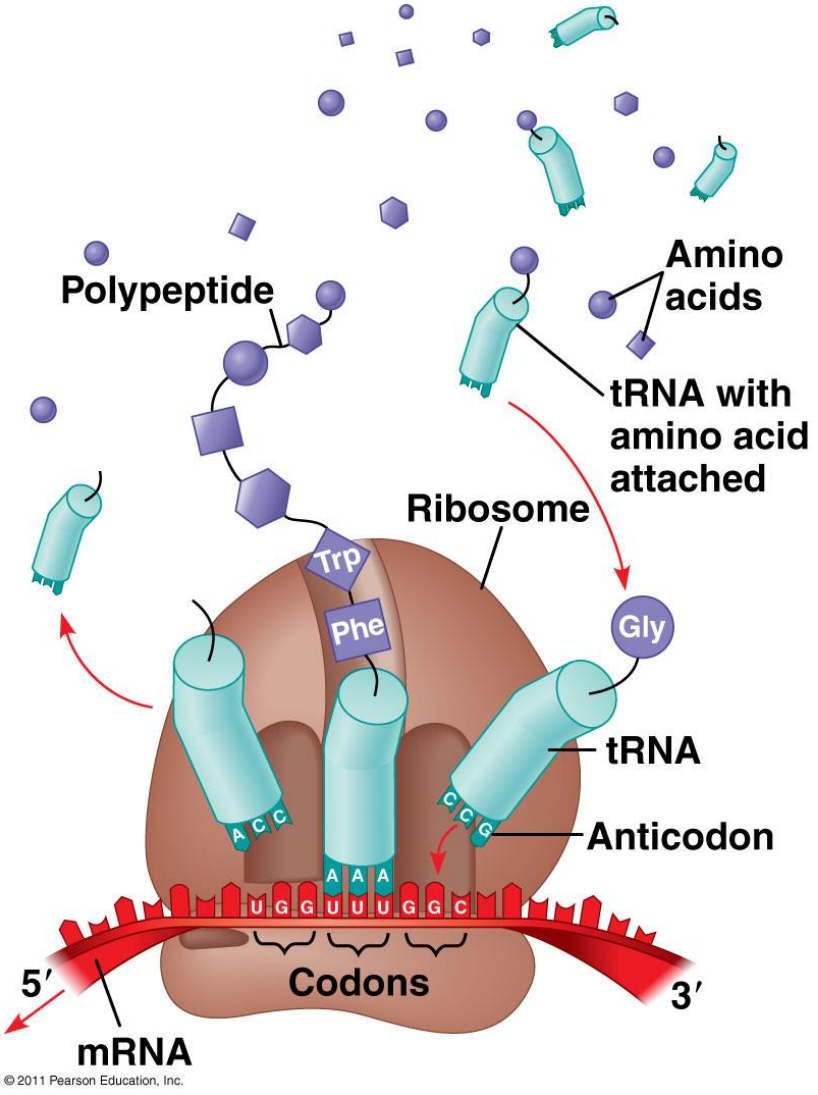
1. Re-read your notes.
2. Talk to a neighbor to fill in any missing information.
3. Highlight key ideas

4. Tell your neighbor 2 facts about the information presented.
5. Ask your neighbor 1 lingering question.

Concept 17.4: Translation is the RNA-directed synthesis of a polypeptide

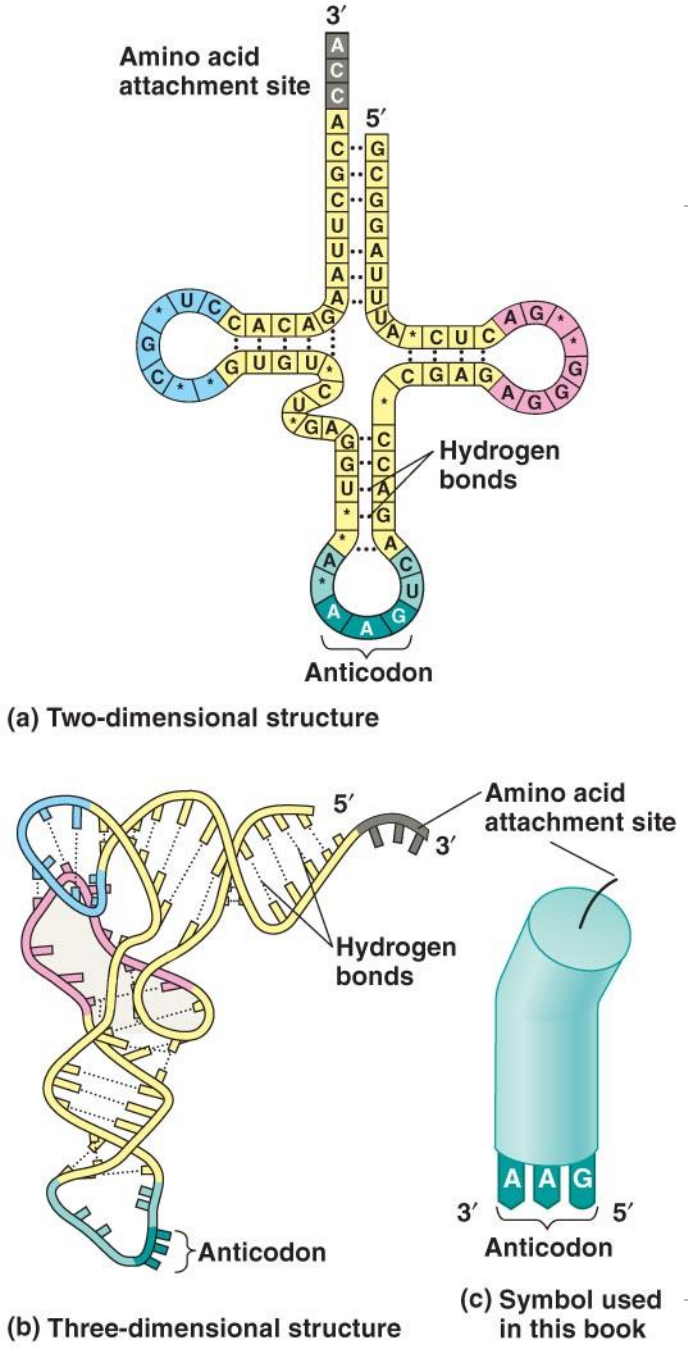
Components of Translation

1. **mRNA** = message
2. **tRNA** = interpreter
3. **Ribosome** = site of translation



tRNA

- Transcribed in nucleus
- Specific to each amino acid
- Function: Transfer AA to ribosomes
- Anticodon: pairs with complementary mRNA codon
- Base-pairing rules between 3rd base of codon & anticodon are not as strict. This is called **wobble**.



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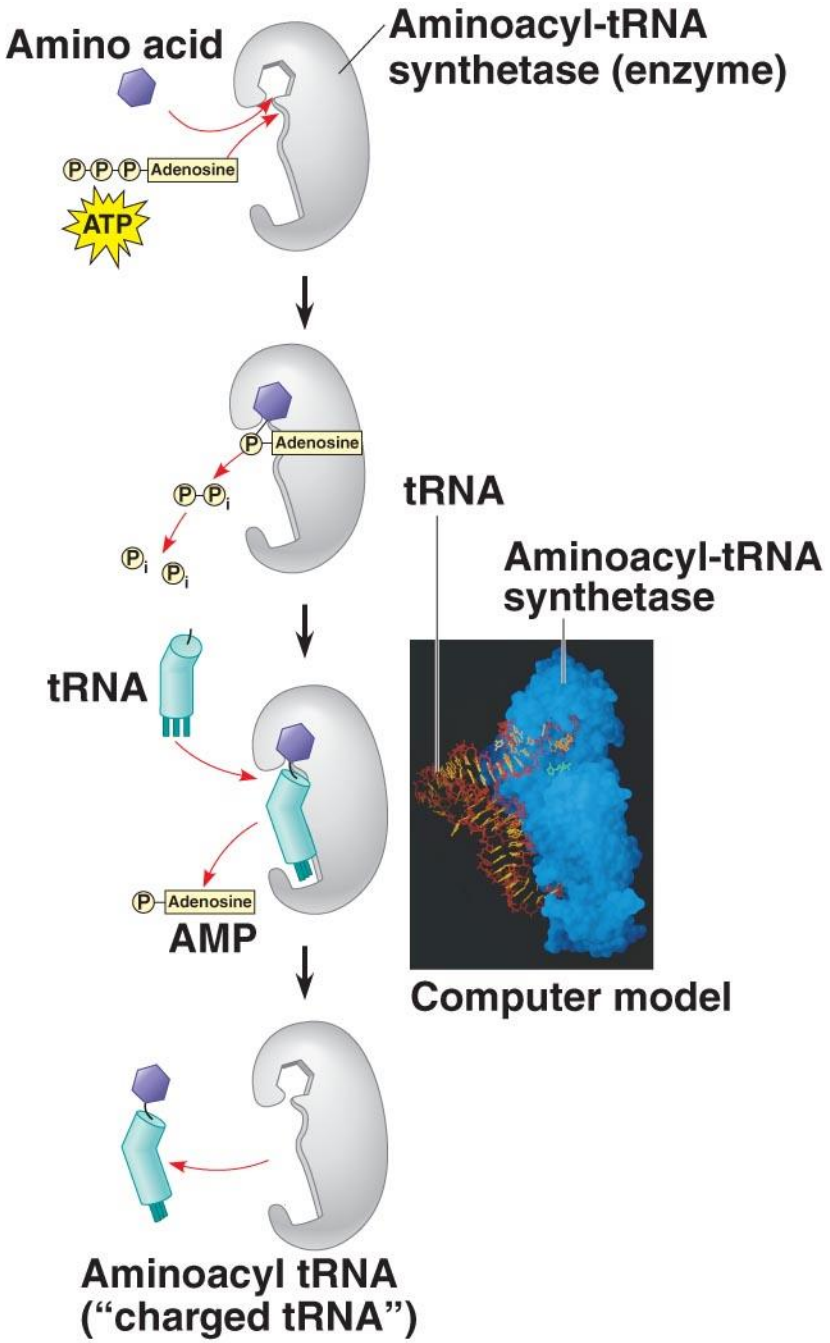
tRNA

- Aminoacyl-tRNA-synthetase: enzyme that binds tRNA to specific amino acid



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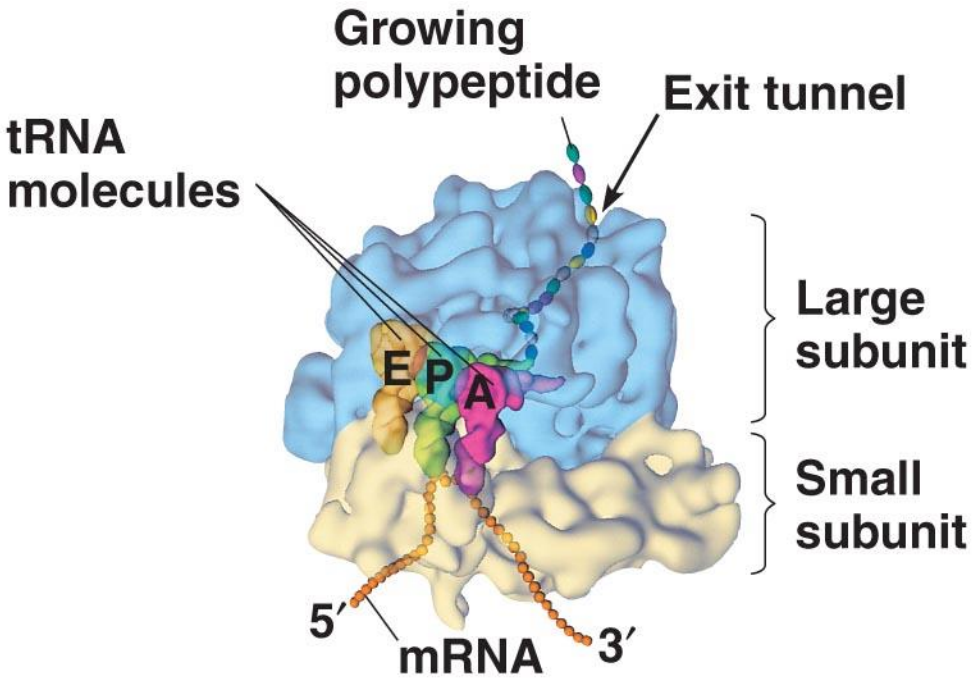
Ribosomes

