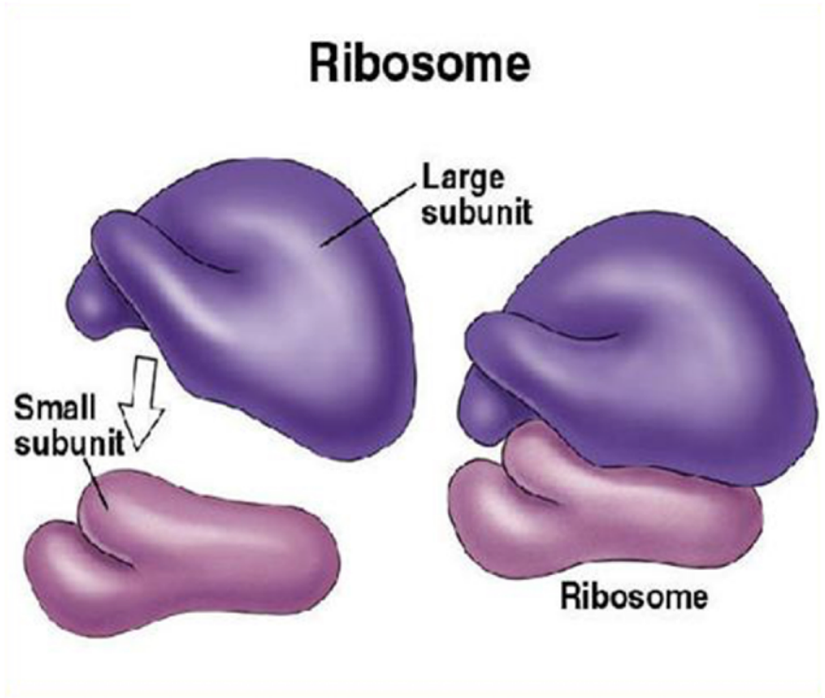
BIOL2107, Fall ’23

Lecture 25

Central Dogma: RNA to Protein, Translation…



DNA

rRNA

tRNA

mRNA

RNA

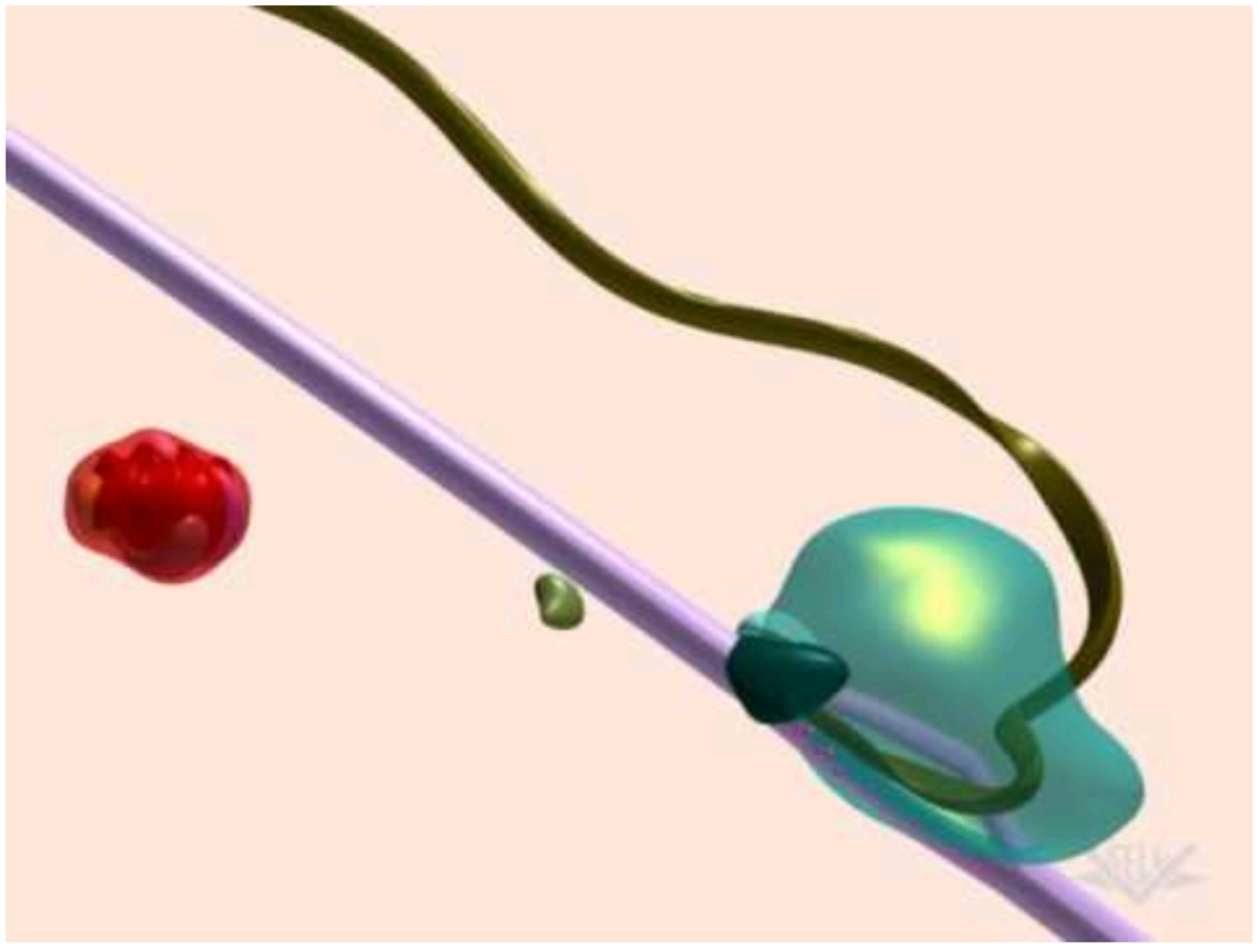
µRNA

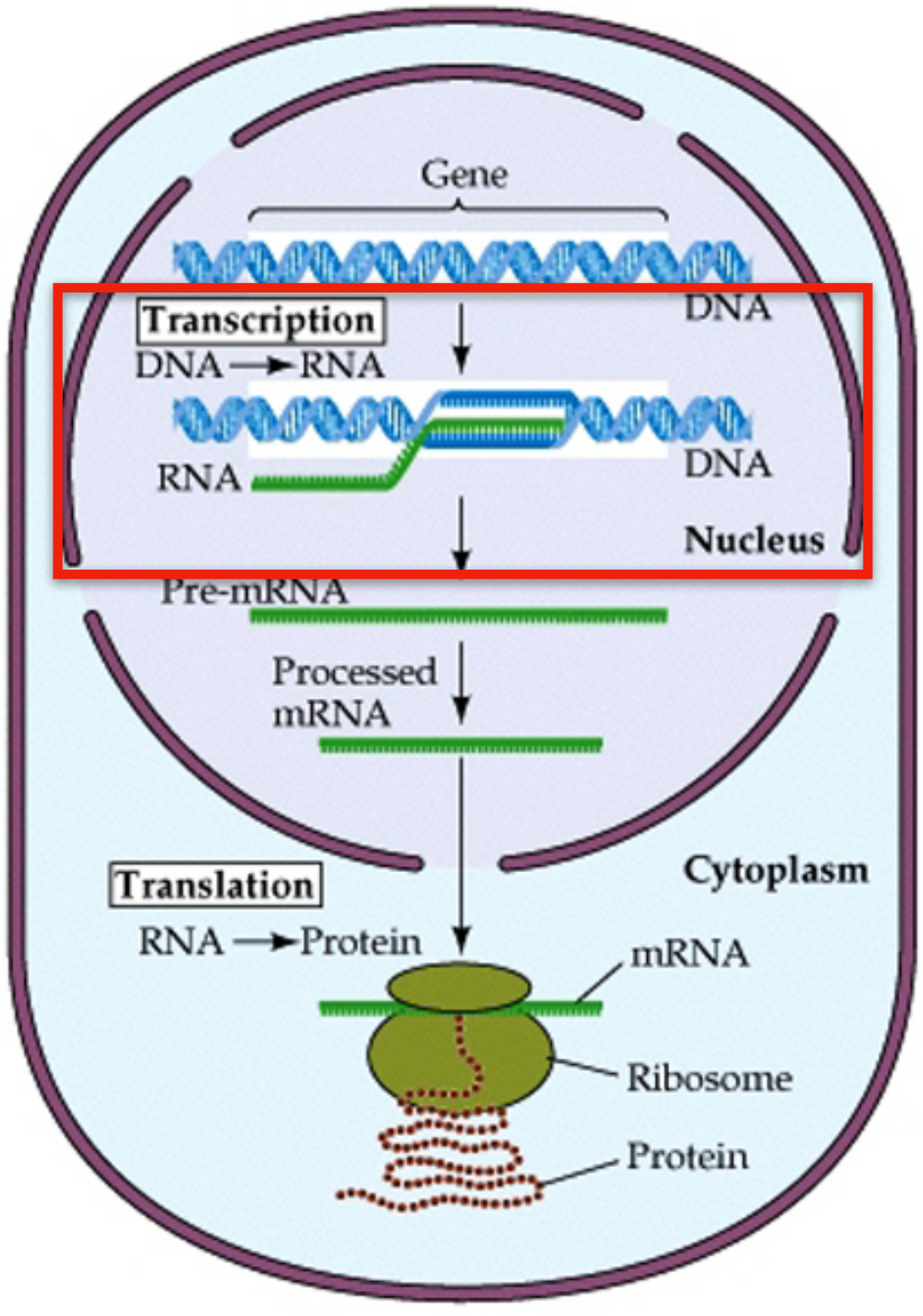
Catalytic

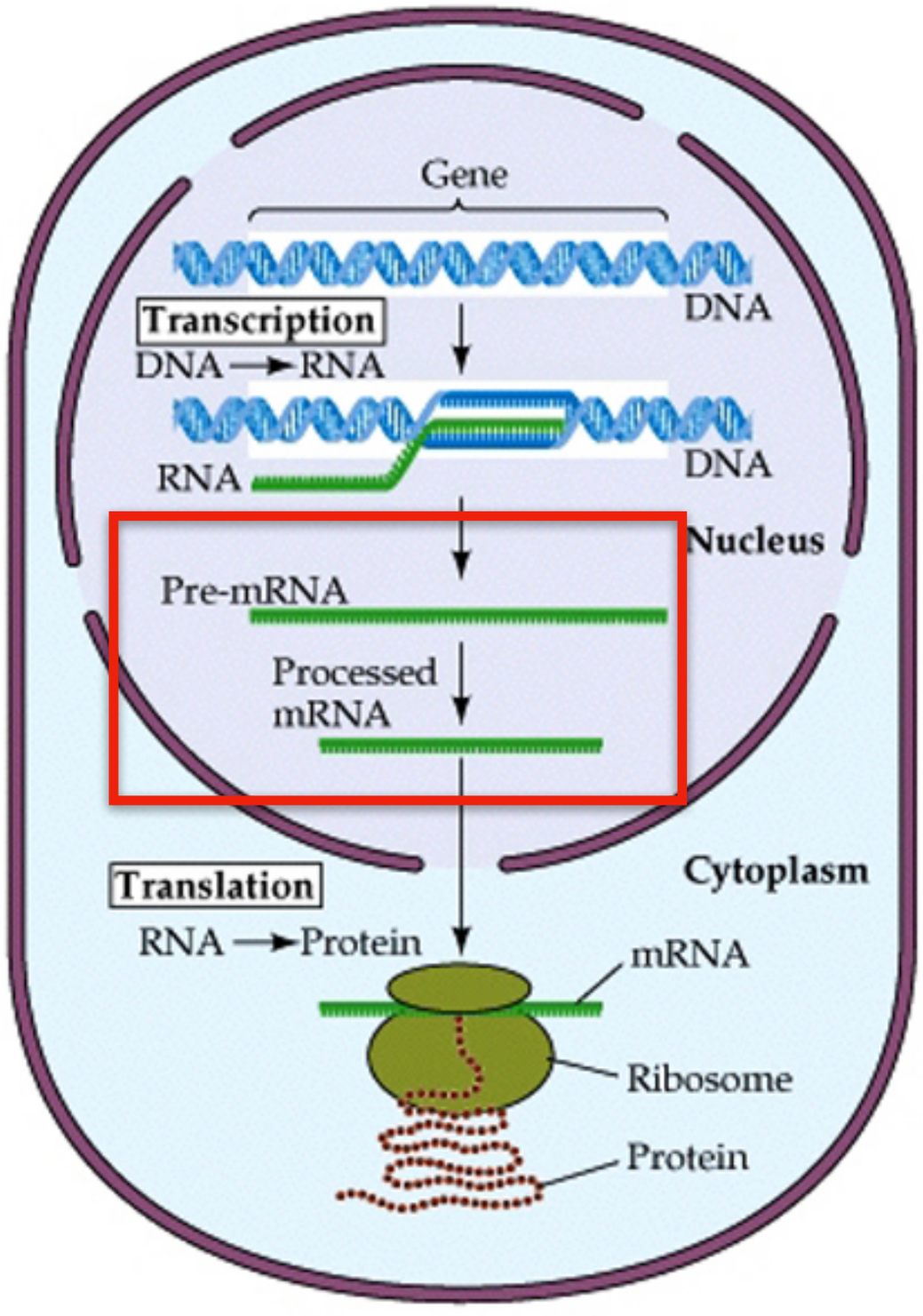
