General and Molecular Biology

Differences in Translation of Prokaryotes and Eukaryotes

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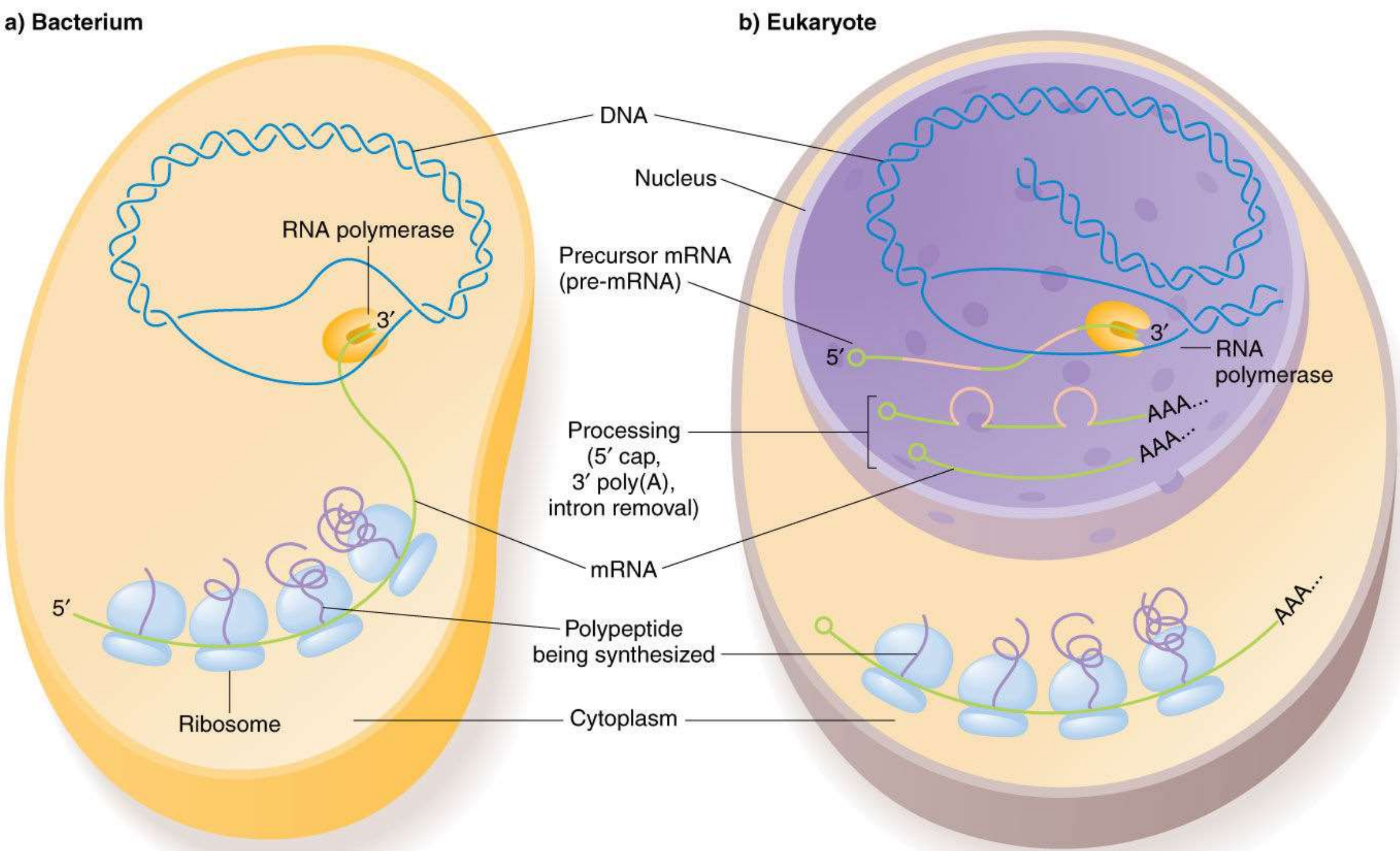
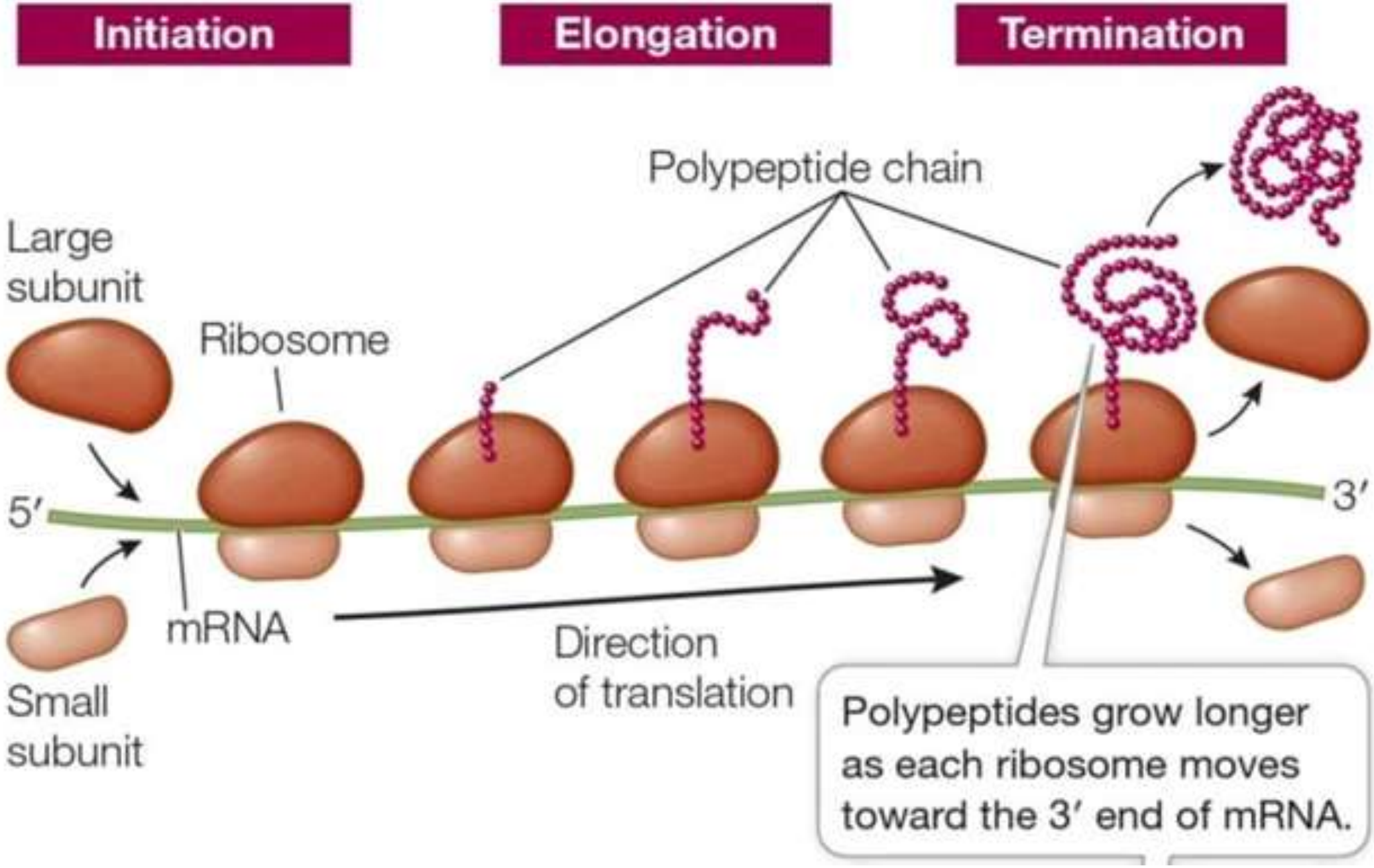
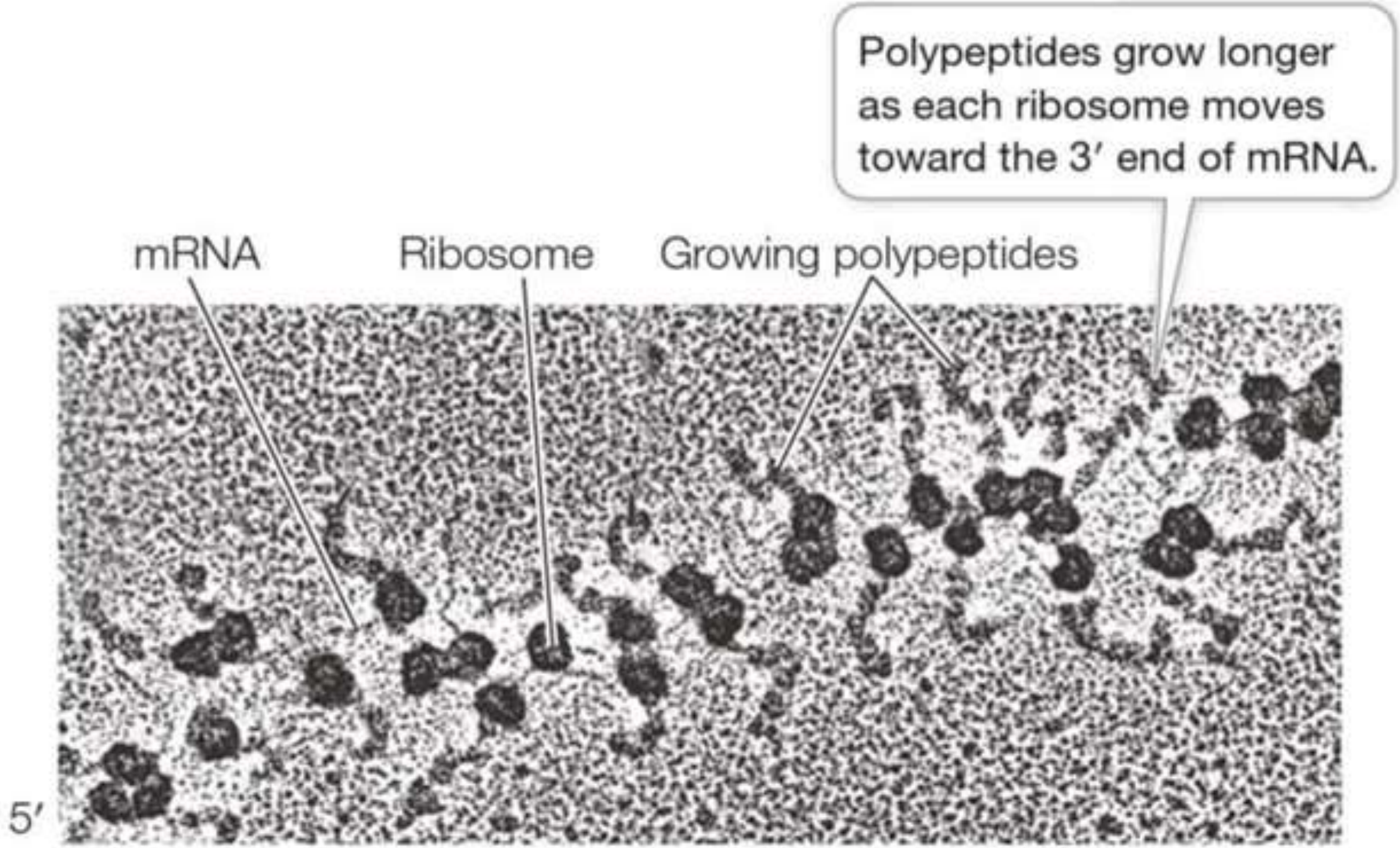