- Ribosome = rRNA + proteins
- made in nucl*eolus*
- 2 subunits



(a) Computer model of functioning ribosome

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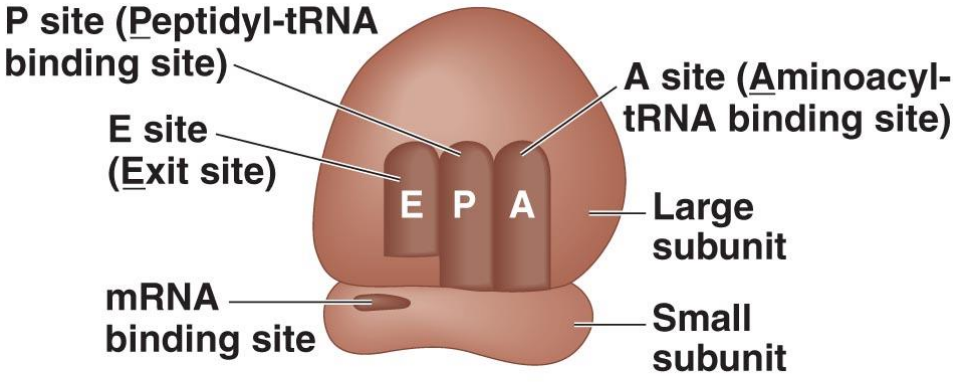
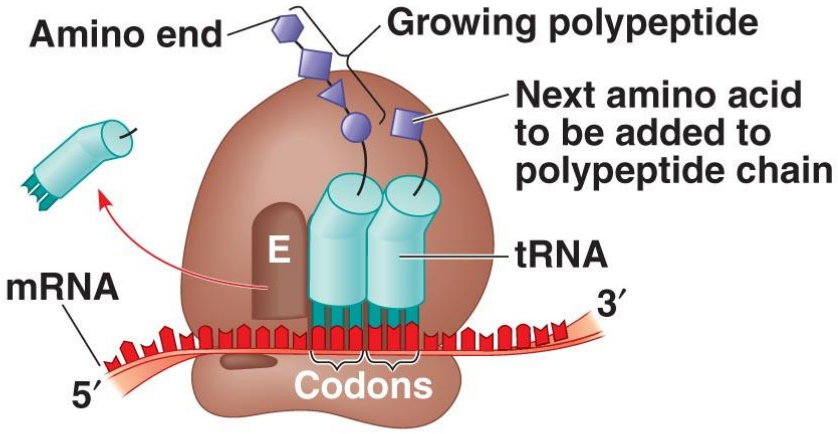
Ribosomes

Active sites:

- **A site**: holds **AA** to be added
- **P site**: holds growing polypeptide chain
- **E site**: exit site for tRNA



(b) Schematic model showing binding sites



(c) Schematic model with mRNA and tRNA

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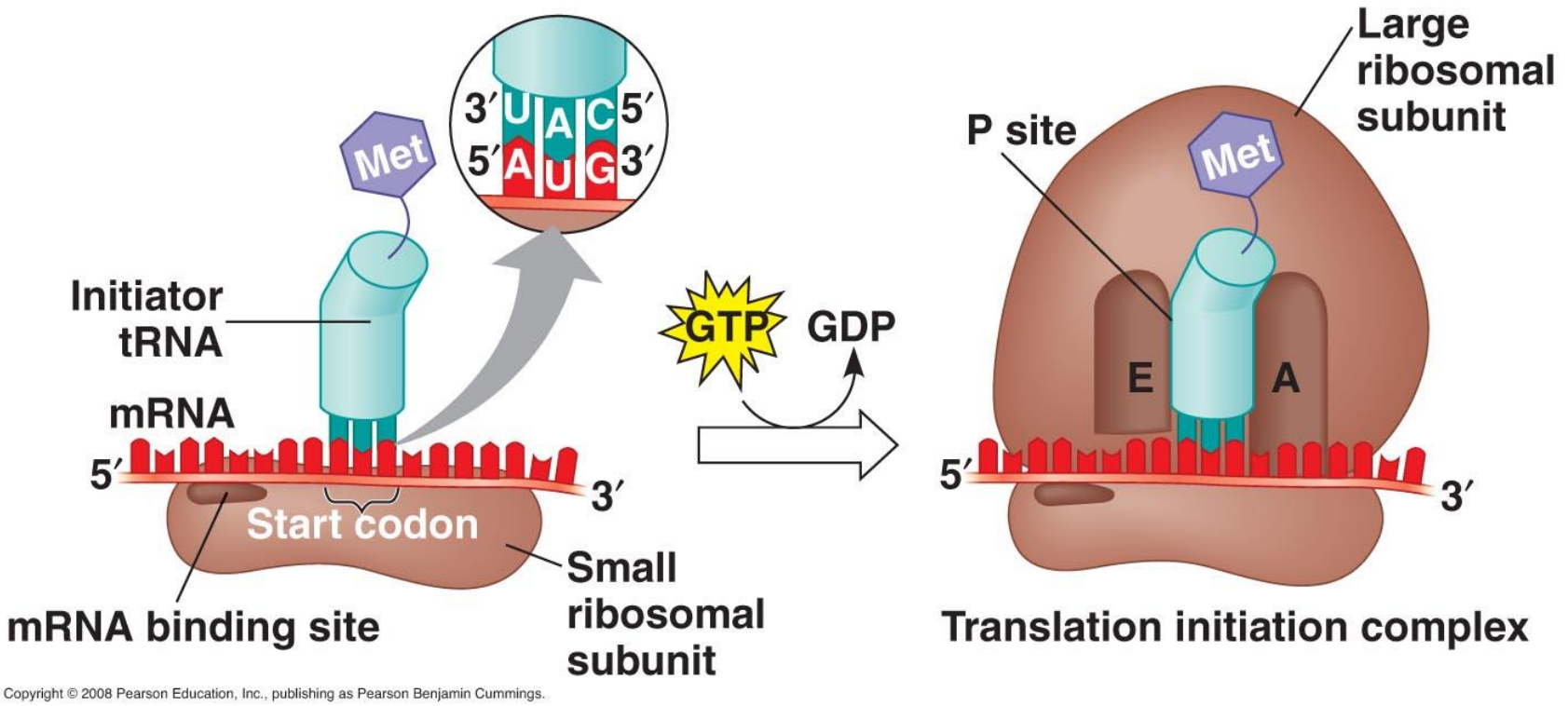
Translation:
1. Initiation



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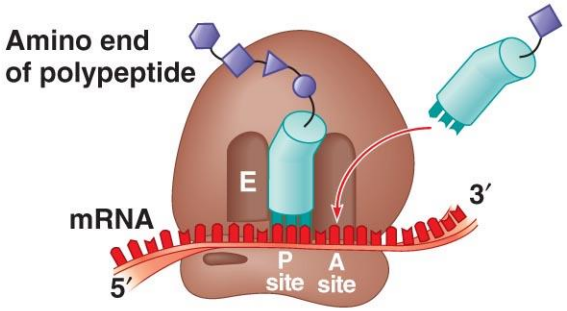
- Small subunit binds to start codon (AUG) on mRNA
- tRNA carrying Met attaches to P site
- Large subunit attaches

2. Elongation



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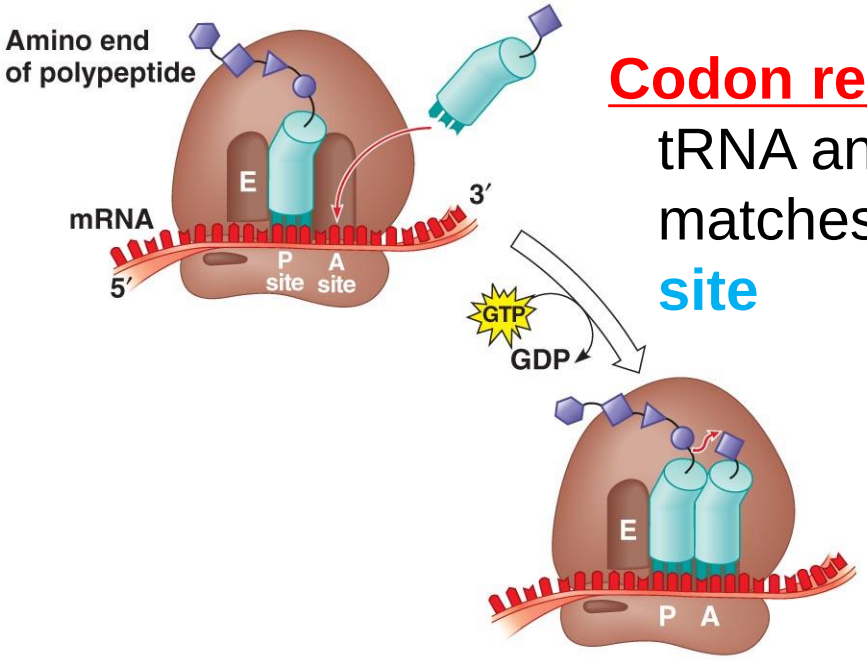
2. Elongation



Codon recognition: tRNA anticodon matches codon in **A site**

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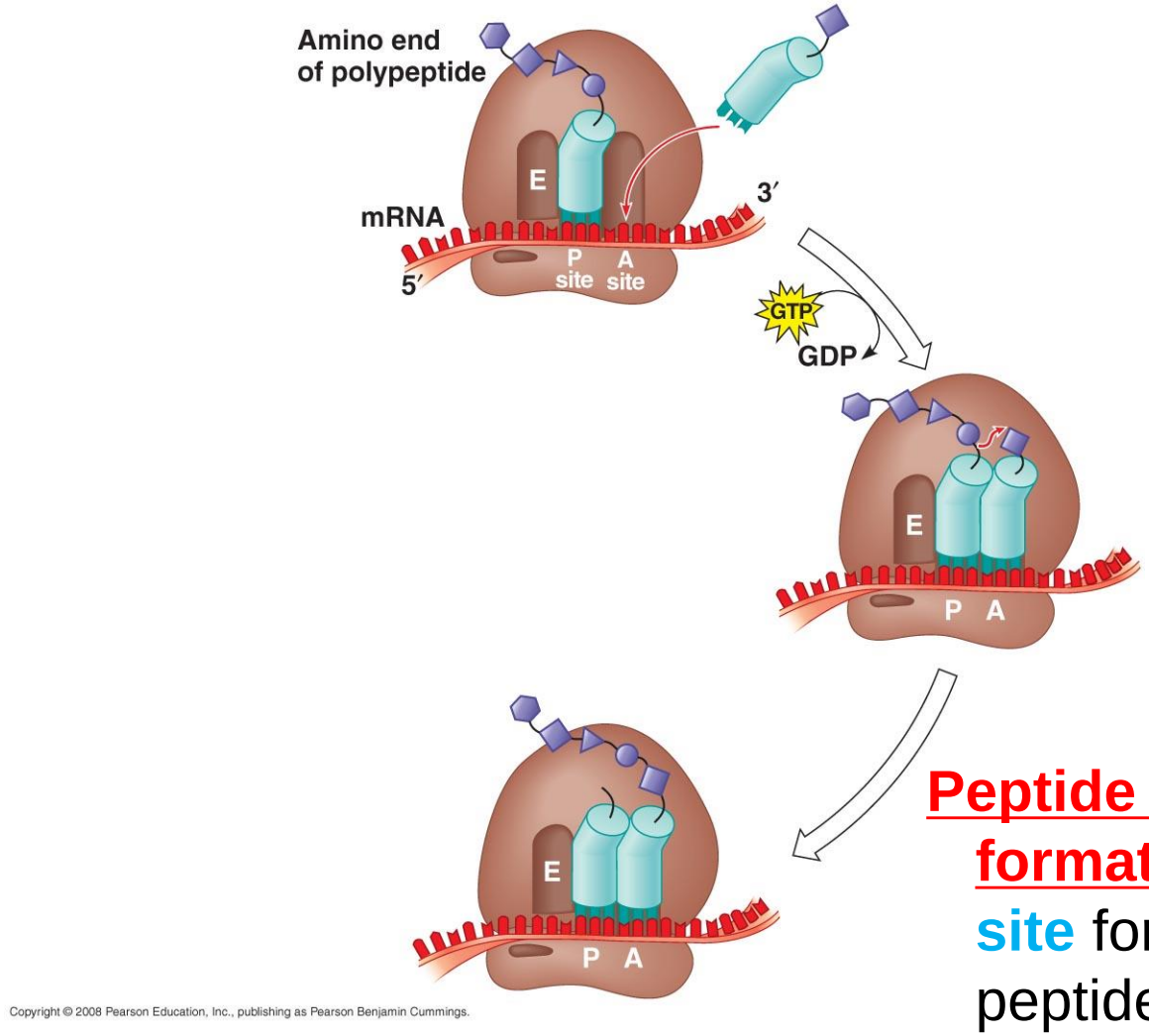
2. Elongation