Structural

Regulatory

Protein




Gene
DNA
Transcription
DNA → RNA
RNA
DNA
Nucleus
Pre-mRNA
Processed
mRNA
Cytoplasm
Translation
RNA → Protein
mRNA
Ribosome
Protein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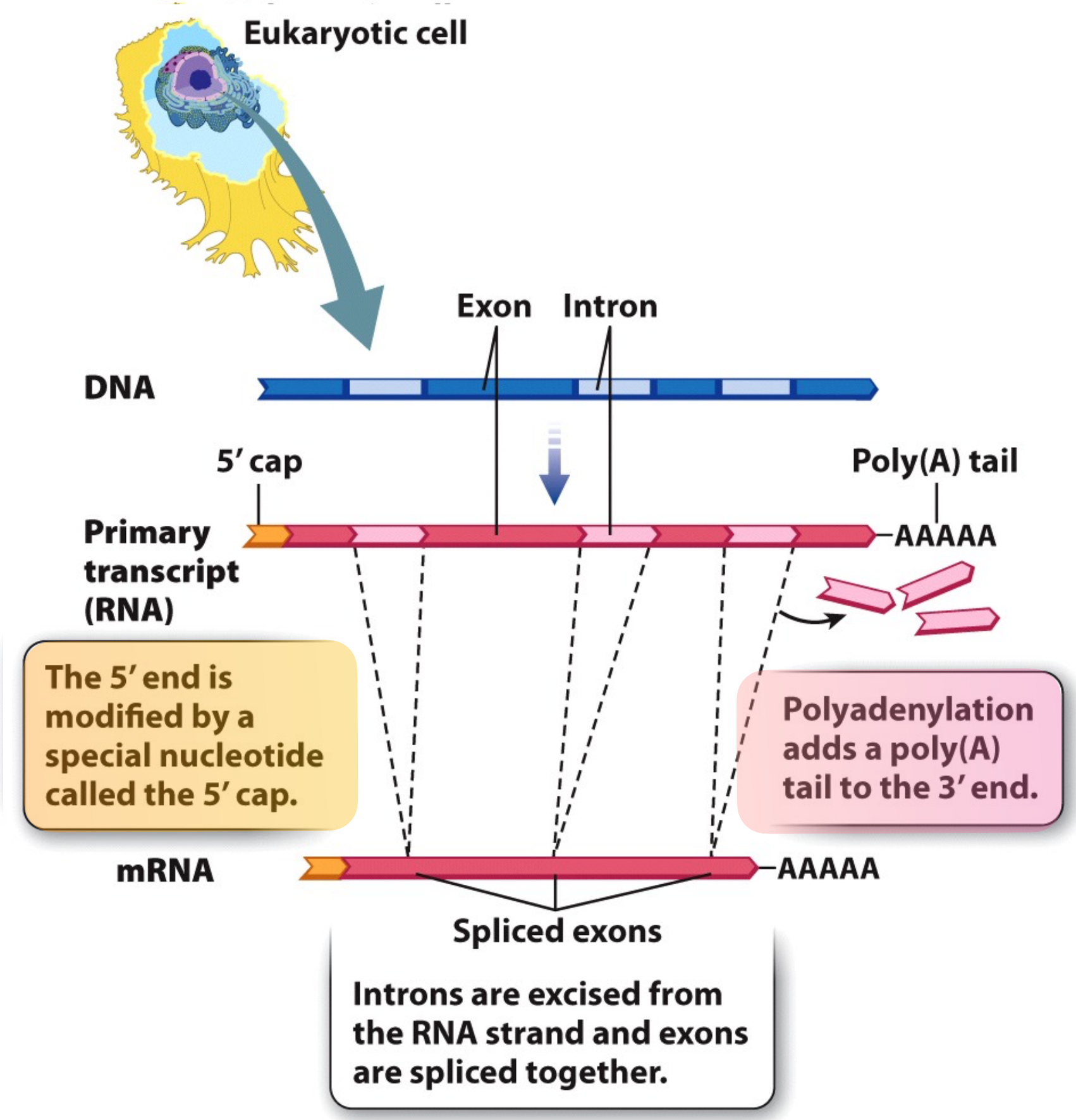
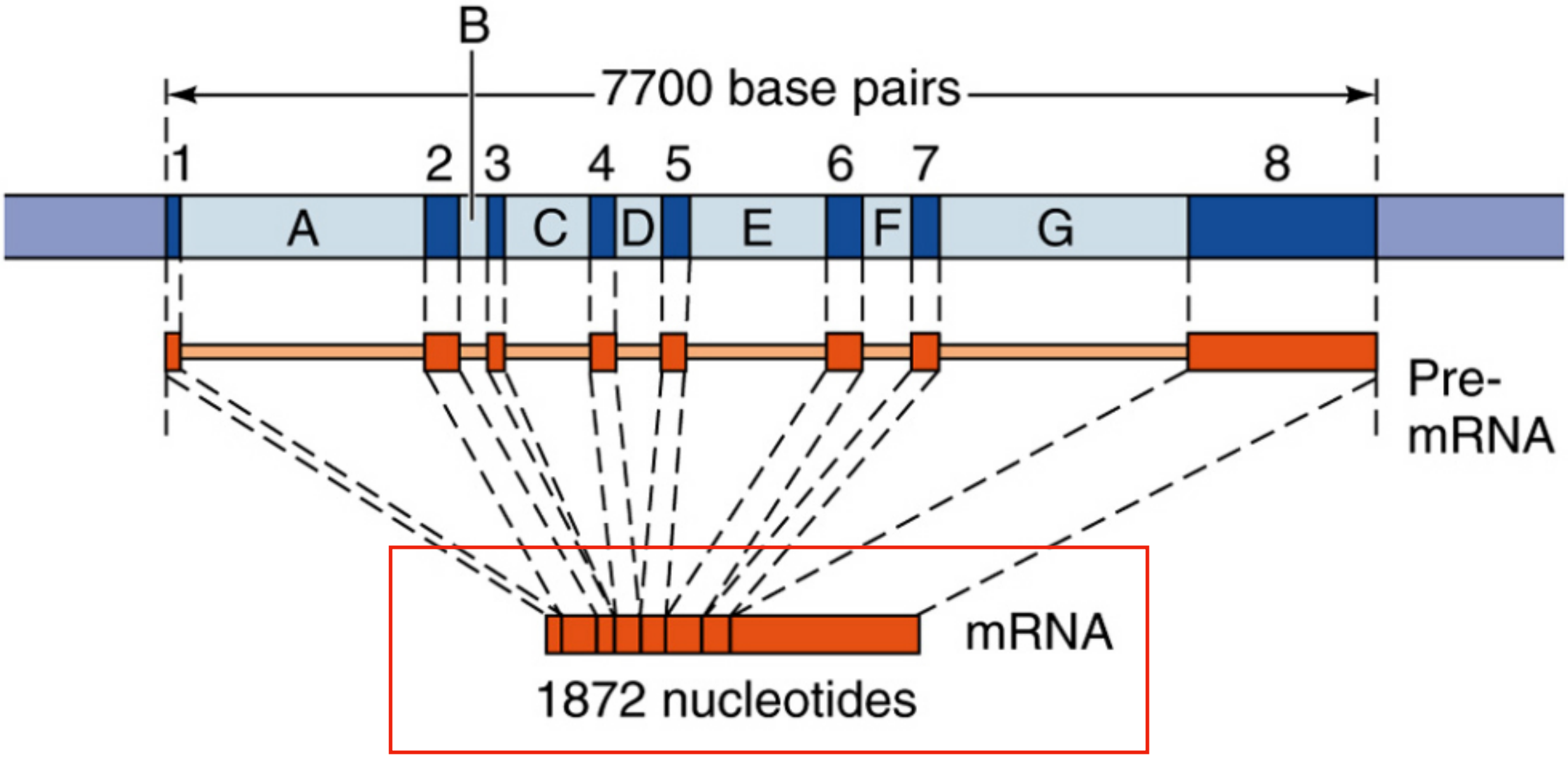