a) Bacterium
b) Eukaryote
DNA
Nucleus
RNA polymerase
3′
Precursor mRNA
(pre-mRNA)
5′
3′
RNA
polymerase
AAA...
AAA...
Processing
(5′ cap,
3′ poly(A),
intron removal)
mRNA
5′
Polypeptide
being synthesized
AAA...
Ribosome
Cytoplasm


Initiation
Elongation
Termination
Polypeptide chain
Large subunit
Ribosome
5′
3′
mRNA
Small subunit
Direction of translation
Polypeptides grow longer as each ribosome moves toward the 3′ end of mRNA.


Polypeptides grow longer as each ribosome moves toward the 3′ end of mRNA.
mRNA
Ribosome
Growing polypeptides
5′

Translation

- Translation in biology is the process by which cells create proteins from the instructions encoded in mRNA (messenger RNA).
- It is one of the key steps in gene expression, following transcription (when DNA is copied into mRNA).
- Translation is almost similar in prokaryotes and eukaryotes apart from some differences.

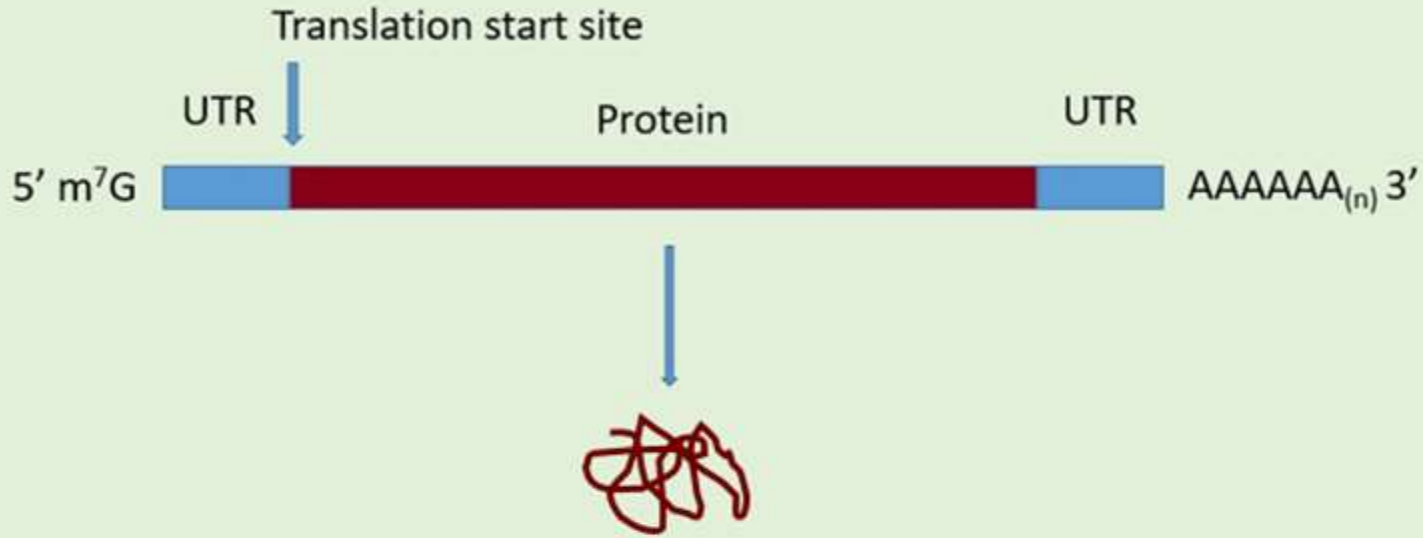
1. Location

- **Prokaryotes:**
- Translation occurs in the cytoplasm, often simultaneously with transcription (coupled process).
- **Eukaryotes:**
- Translation occurs in the cytoplasm, after transcription and RNA processing in the nucleus.

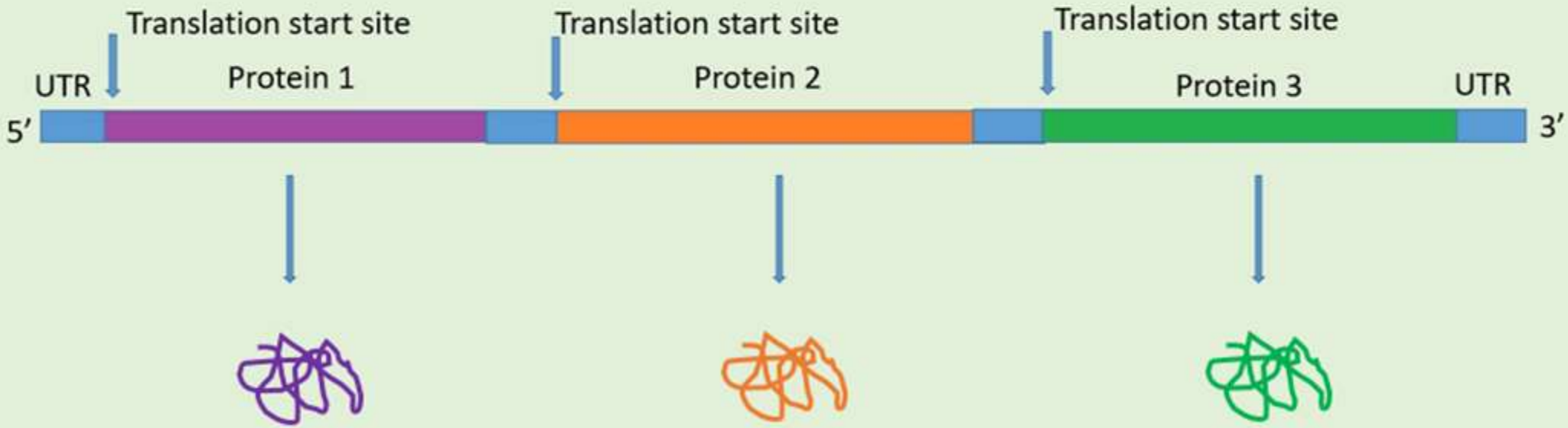
2. mRNA Structure

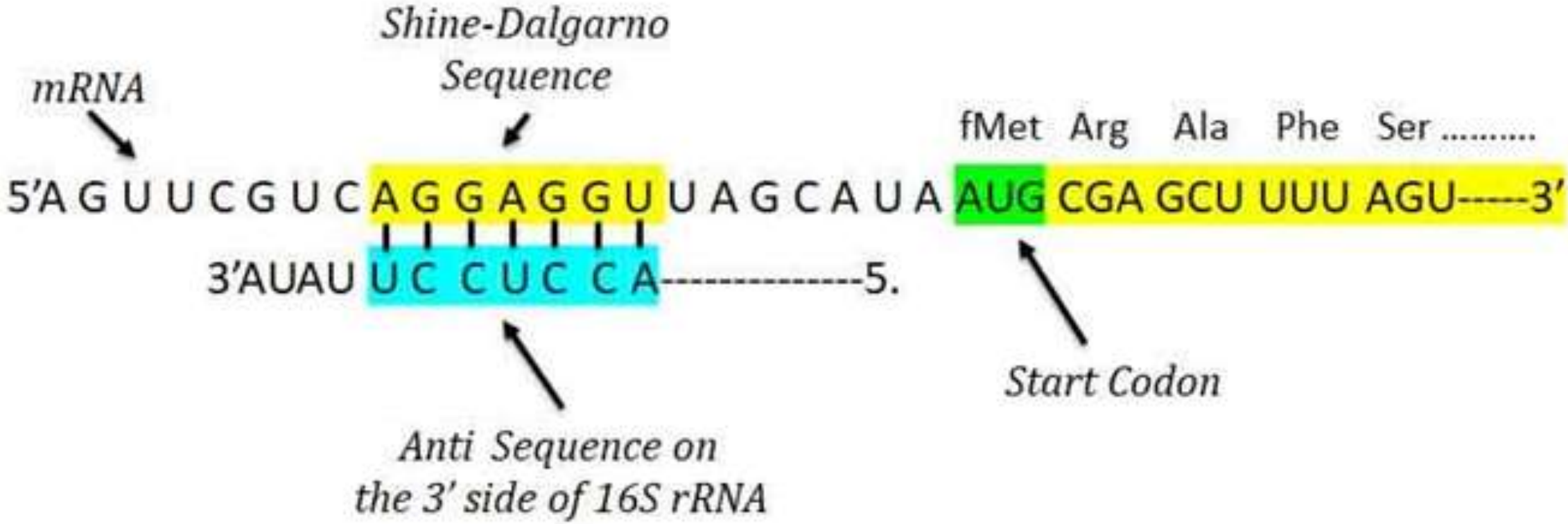
- **Prokaryotes:**
- mRNA is often polycistronic (encodes multiple proteins from a single mRNA transcript).
- No 5′ cap or poly-A tail.
- Contains a Shine-Dalgarno sequence for ribosome binding
- **Eukaryotes:**
- mRNA is monocistronic (encodes a single protein per mRNA).
- Has a 5′ cap and a 3′ poly-A tail for stability and translation initiation.
- Uses a Kozak sequence (5'-GCC(A/G)CCAUGG-3') for ribosome recognition.