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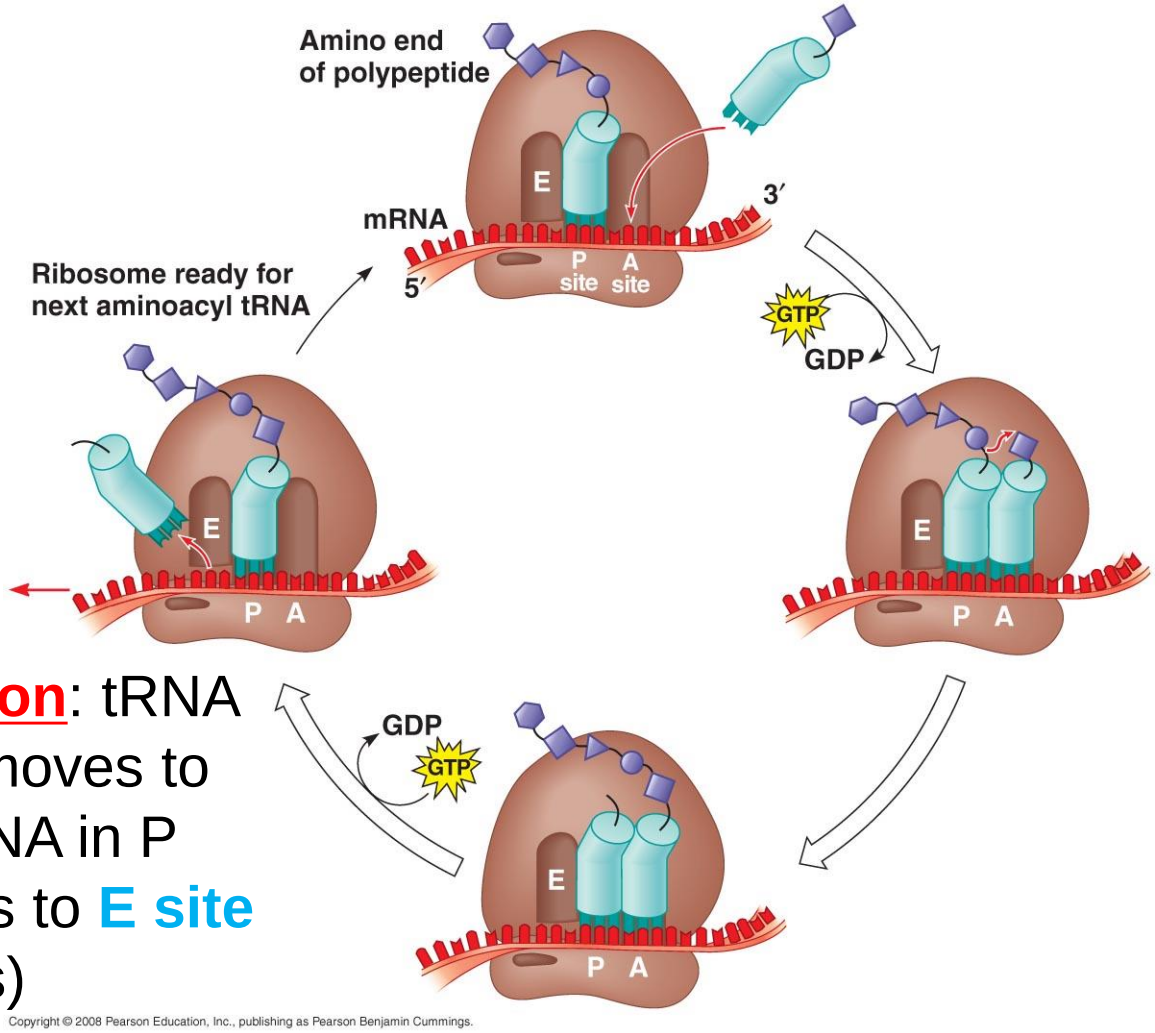
Peptide bond formation: AA in **A site** forms bond with peptide in **P site**

2. Elongation



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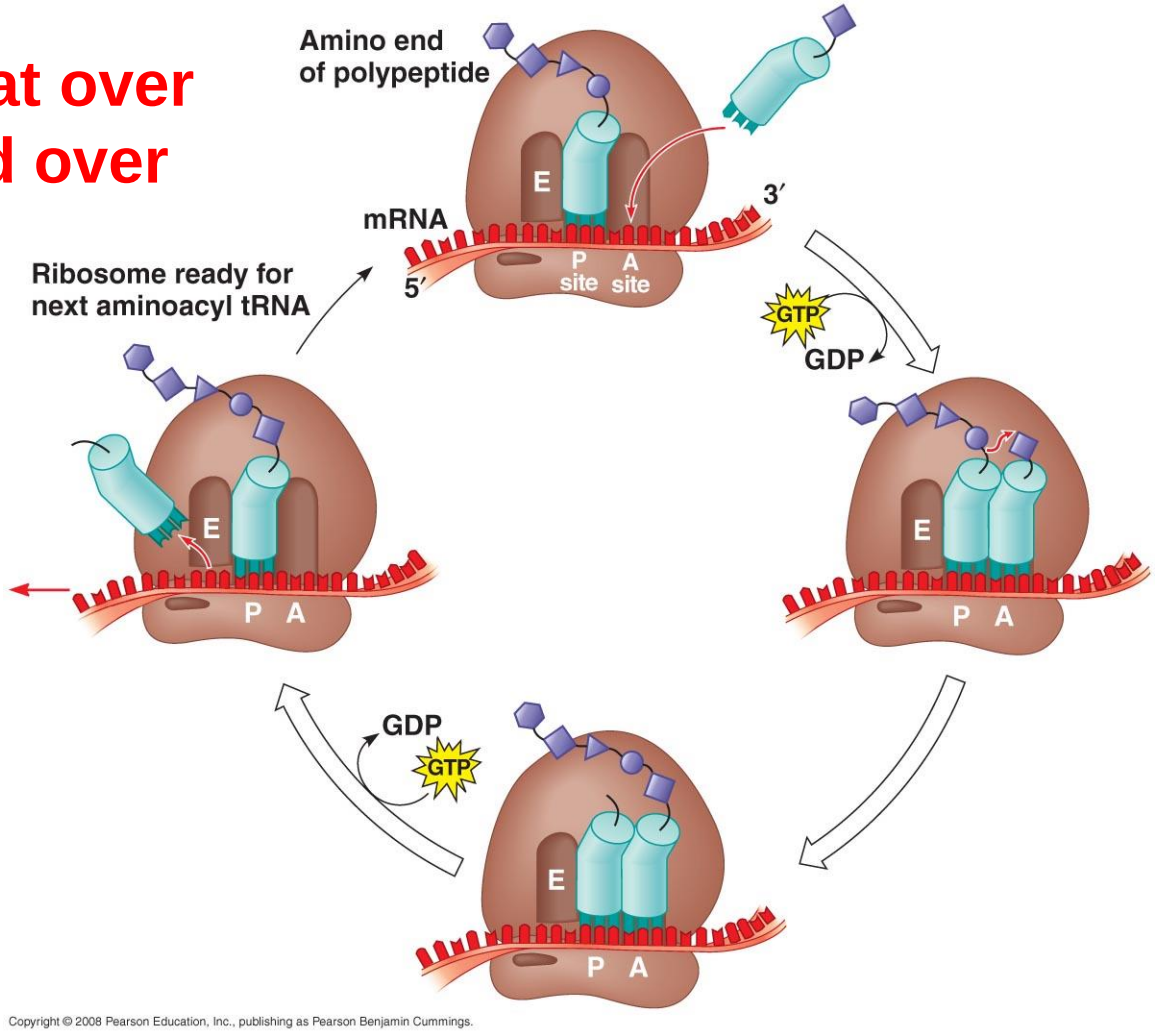
Translocation: tRNA in **A site** moves to **P site**; tRNA in P site moves to **E site** (then exits)

2. Elongation

Repeat over and over



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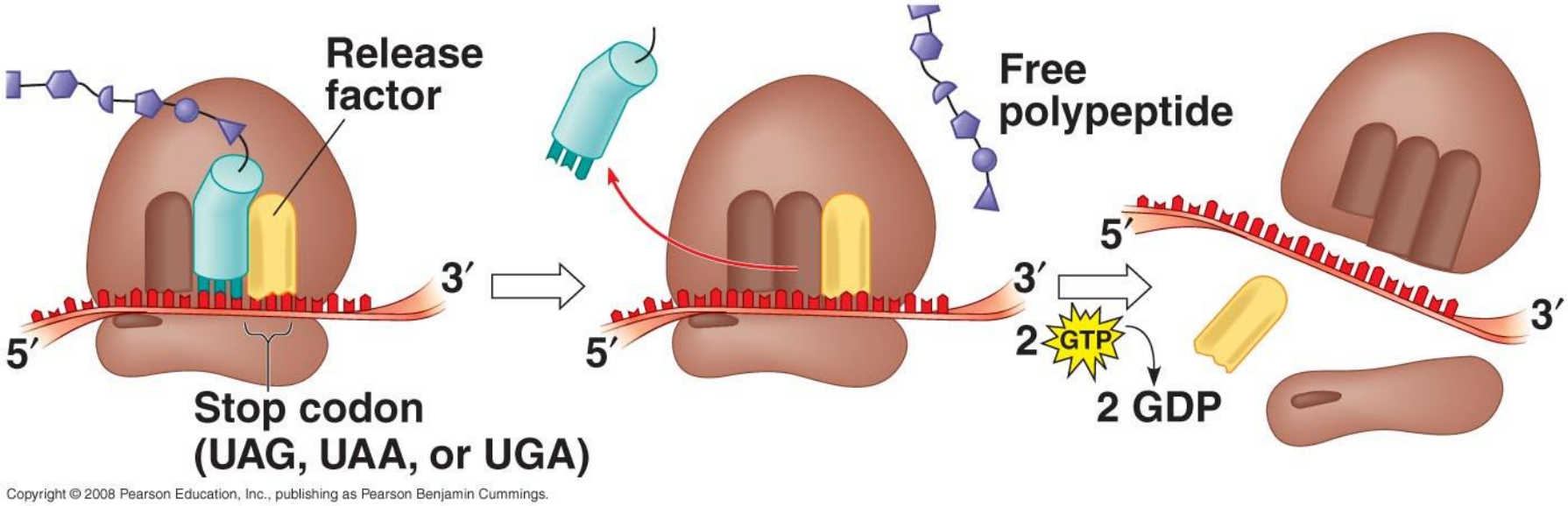
3.Termination

- **Stop codon** reached and translation stops
- **Release factor** binds to stop codon; polypeptide is released
- Ribosomal subunits dissociate