Figure 3.22
Biology: How Life Works


B
7700 base pairs
1
2
3
4
5
6
7
8
A
C
D
E
F
G
Pre-
mRNA
mRNA
1872 nucleotides

1 error in 1x 10^9 (1 in 1,000,000,000) bases replicated

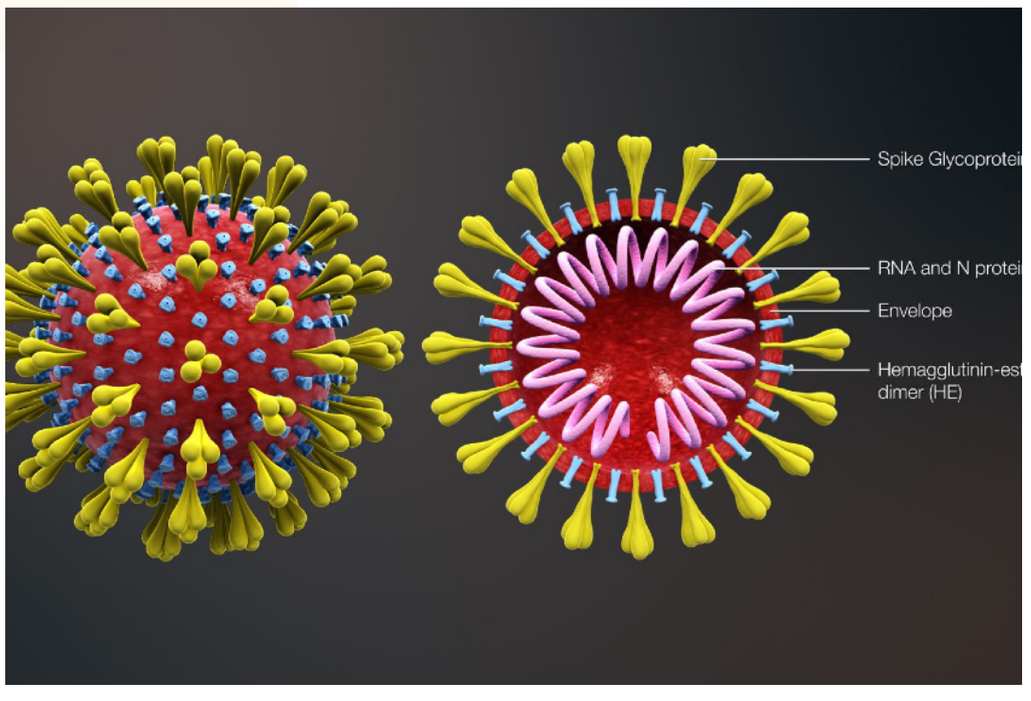
1 error in 1x 10^4 (1 in 10,000) bases replicated