Eukaryotic mRNA



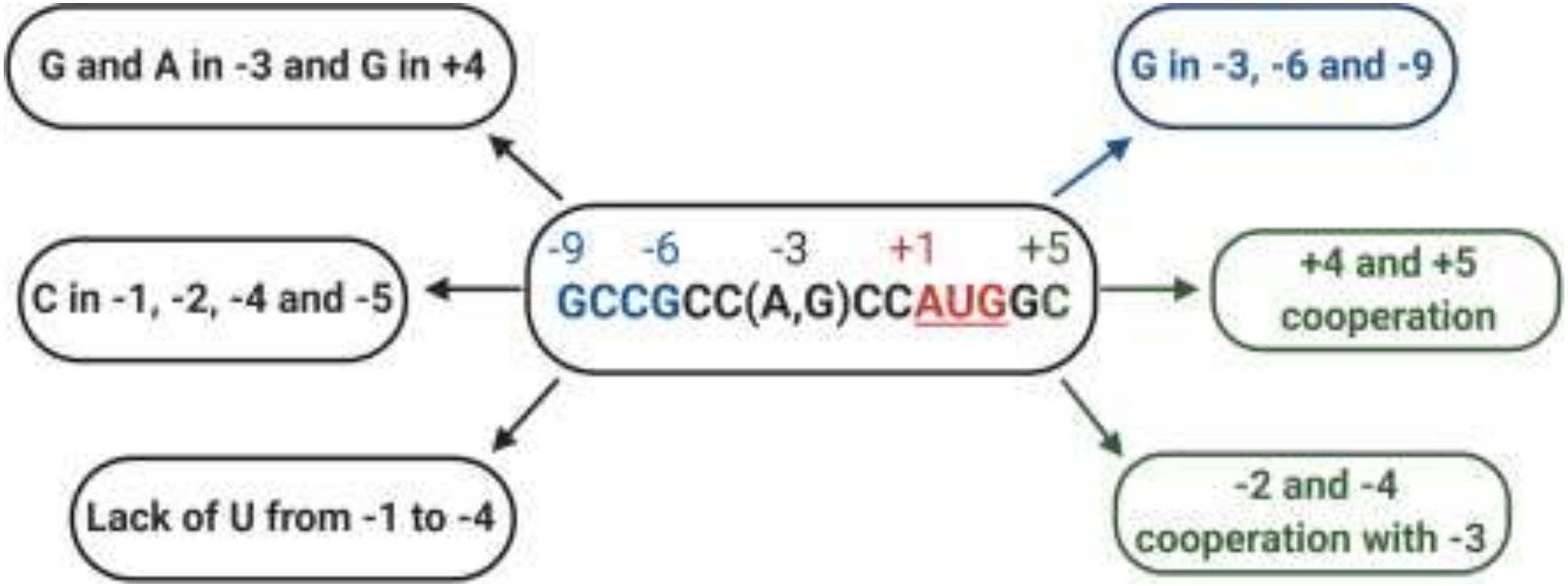
Prokaryotic mRNA





Shine Dalgarno Sequence

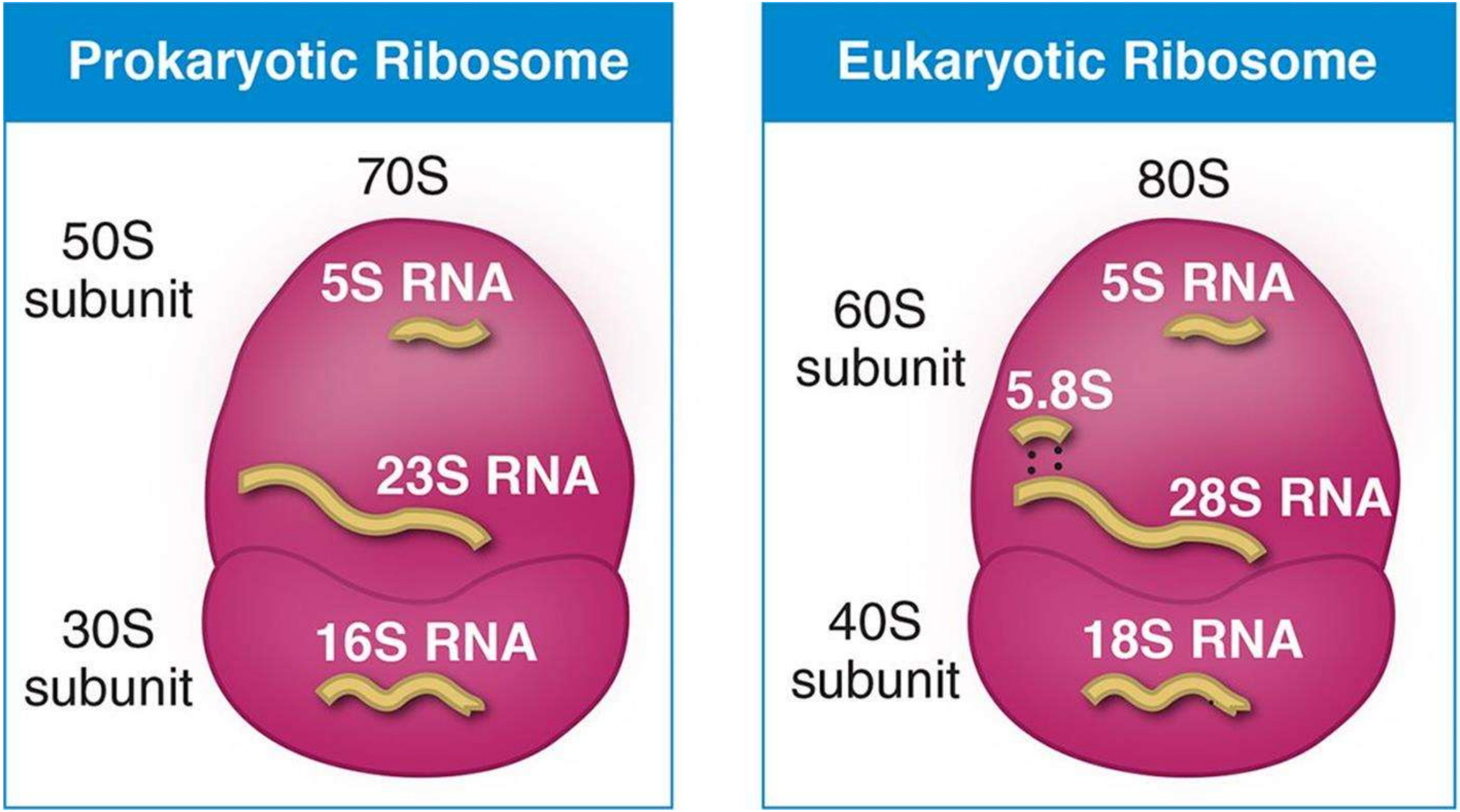
Kozak sequence (5'-GCC(A/G)CCAUGG-3’) in Eukaryotes



	Shine Dalgarno	Kozak Sequence
DEFINITION	Shine Dalgarno sequence is a ribosomal binding site found in bacterial and archaeal messenger RNA	Kozak sequence is a protein translation initiation site in most eukaryotic messenger RNA
SEQUENCE	5'AGGAGGU3'	5' (gcc) gccRccAUGG-3'
DISCOVERED BY	Australian scientists John Shine and Lynn Dalgarno	American scientist Marilyn Kozak
AUG CODON	Located around 8 bases upstream of the start codon AUG	Surrounds the AUG codon
SMALLER SUBUNIT OF RIBOSOME BINDS TO THE SEQUENCE	30S subunit	40S subunit
EXAMPLES	Bacteria, archaea, chloroplast, and mitochondria	Vertebrates such as cow, cat, dog, chicken, guinea pig, hamster, mouse, pig rabbit, sheep, Xenopus