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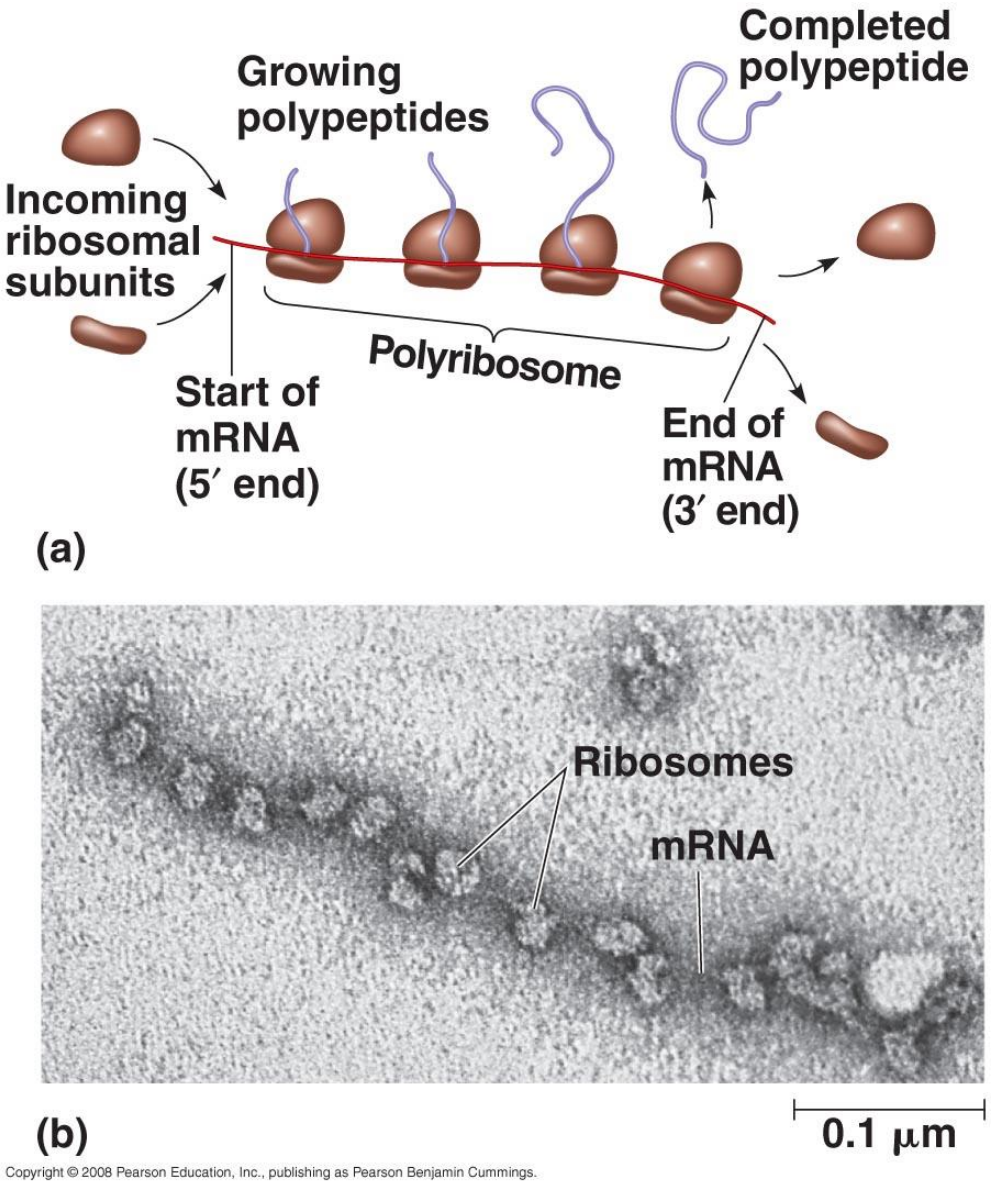
Polyribosomes

- A single mRNA can be translated by several ribosomes at the same time



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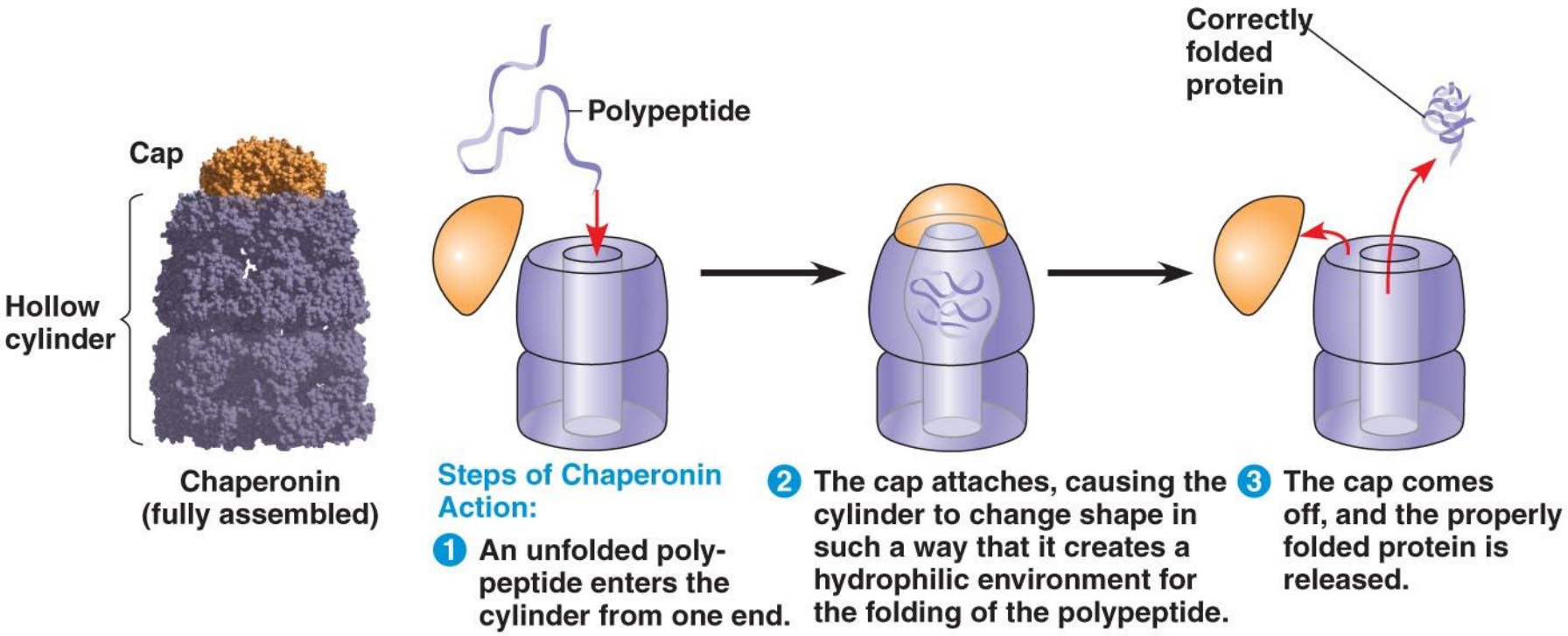
Protein Folding

- During synthesis, polypeptide chain coils and folds spontaneously
- **Chaperonin**: protein that helps polypeptide fold correctly



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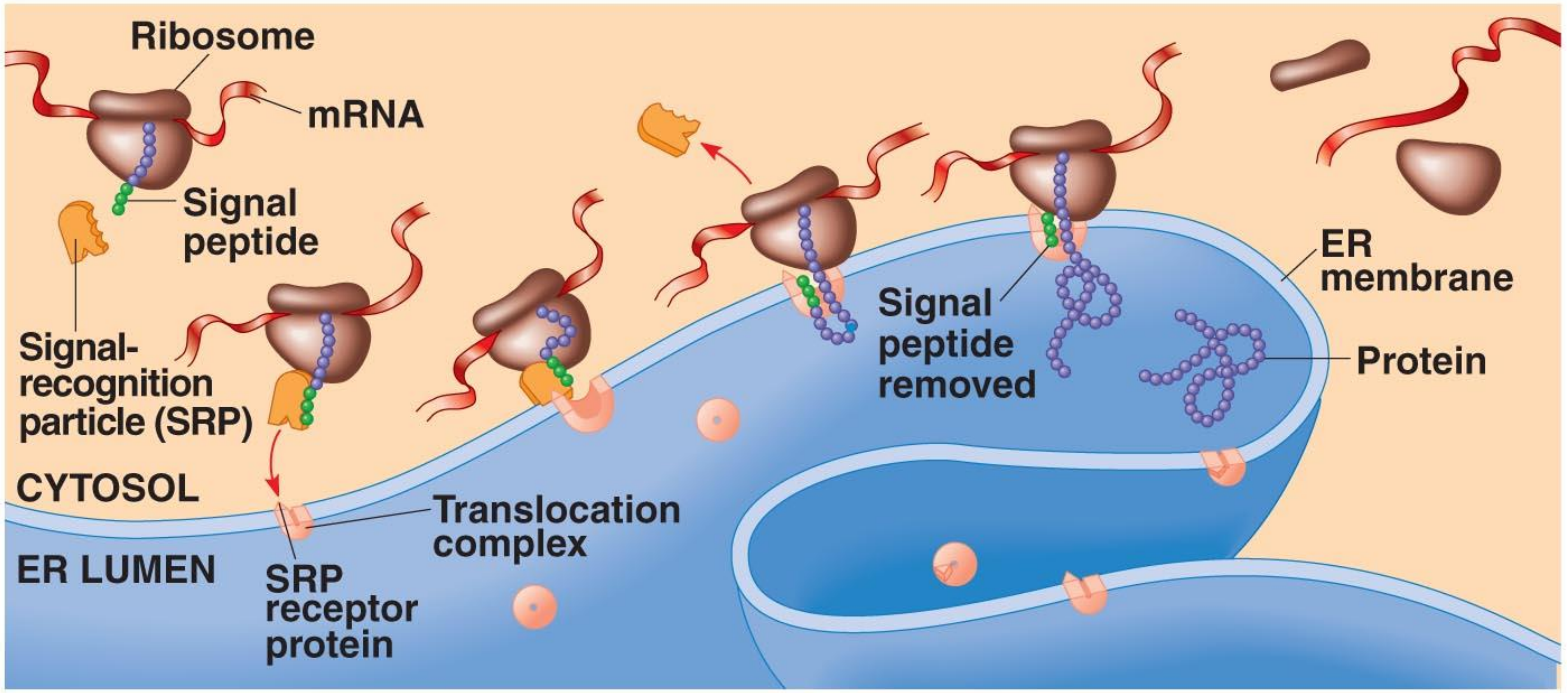
Types of Ribosomes

- **Free ribosomes**: synthesize proteins that stay in cytosol and function there
- **Bound ribosomes** (to ER): make proteins of endomembrane system (nuclear envelope, ER, Golgi, lysosomes, vacuoles, plasma membrane) & proteins for secretion
  - Uses **signal peptide** to target location

Cellular "Zip Codes"

- Signal peptide: 20 AA at leading end of polypeptide determines destination
- Signal-recognition particle (SRP): brings ribosome to ER



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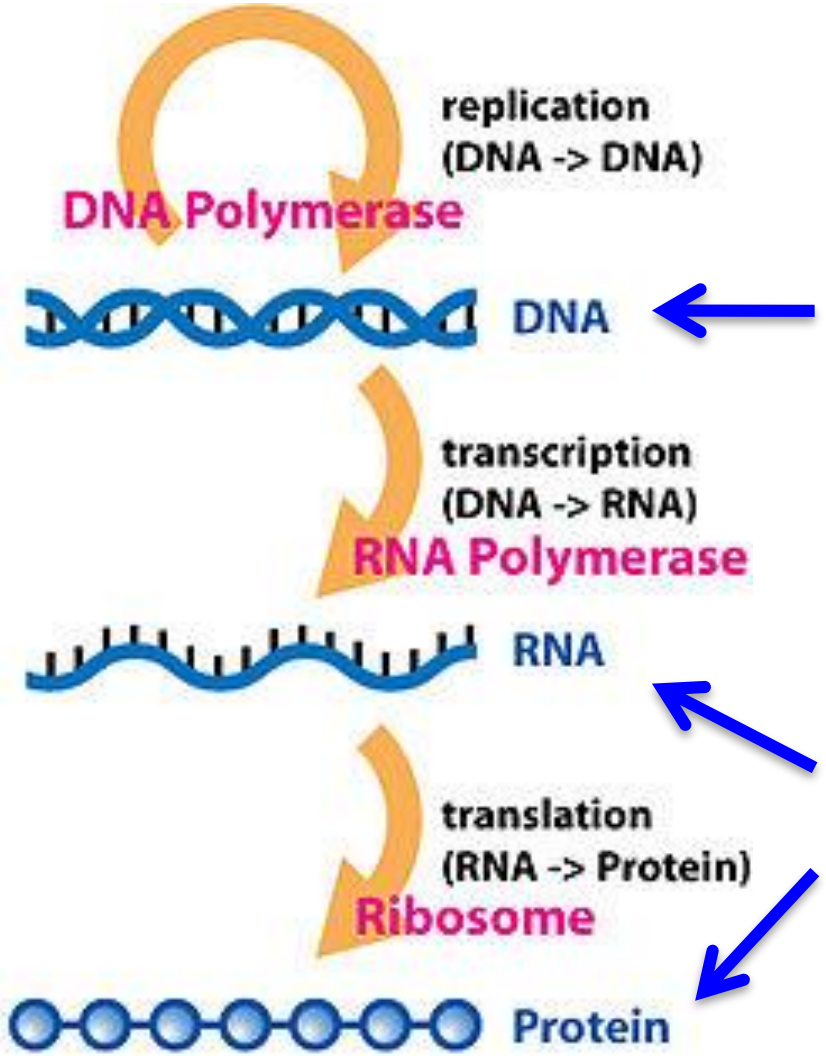
Re-Read, Review, & Reflect