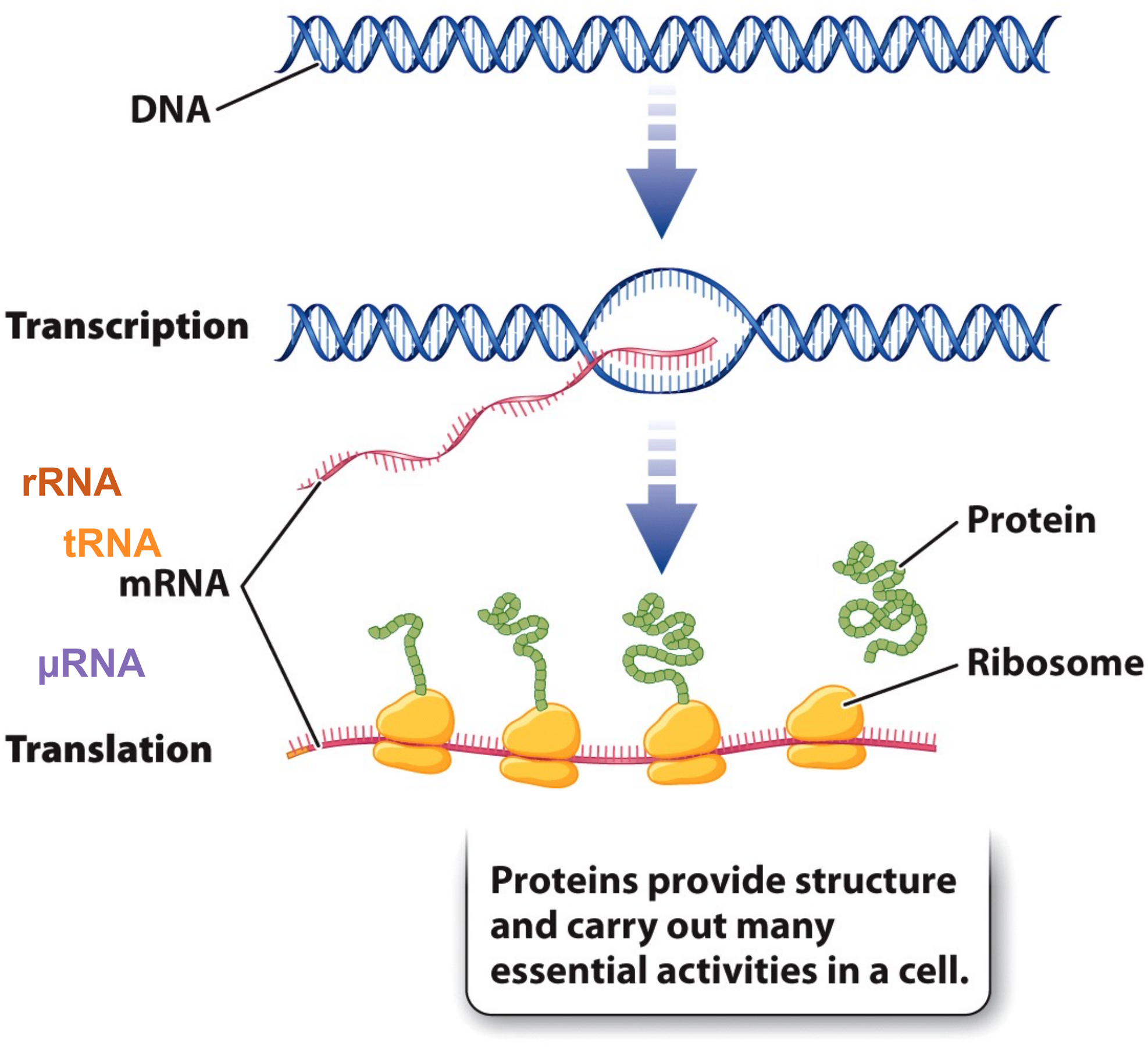
e.g HIV

e.g SarsCoV-2

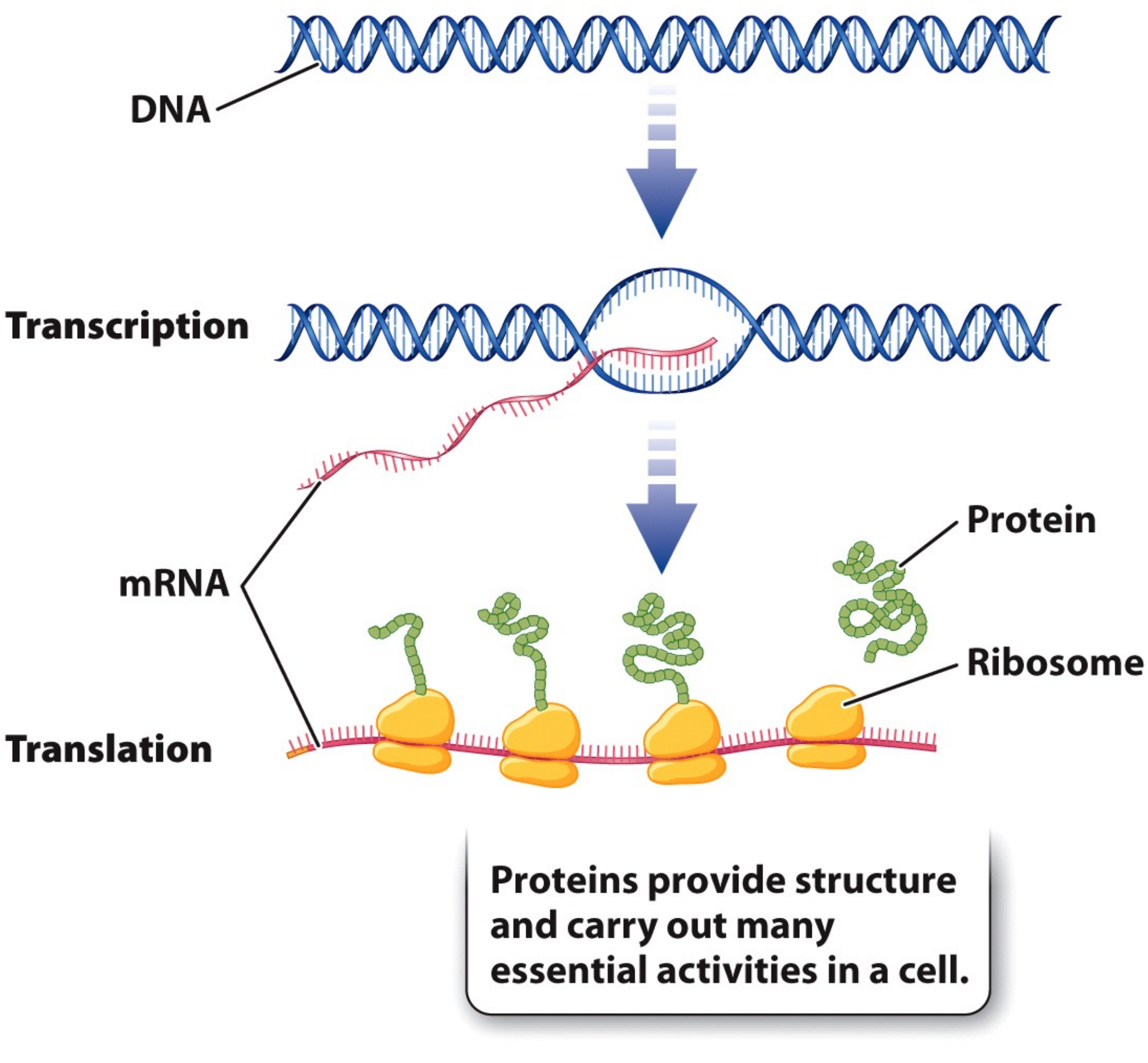
Fig. 1

Genomic organization of representative α, β, and γ CoVs. An illustration of the MHV genome is depicted at the *top*. The expanded regions below show the structural and accessory proteins in the 3′ regions of the HCoV-229E, MHV, SARS-CoV, MERS-CoV and IBV. Size of the genome and individual genes are approximated using the legend at the *top* of the diagram but are not drawn to scale. *HCoV-229E* human coronavirus 229E, *MHV* mouse hepatitis virus, *SARS-CoV* severe acute respiratory syndrome coronavirus, *MERS-CoV* Middle East respiratory syndrome coronavirus, *IBV* infectious bronchitis virus





Proteins provide structure and carry out many essential activities in a cell.