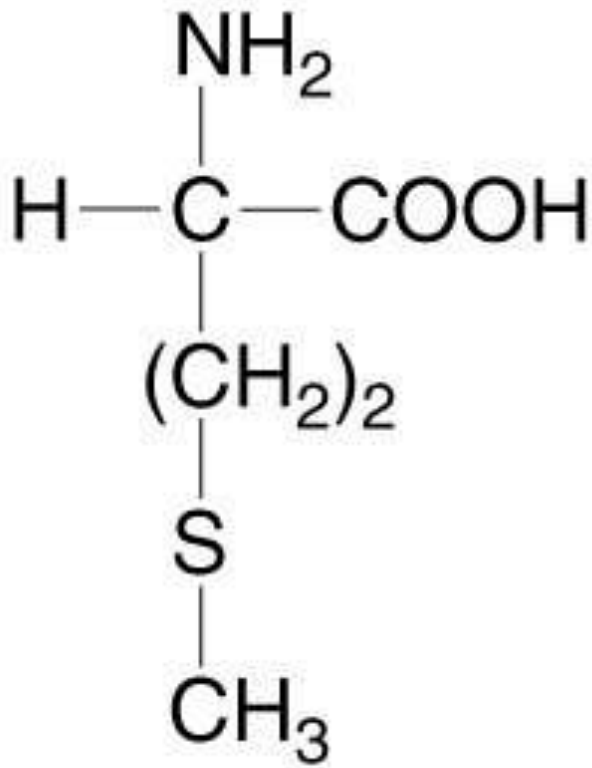
3. Ribosomes

- **Prokaryotes:**
- Smaller ribosomes (70S), composed of 50S (large subunit) and 30S (small subunit).
- **Eukaryotes:**
- Larger ribosomes (80S), composed of 60S (large subunit) and 40S (small subunit).

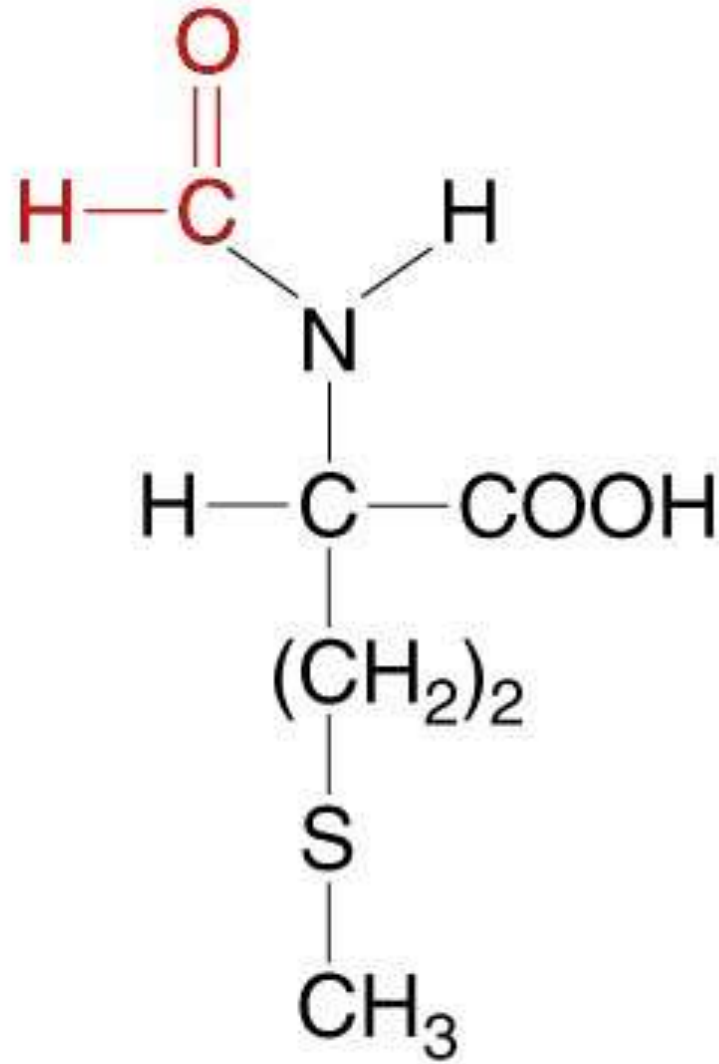

Prokaryotic Ribosome
70S
50S subunit
5S RNA
23S RNA
30S subunit
16S RNA
Eukaryotic Ribosome
80S
60S subunit
5S RNA
5.8S
28S RNA
40S subunit
18S RNA

4. Initiation

- **Prokaryotes:**
- Initiator tRNA carries N-formylmethionine (fMet).
- Translation initiation requires three initiation factors (IF1, IF2, IF3).
- The Shine-Dalgarno sequence aligns the mRNA with the ribosome.
- **Eukaryotes:**
- Initiator tRNA carries methionine (Met).
- Initiation is more complex, involving multiple eukaryotic initiation factors (eIFs).
- The 5′ cap and poly-A tail enhance ribosome assembly, and ribosomes scan for the start codon.



Methionine



N-Formylmethionine

5. Elongation

- Elongation factors in Prokaryotes include.

Prokaryotic Factors	Function	GTP Hydrolase
EF-Tu	chaperones aminoacyl-tRNA into ribosome	Yes
EF-Ts	Recharges EF-Tu with GDP-GTP exchange	No
EF-G	Required for translocation of mRNA and tRNAs after peptide bond formation	Yes
EF-P	Helps facilitate protein exit through tunnel and prevent stalling	No

5. Elongation

- Elongation factors in eukaryotes are following.