1. Re-read your notes.
2. Talk to a neighbor to fill in any missing information.
3. Highlight key ideas

4. Tell your neighbor 2 facts about the information presented.
5. Ask your neighbor 1 lingering question.

Concept 17.5: Point mutations can affect protein structure and function

The Central Dogma



Mutations happen here

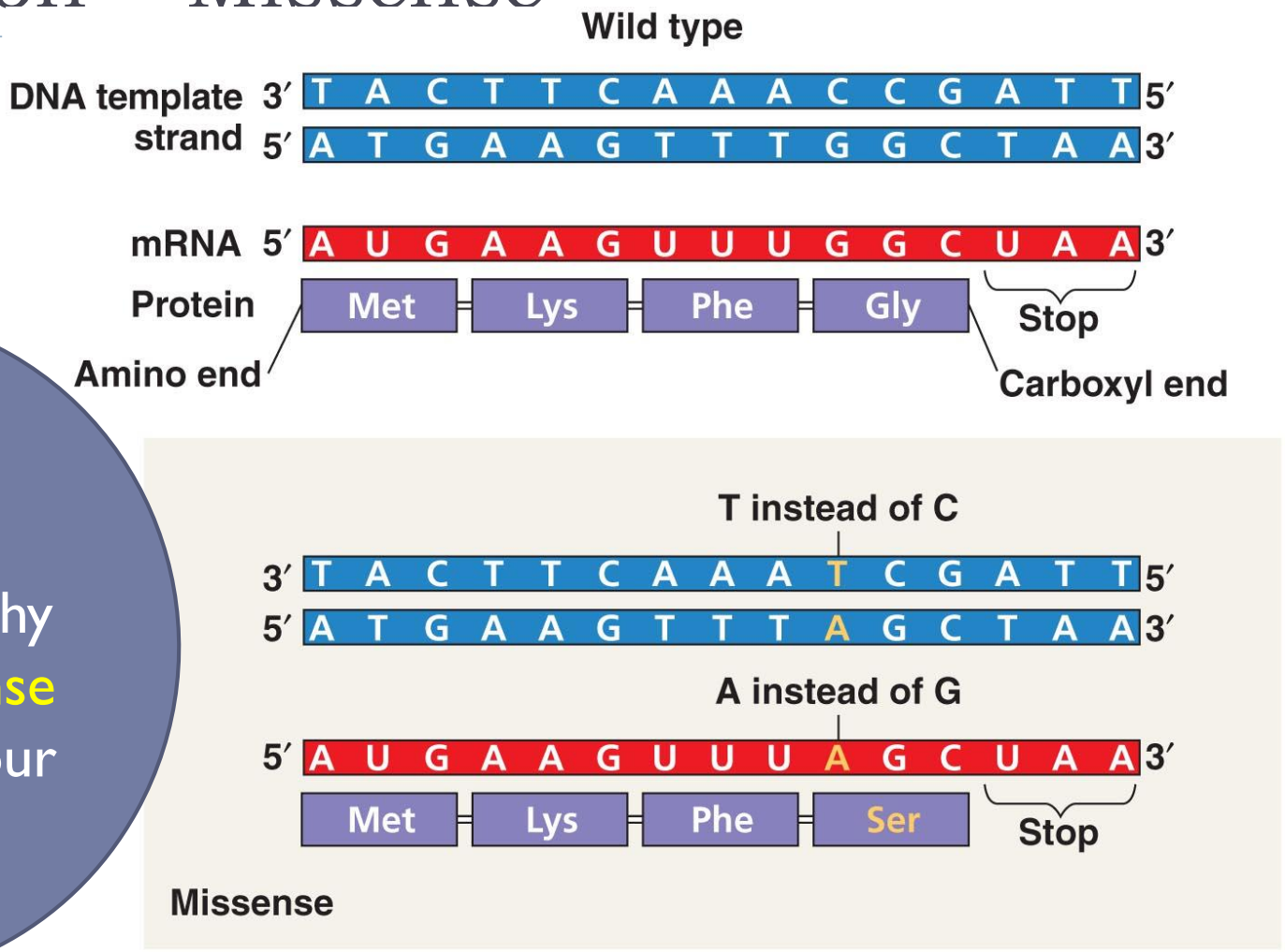
Effects play out here

Mutations = changes in the genetic material of a cell

- Large scale mutations: chromosomal; always cause disorders or death
  - nondisjunction, translocation, inversions, duplications, large deletions
- Point mutations: alter **1 base pair** of a gene
  1. **Base-pair substitutions** – replace 1 with another
     - Missense: different amino acid
     - Nonsense: stop codon, not amino acid
  2. **Frameshift** – mRNA read incorrectly; nonfunctional proteins
     - Caused by insertions or deletions

If substitution results in the *SAME* AA being inserted, then it is a SILENT mutation

Substitution = Missense



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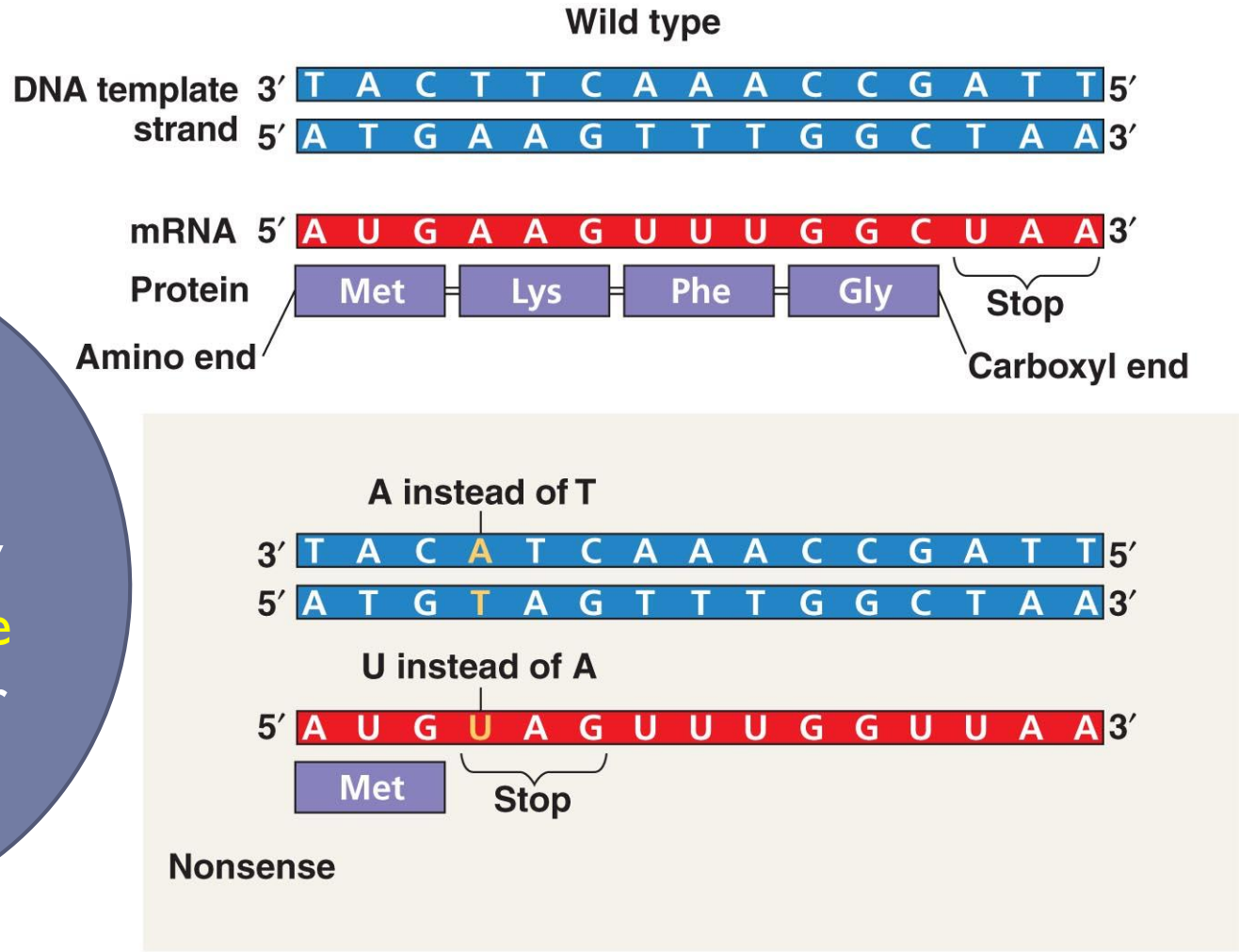
Turn & Talk

Explain how/why this is a missense mutation to your neighbor

Substitution = Nonsense

Turn & Talk

Explain how/why this is a nonsense mutation to your neighbor



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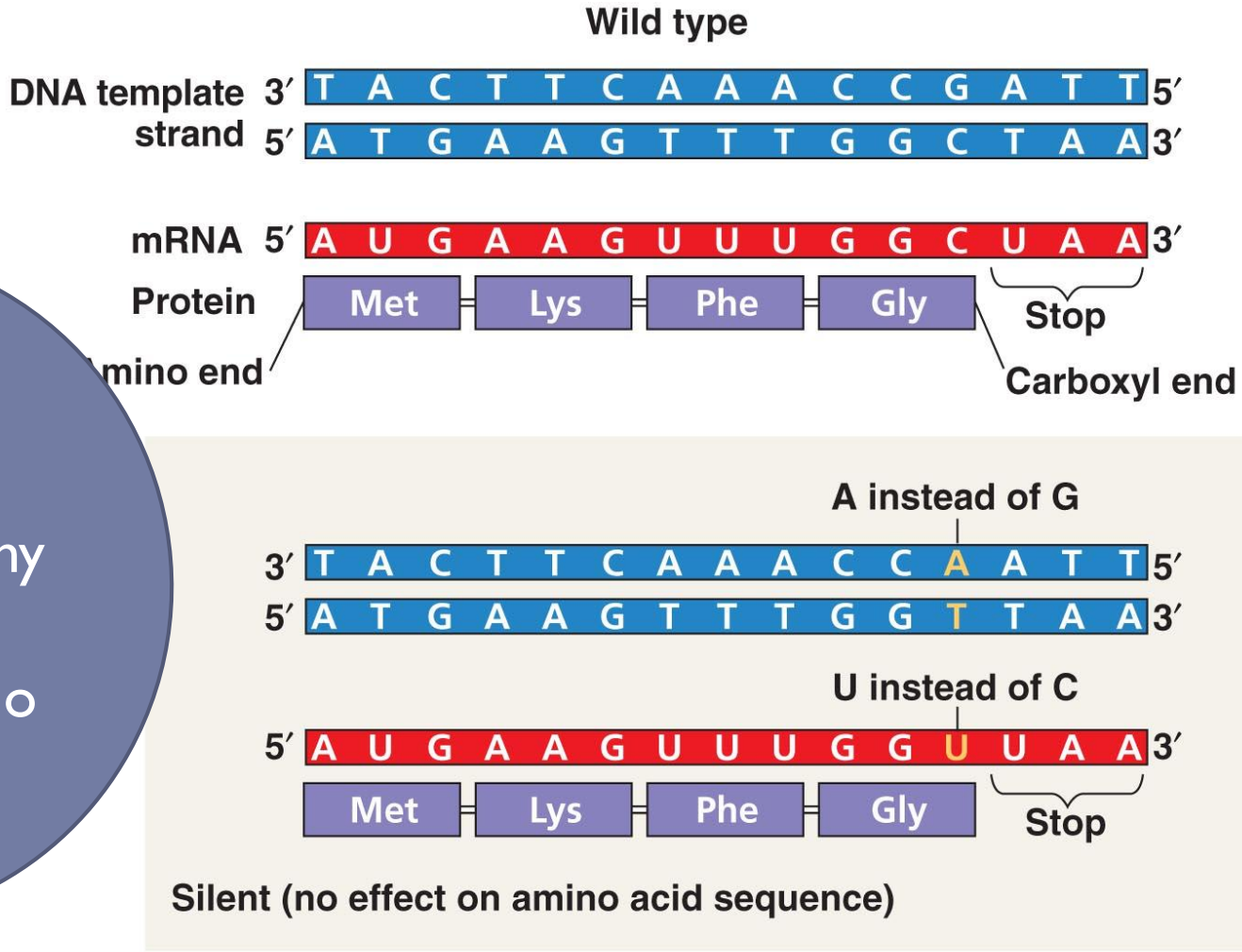
Substitution = **Silent (no effect)**

Turn & Talk

Explain how/why this is silent mutation has no effect.