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“Universal” Genetic Code

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Four possibilities for the first base, multiplied by four for the second, multiplied by four for the third yields… **64 possibilities**

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Four possibilities for the first base, multiplied by four for the second, multiplied by four for the third yields… **64 possibilities**

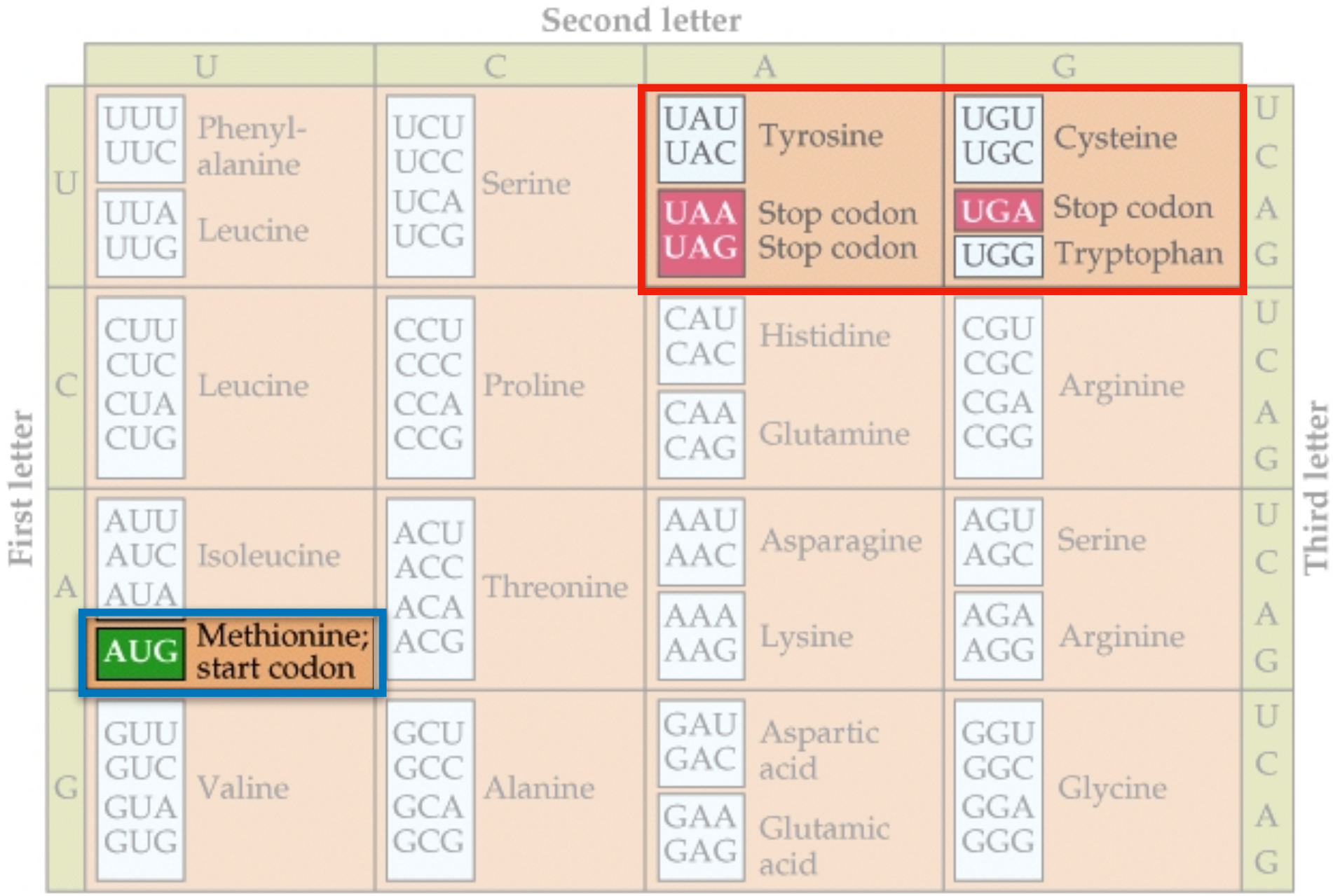
The “Universal” Genetic Code is a 3 base/letter code…

T / HER / EDC / ATG / OTT / HER / ATO / FFT / HEM / AT

TH / ERE / DCA / TGO / TTH / ERA / TOF / FTH / EMA / T

THE/ RED / CAT / GOT / THE / RAT / OFF / THE / MAT

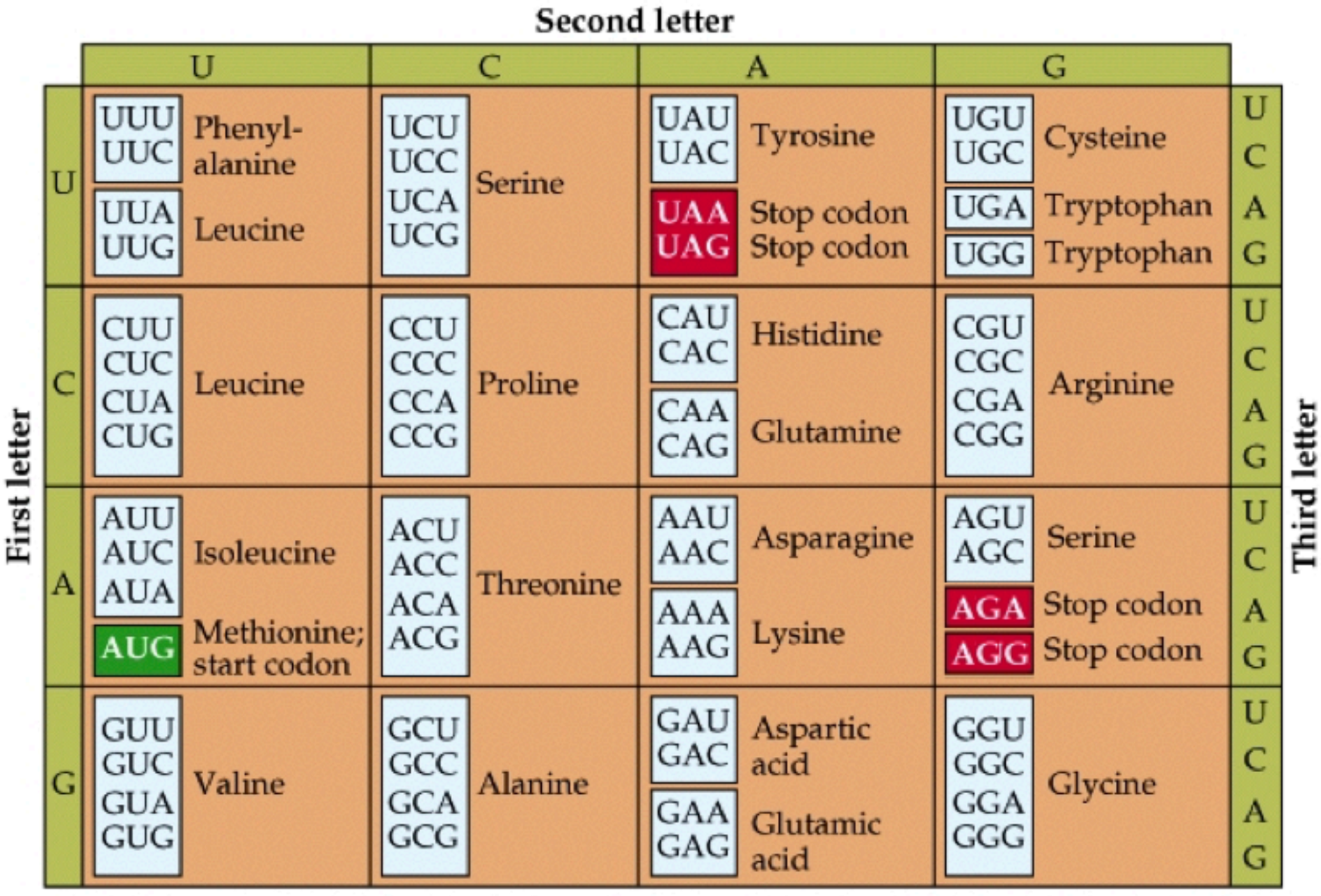
“Universal” Genetic Code



AUG, which codes for the amino acid **methionine**, is called the ***start*** **codon**, which initiates the translational process.

Three of the possible codons are **STOP CODONS** (**UAA**, **UAG**, and **UGA**), which direct the ribosomes to STOP reading the mRNA; that is, they end translation.