Eukaryotic Factors	Function'	GTP Hydrolase'
eEF-1α	chaperones aminoacyl-tRNA into ribosome	Yes
eEF-1βγ	Recharges eEF-1a with GDP-GTP exchange	No
eEF-2	Required for translocation of mRNA and tRNAs after peptide bond formation	Yes
eIF5A	Helps facilitate protein exit through tunnel and prevent stalling	No

6. Termination

- **Prokaryotes:**
- Release factors (RF1 and RF2) recognize stop codons (UAA, UAG, UGA).
- **Eukaryotes:**
- A single release factor (eRF1) recognizes all stop codons.

7. Post-Translation Modifications

- **Prokaryotes:**
- Minimal post-translational modifications.
- **Eukaryotes:**
- Extensive post-translational modifications (e.g., phosphorylation, glycosylation) in the ER and Golgi apparatus.

8. Speed of Translation

- **Prokaryotes:**
- Translation is rapid and occurs concurrently with transcription.
- About 15–20 amino acids are added per second.
- **Eukaryotes:**
- Translation is slower and temporally separated from transcription.
- About 5–10 amino acids are added per second.

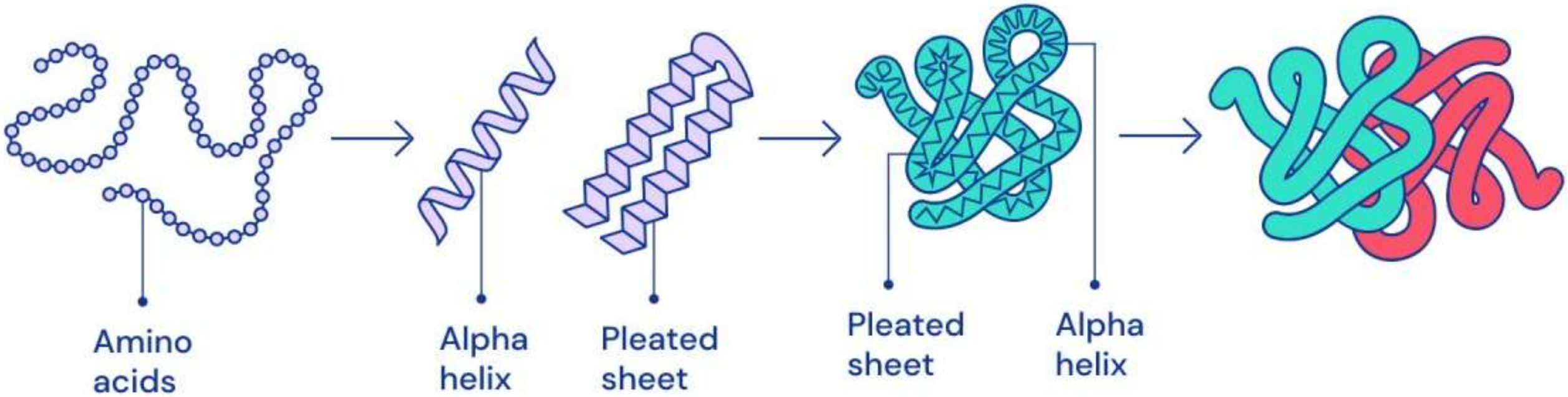
Feature	Prokaryotes	Eukaryotes
Location	Cytoplasm	Cytoplasm (after nucleus)
mRNA Type	Polycistronic	Monocistronic
Ribosome Size	70S	80S
Initiator tRNA	fMet	Met
Key Sequences	Shine-Dalgarno sequence	Kozak sequence
Initiation Factors	IF1, IF2, IF3	Multiple eIFs
Elongation Factors	EF-Tu, EF-Ts, EF-G	eEF1, eEF2
Release Factors	RF1, RF2	eRF1
Post-Translation	Minimal	Extensive

Proofreading

- **Proofreading Mechanisms:**
- Aminoacyl-tRNA synthetases have proofreading abilities to ensure that the correct amino acid is attached to the corresponding tRNA. If the wrong amino acid is attached, the enzyme can hydrolyze the incorrect product and attach the correct one.
- **GTP Hydrolysis:**
- Many steps in translation, especially the binding and translocation of tRNAs, are coupled with GTP hydrolysis. This coupling ensures that errors in codon recognition are minimized because GTP hydrolysis only occurs if the correct tRNA is bound.

Post-Translational Modifications in Eukaryotes

- Once a protein is synthesized, it often undergoes further modifications that are essential for its proper function. These modifications include:
- **1. Folding:** The protein must fold into its correct 3D shape.
- **2. Chemical Modifications:** Proteins can undergo phosphorylation, methylation, glycosylation, or acetylation, which regulate their function, localization, or interactions with other molecules.
- **3. Transportation:** Proteins may be transported to specific areas in the cell (e.g., the nucleus, mitochondria, or plasma membrane) to carry out their functions.


Amino acids
Alpha helix
Pleated sheet
Pleated sheet
Alpha helix


Thank
You!