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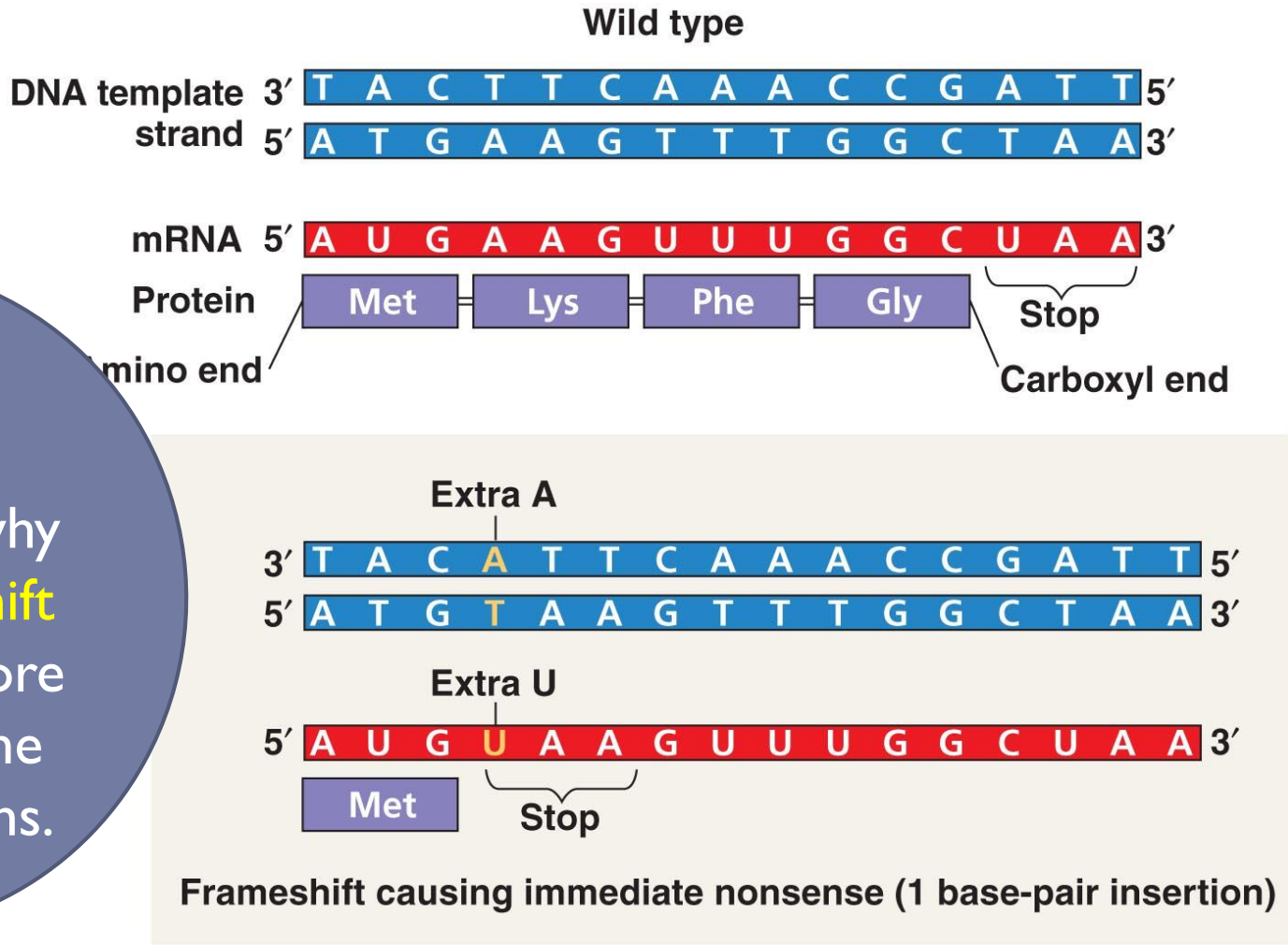
Insertion = Frameshift Mutation

Turn & Talk

Explain how/why this is frameshift mutation is more severe than the point mutations.



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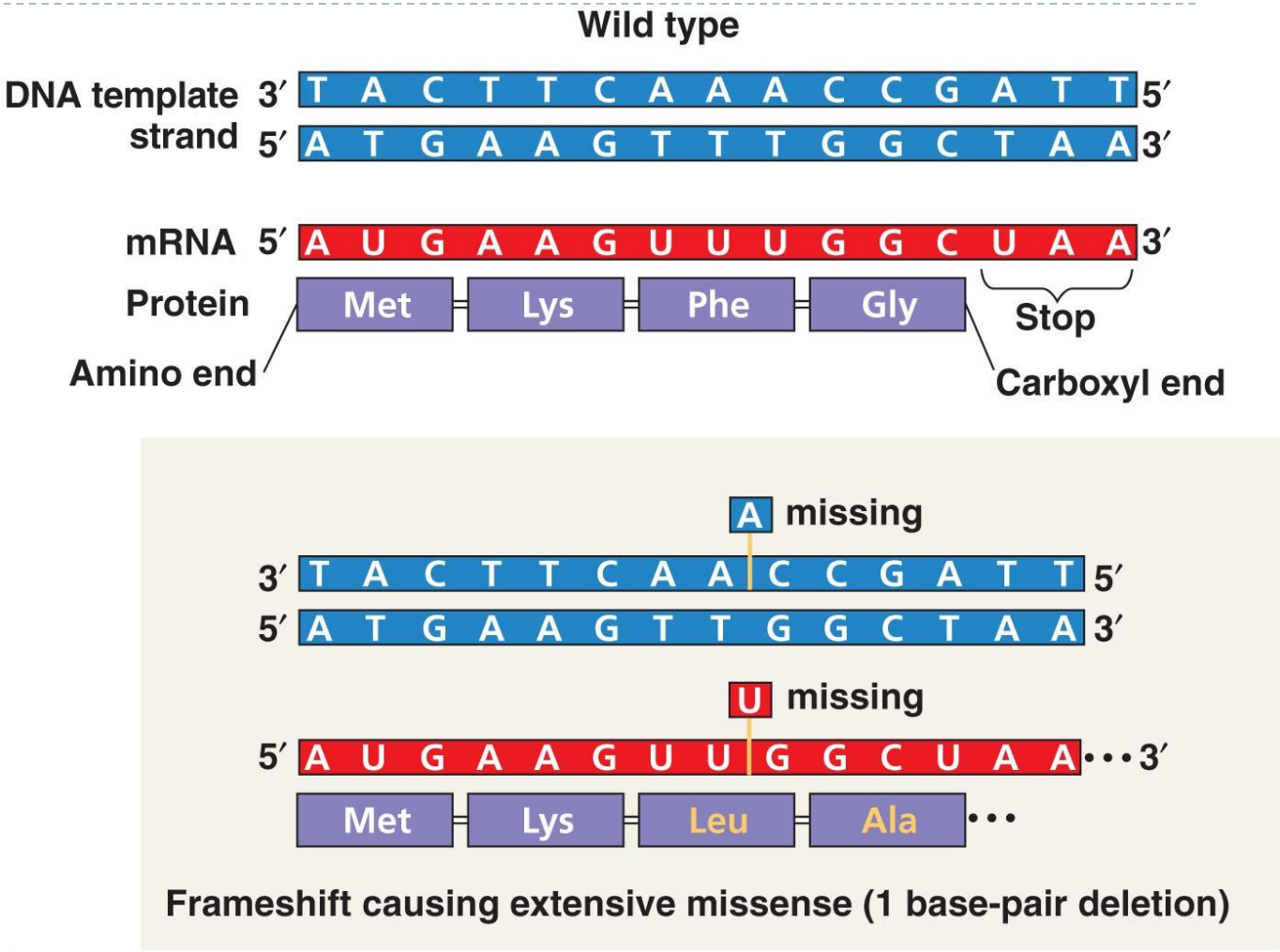
Deletion = Extensive missense, premature termination

Frameshift mutations are usually very bad.

However, the degree of the effect varies depending *where* on the chromosome it occurs



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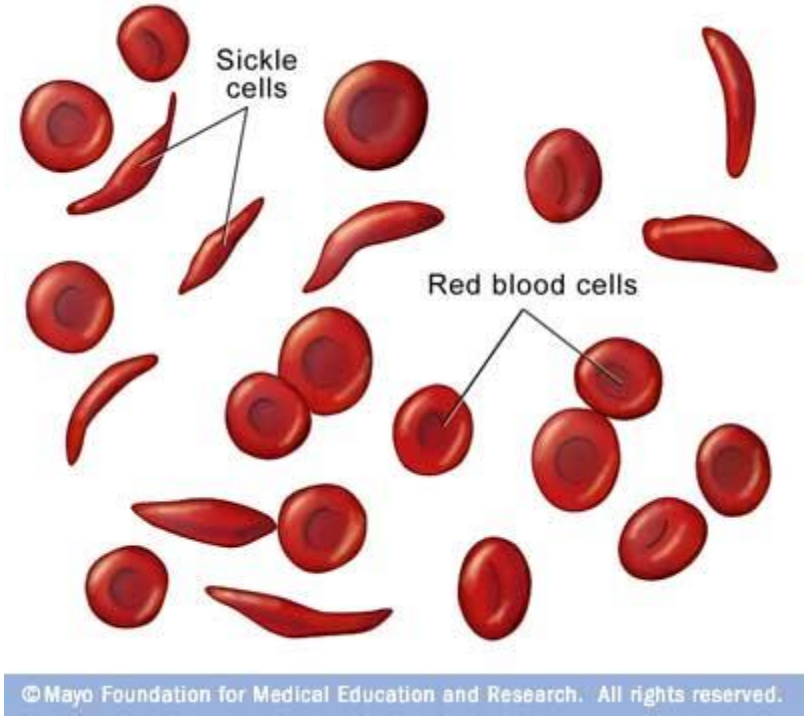
Sickle Cell Disease

Symptoms
Anemia
Pain
Frequent infections
Delayed growth
Stroke
Pulmonary hypertension
Organ damage
Blindness
Jaundice
gallstones