"Universal" Genetic Code



Four possibilities for the first base, x four for the second, x four for the third yields **64 possibilities options**

Only 20 amino acids, so the code is "redundant"

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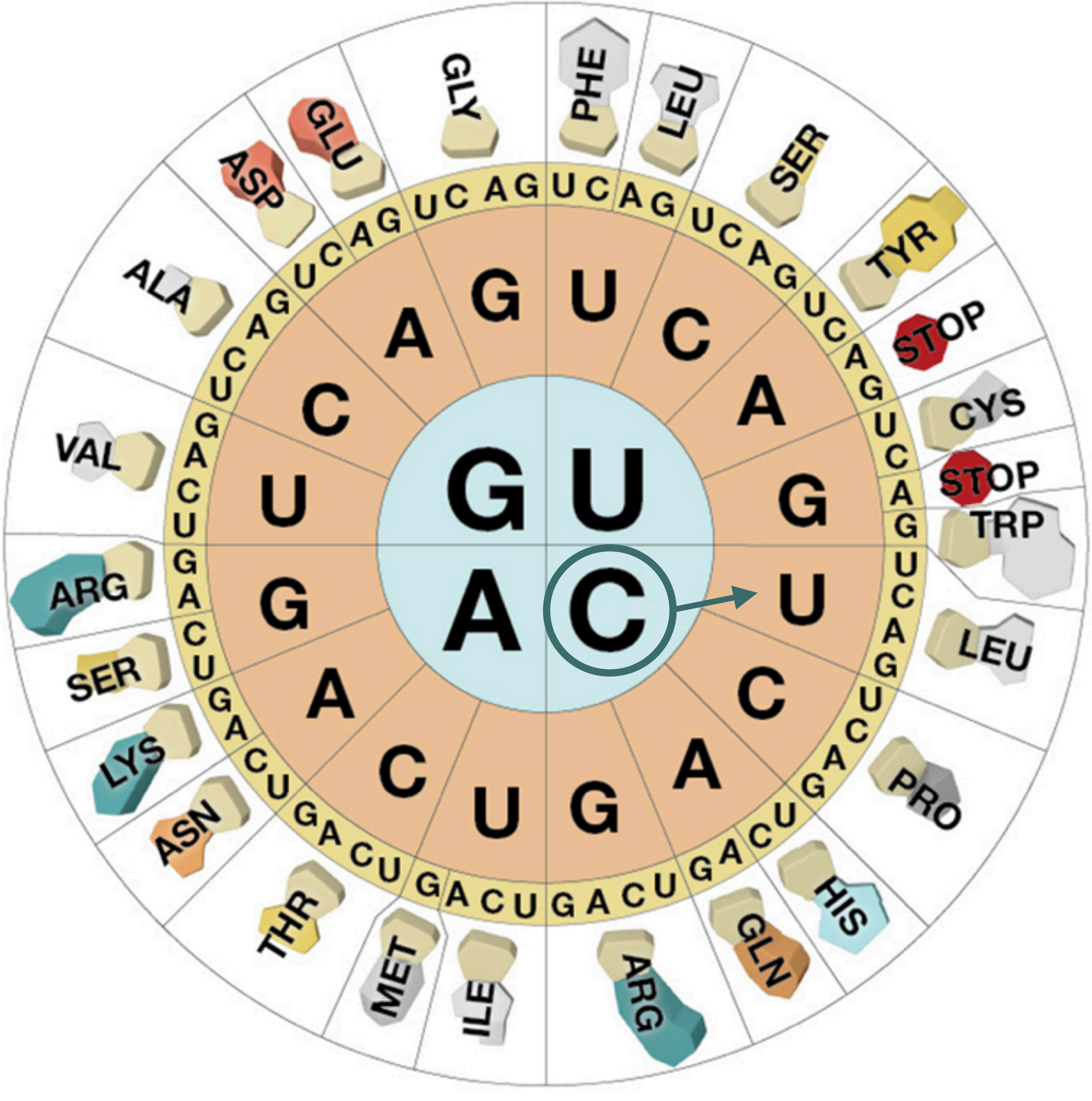
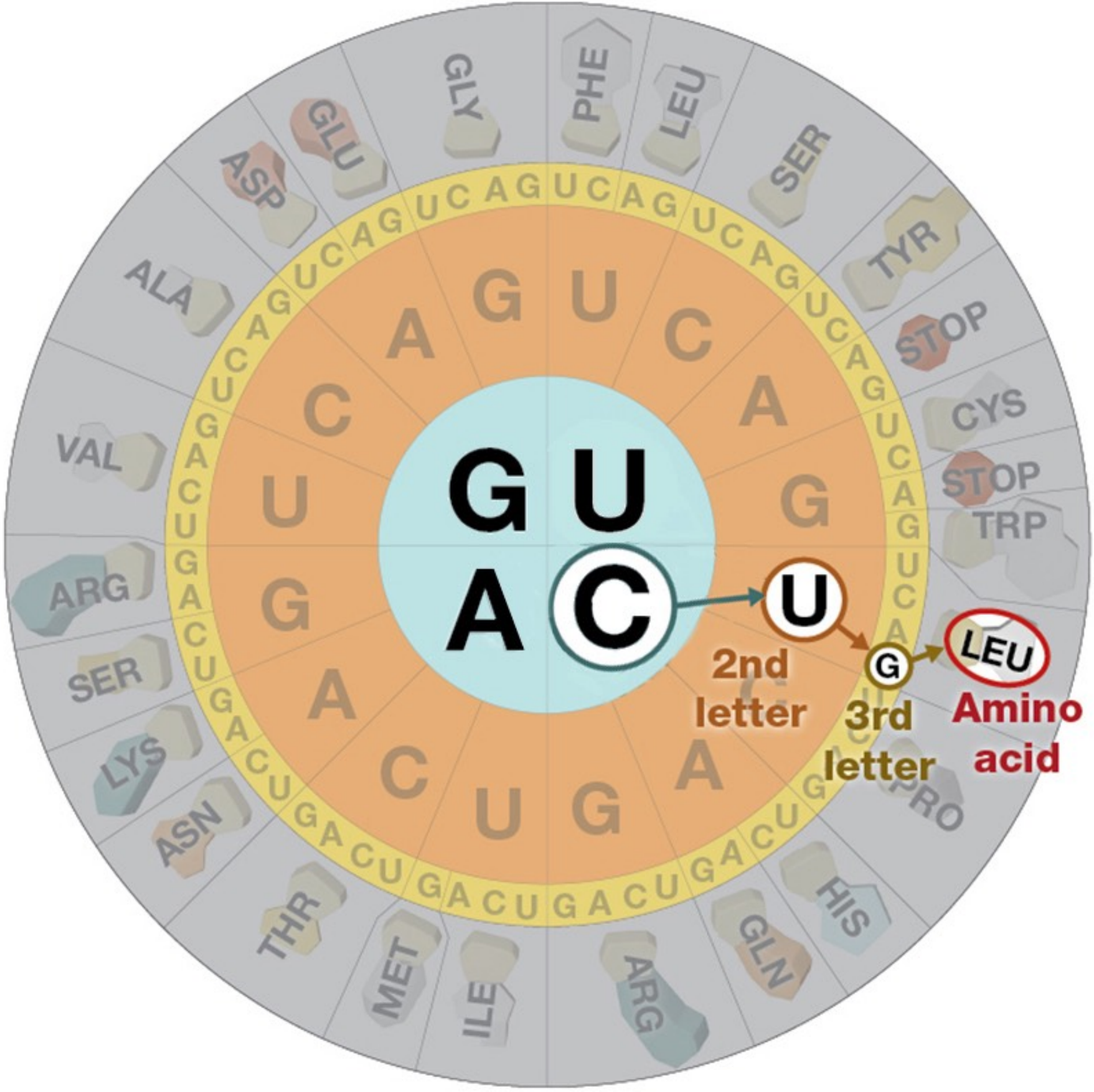
The genetic code is **redundant** but not **ambiguous.** This means that many amino acids have more than **one codon**, but only one amino acid is specified for any one codon.