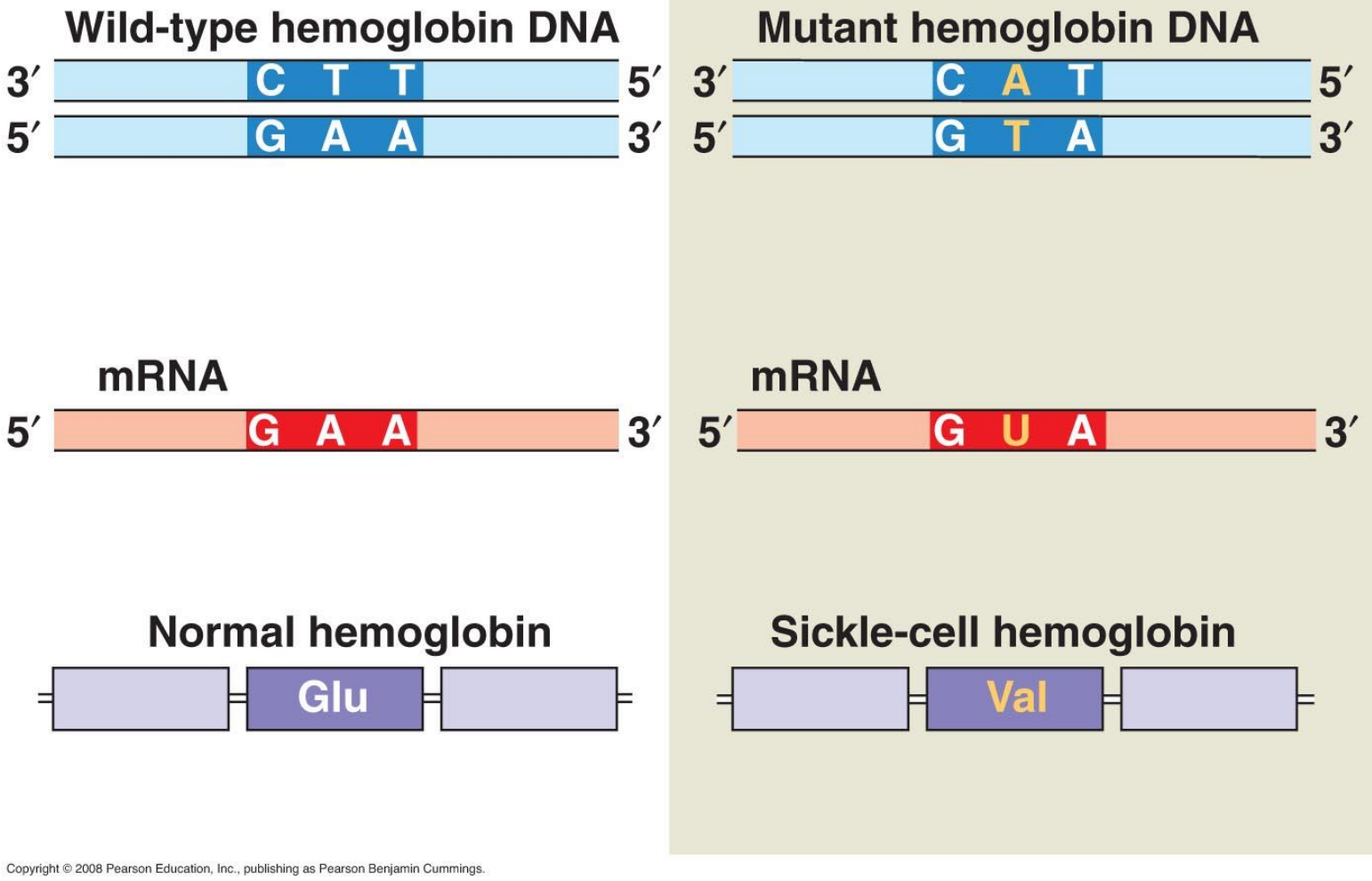
Caused by a genetic defect

Carried by 5% of humans

Carried by up to 25% in some regions of Africa

Life expectancy
42 in males 48 in females

Sickle-Cell Disease = Point Mutation



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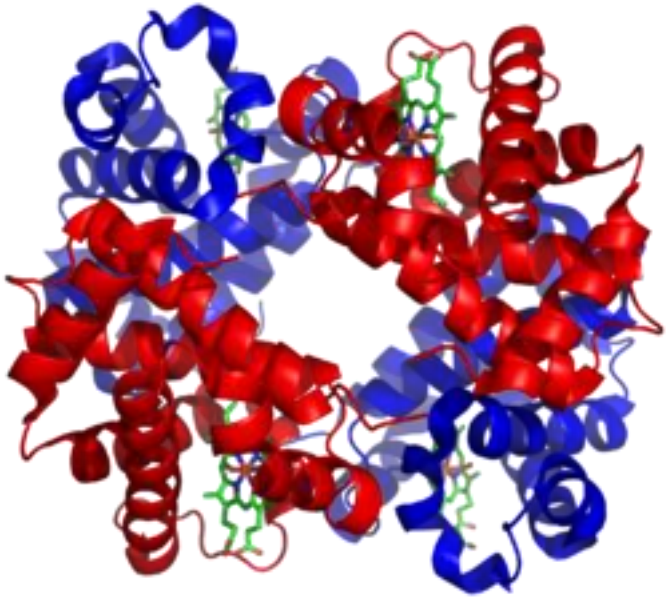
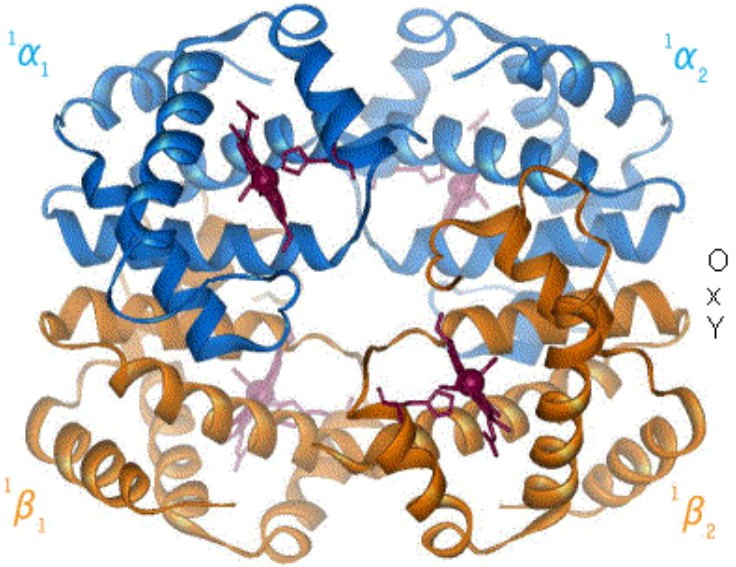
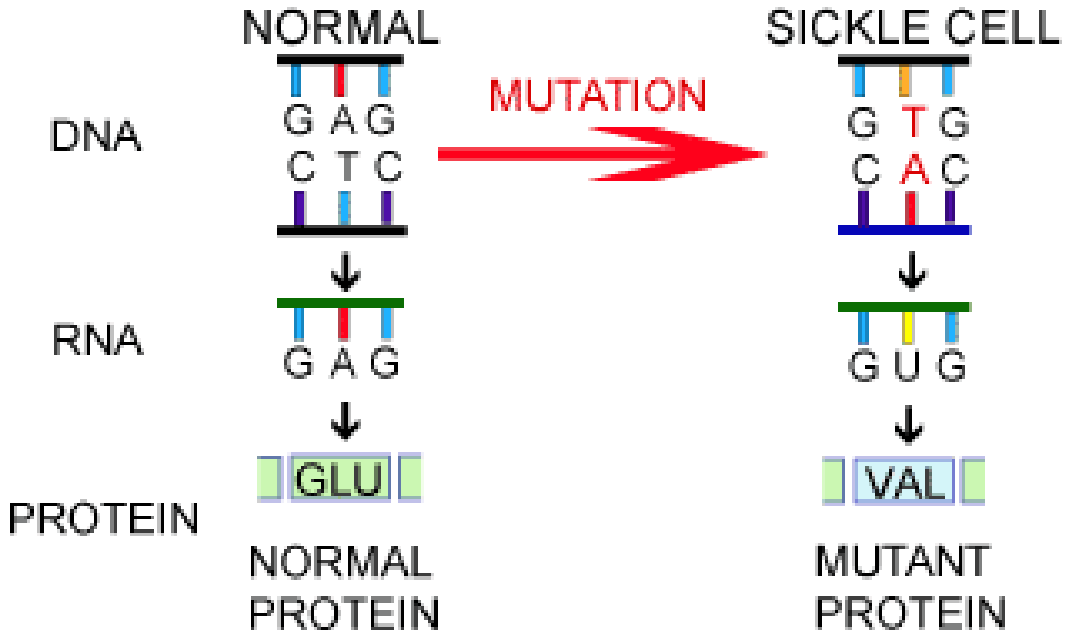
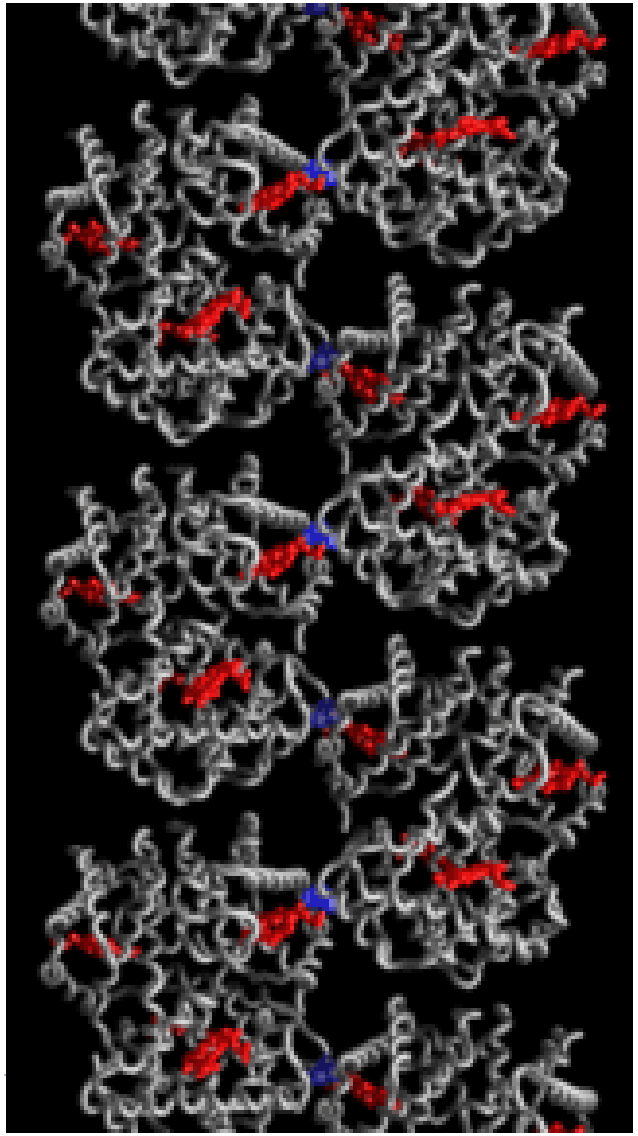
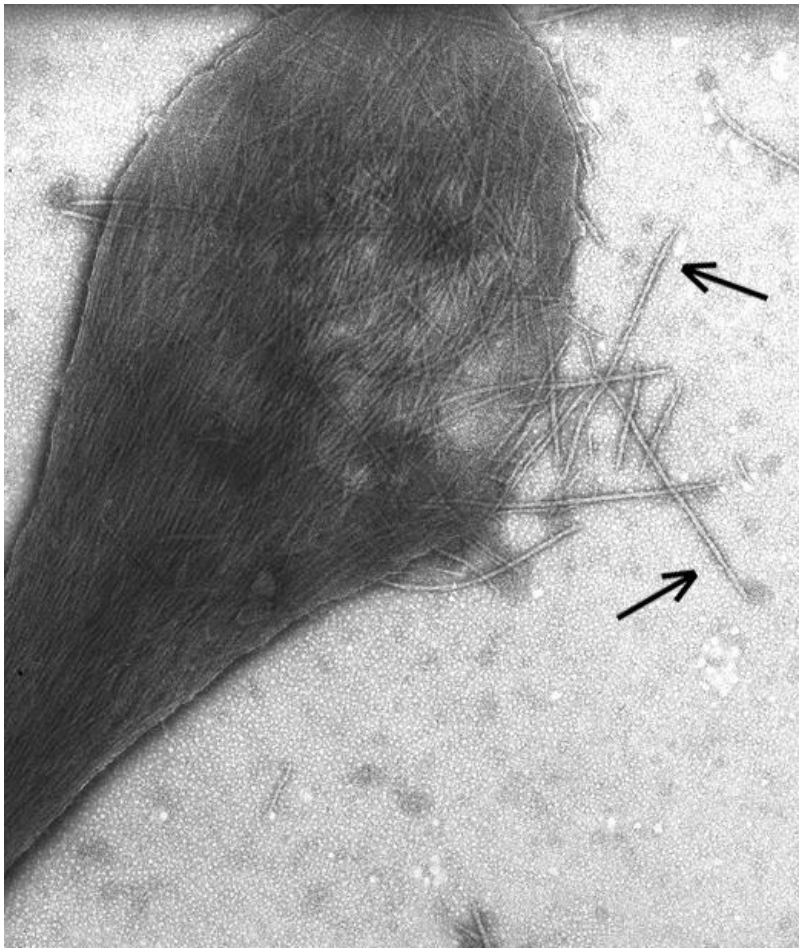