G
U
A
C
GLY
PHE
LEU
SER
TYR
STOP
CYS
STOP
TRP
LEU
PRO
HIS
GLN
ARG
ILE
MET
THR
ASN
LYS
SER
ARG
VAL
ALA
ASP
GLU


GLY
PHE
LEU
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TYR
STOP
CYS
STOP
TRP
PRO
HIS
GLN
ARG
ILE
MET
THR
ASN
LYS
SER
ARG
VAL
ALA
ASP
GLU
G U
A C
U
2nd letter
G
3rd letter
LEU
Amino acid

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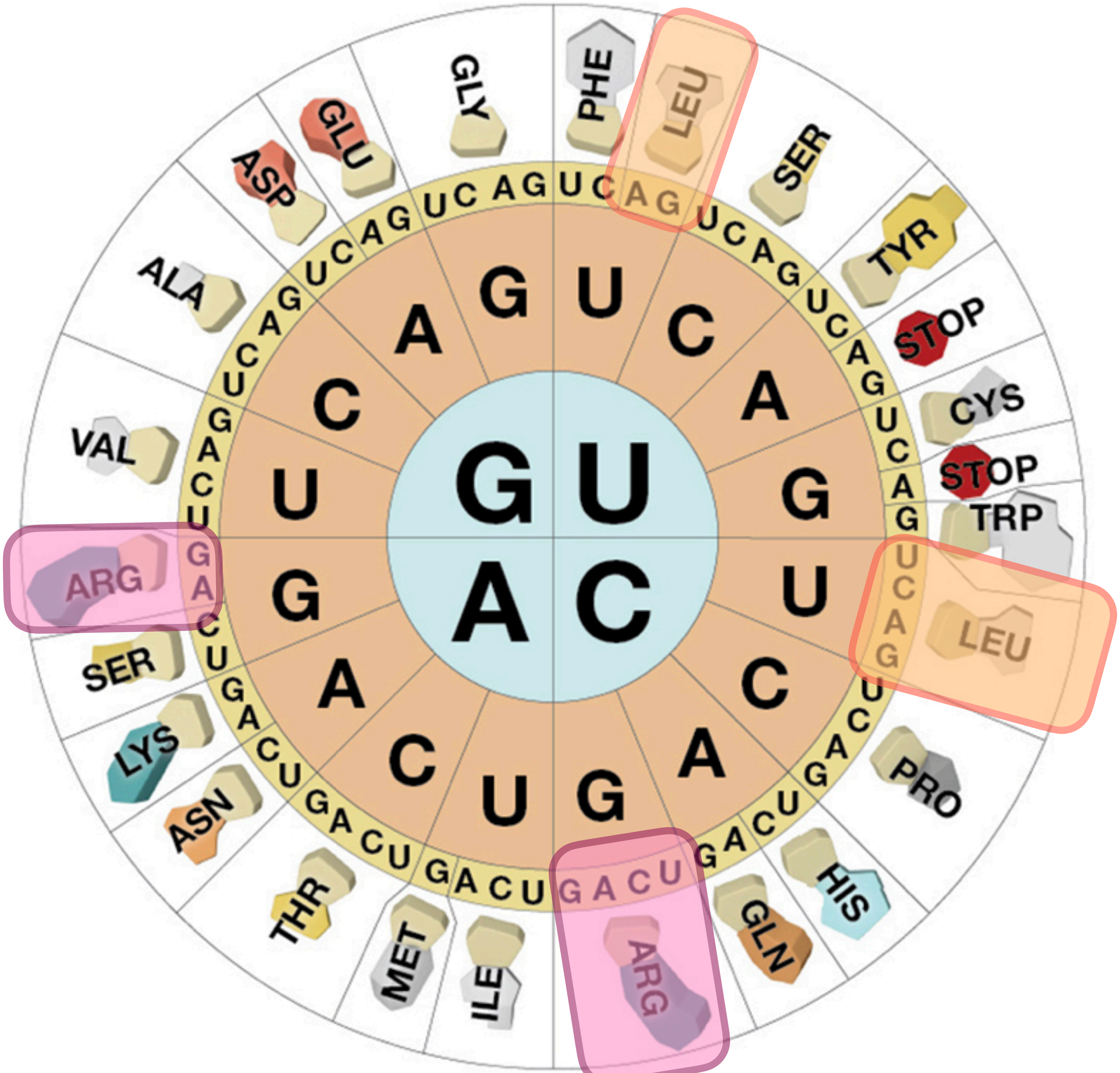
G U
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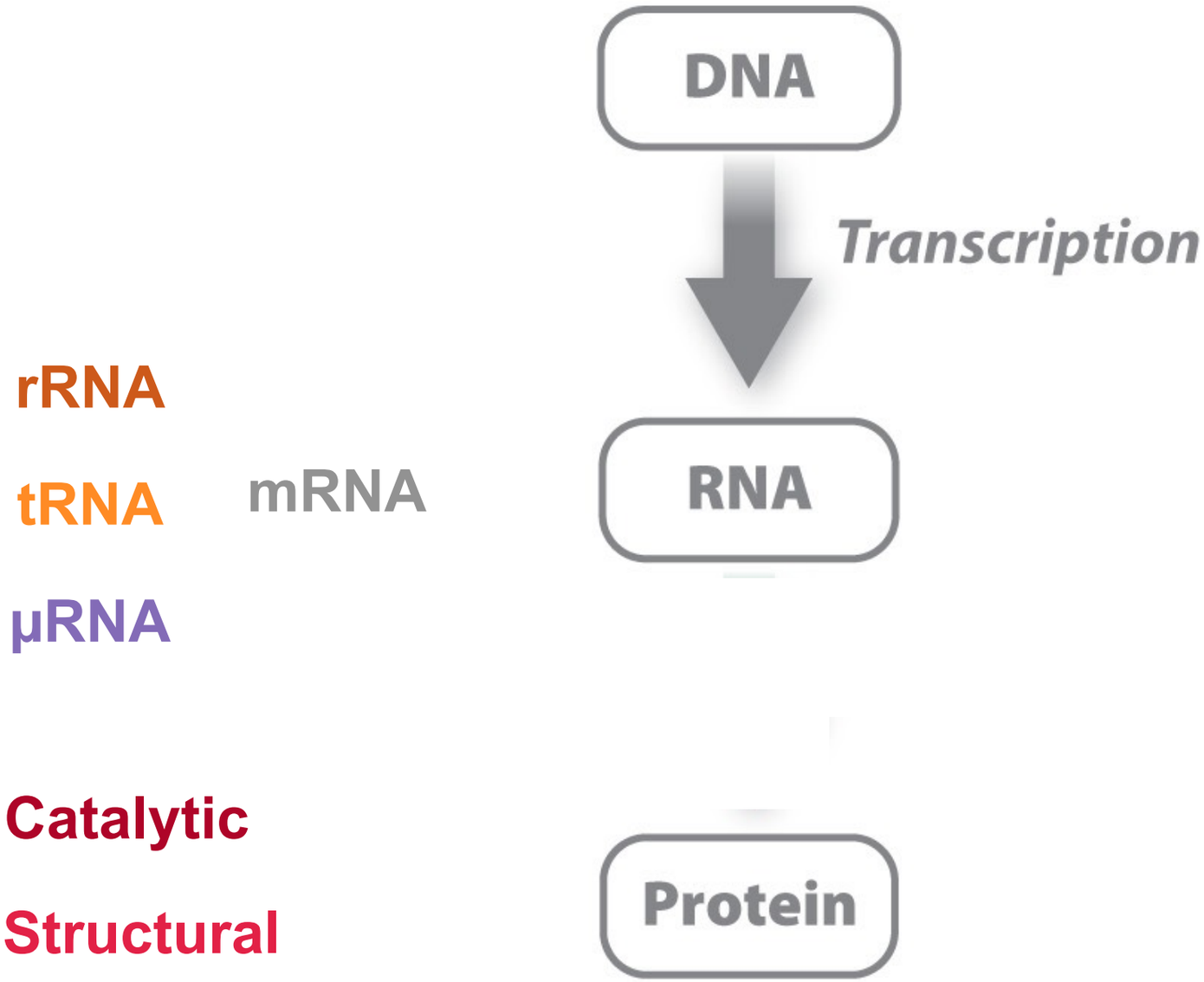
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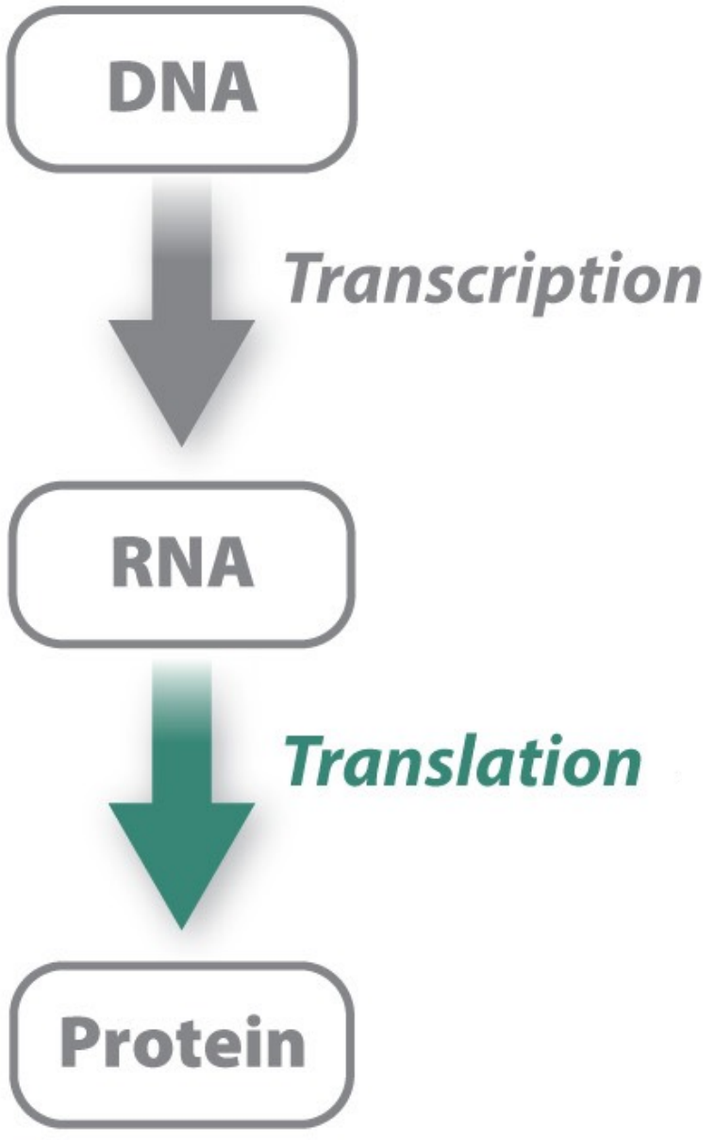