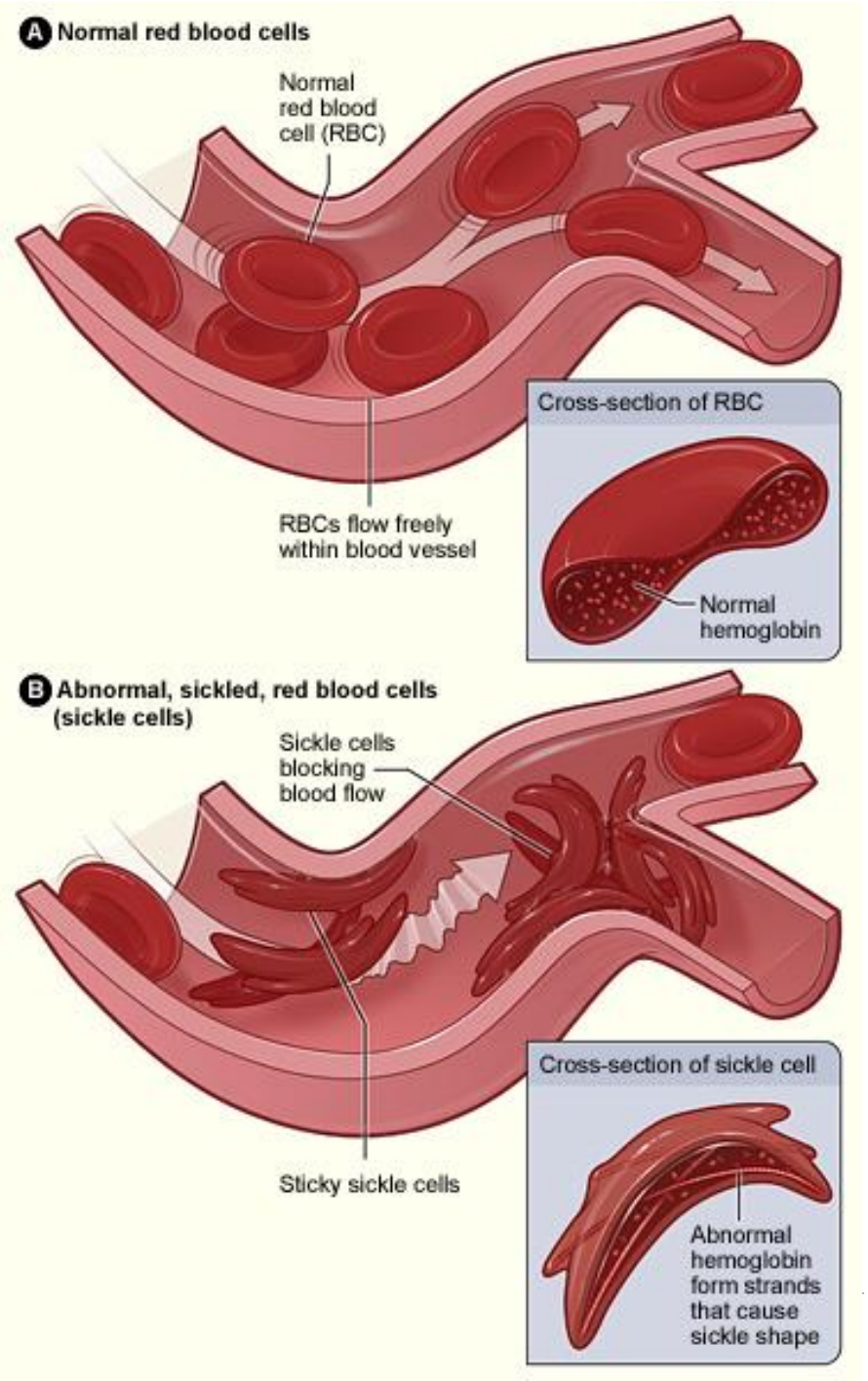

$^1\alpha_1$
$^1\alpha_2$
O
X
Y
$^1\beta_1$
$^1\beta_2$


NORMAL
SICKLE CELL
DNA
G A G
C T C
MUTATION
G T G
C A C
RNA
G A G
G U G
PROTEIN
GLU
VAL
NORMAL PROTEIN
MUTANT PROTEIN

Sickle cell hemoglobin forms long, inflexible chains

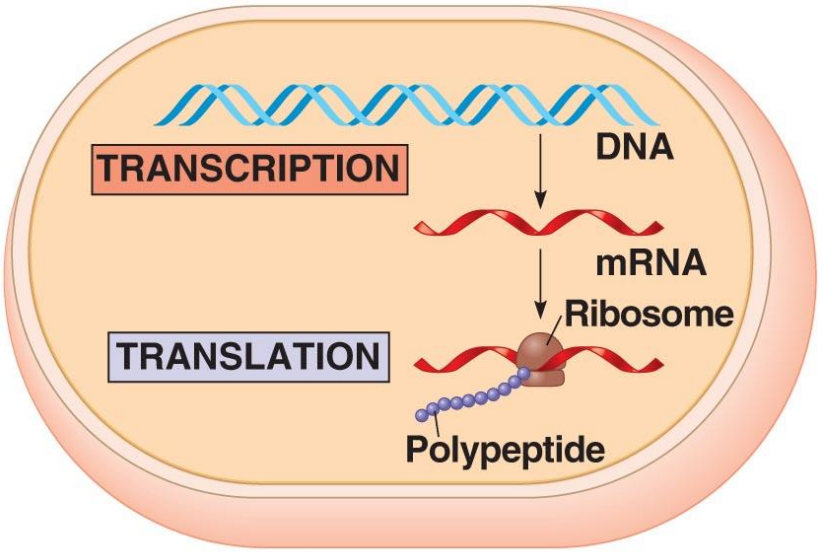





A Normal red blood cells
Normal red blood cell (RBC)
RBCs flow freely within blood vessel
Cross-section of RBC
Normal hemoglobin
B Abnormal, sickled, red blood cells (sickle cells)
Sickle cells blocking blood flow
Sticky sickle cells
Cross-section of sickle cell
Abnormal hemoglobin form strands that cause sickle shape

Comparison: Prokaryotes vs. Eukaryotes

Prokaryote vs. Eukaryote



(a) Bacterial cell

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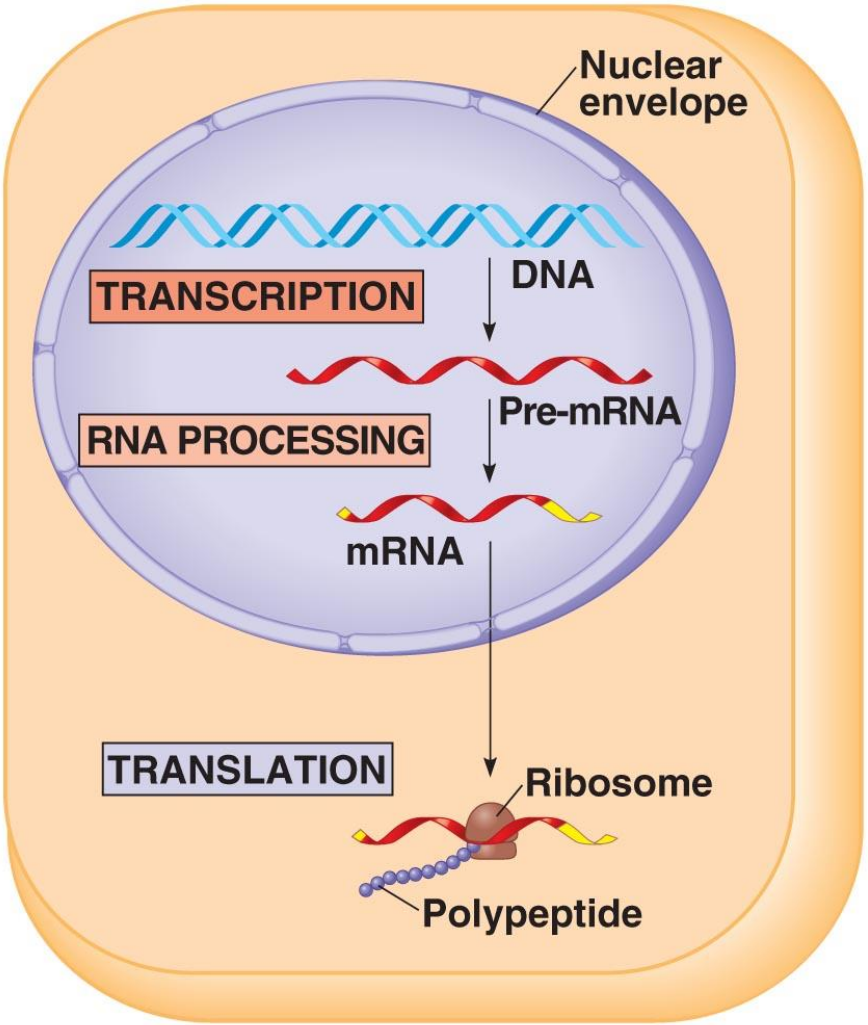
How many differences can you find in your notes? Work with a partner to fill in the chart!



(b) Eukaryotic cell

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Prokaryotes vs. Eukaryotes

Prokaryotes

- Transcription and translation both _____
- DNA/RNA _____
- RNA polymerase binds _____
- Transcription makes _____
- No _____

Eukaryotes

- Transcription in _____; translation in _____
- DNA in _____, RNA _____
- RNA polymerase binds to _____
- Transcription _____ → RNA processing → _____
- _____ (stay), _____ (cut out)

Prokaryotes vs. Eukaryotes

Prokaryotes

- Transcription and translation both in cytoplasm
- DNA/RNA in cytoplasm
- RNA polymerase binds directly to promoter
- Transcription makes mRNA (not processed)
- No introns

Eukaryotes

- Transcription in nucleus; translation in cytoplasm
- DNA in nucleus, RNA travels in/out nucleus
- RNA polymerase binds to TATA box & transcription factors
- Transcription makes pre-mRNA → RNA processing → final mRNA
- Exons (stay), introns (cut out)

Re-Read, Review, & Reflect

1. Re-read your notes.
2. Talk to a neighbor to fill in any missing information.
3. Highlight key ideas

4. Tell your neighbor 2 facts about the information presented.
5. Ask your neighbor 1 lingering question.

Molecular Genetics of Color Mutations in Rock Pocket Mice

- Read: *Introduction*

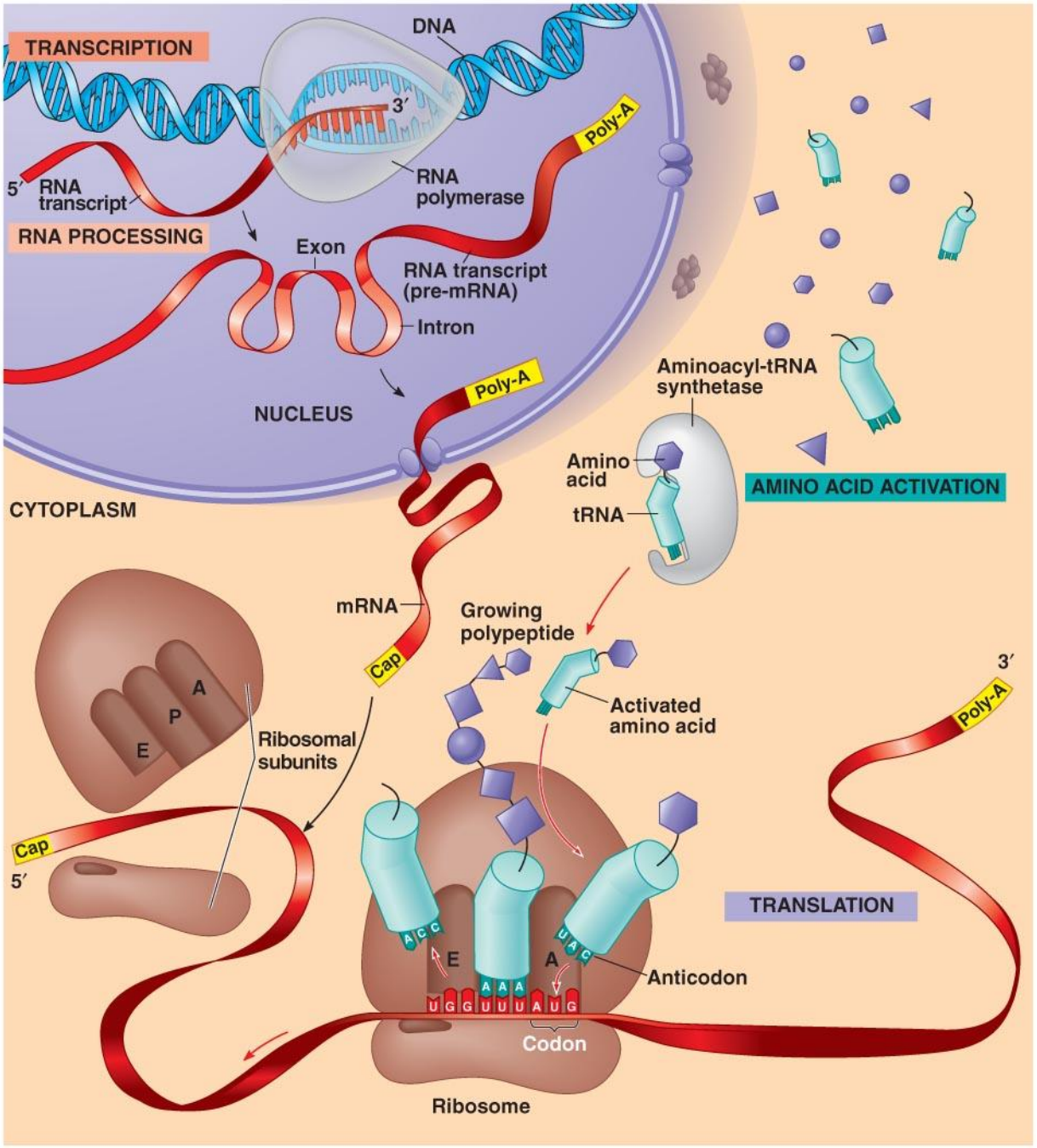
- Recall or Watch: *The Making of the Fittest: Natural Selection and Adaptation (Rock Pocket Mice)*

- Do the following:

1. Follow the directions to transcribe and translate the Mc1r gene.
2. Find the 5 gene mutations
3. Determine the type of mutation for each of the 5 and color them accordingly
4. Answer the questions

A Summary of Protein Synthesis (p. 348)

Most current definition for a gene: A region of DNA whose final product is either a polypeptide or an RNA molecule



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