DNA
Transcription
RNA
Translation
Protein

DNA

Transcription

RNA

Translation

Protein

Messenger RNA (mRNA)

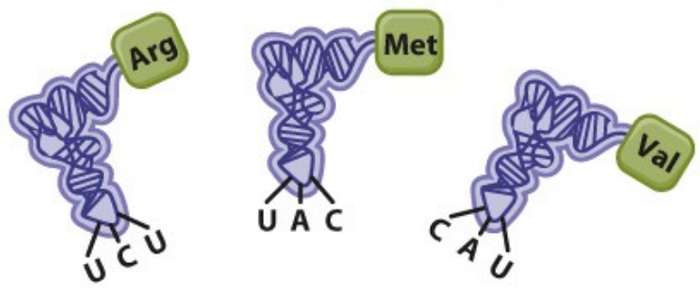
Initiation factors

Elongation factors

Release factors

Aminoacyl tRNA synthetases

Transfer RNA (tRNA)



Ribosome (ribosomal RNA + ribosomal proteins)

DNA

Transcription

RNA

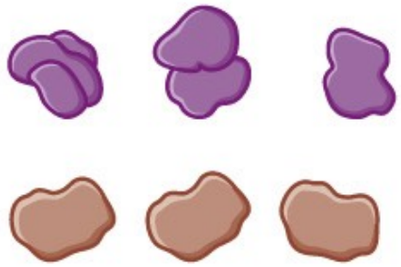
Translation

Protein

Messenger RNA (mRNA)

Initiation factors

Elongation factors



Release factors

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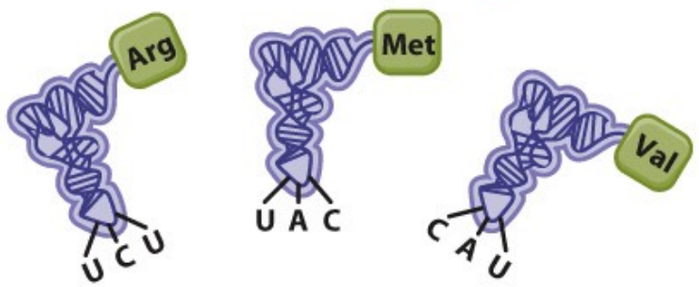

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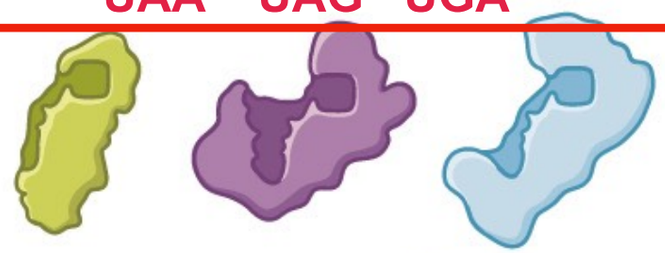
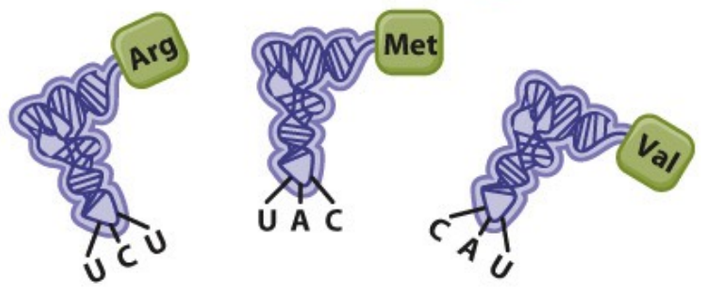


Transfer RNA (tRNA)



Ribosome (ribosomal RNA + ribosomal proteins)

DNA

Transcription

RNA

Translation

Protein

Messenger RNA (mRNA)

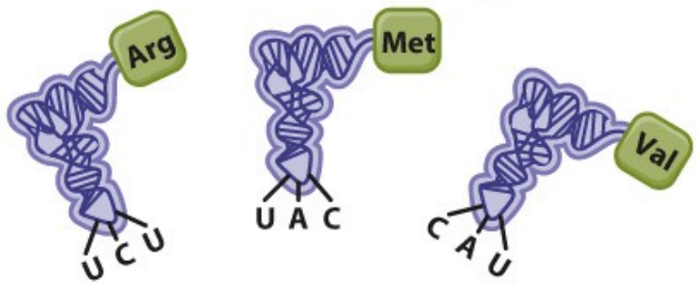
Initiation factors

Elongation factors

Release factors

Aminoacyl tRNA synthetases

Transfer RNA (tRNA)



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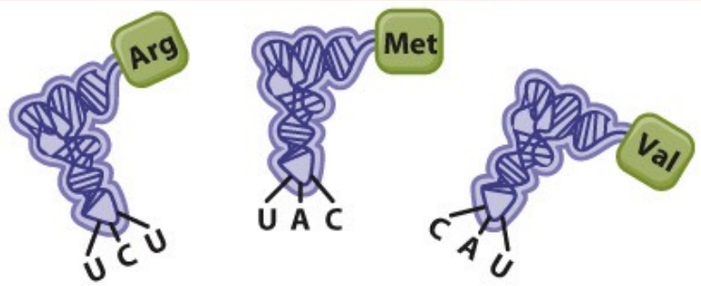

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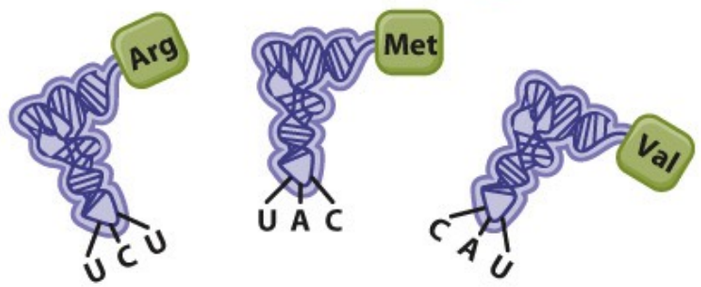

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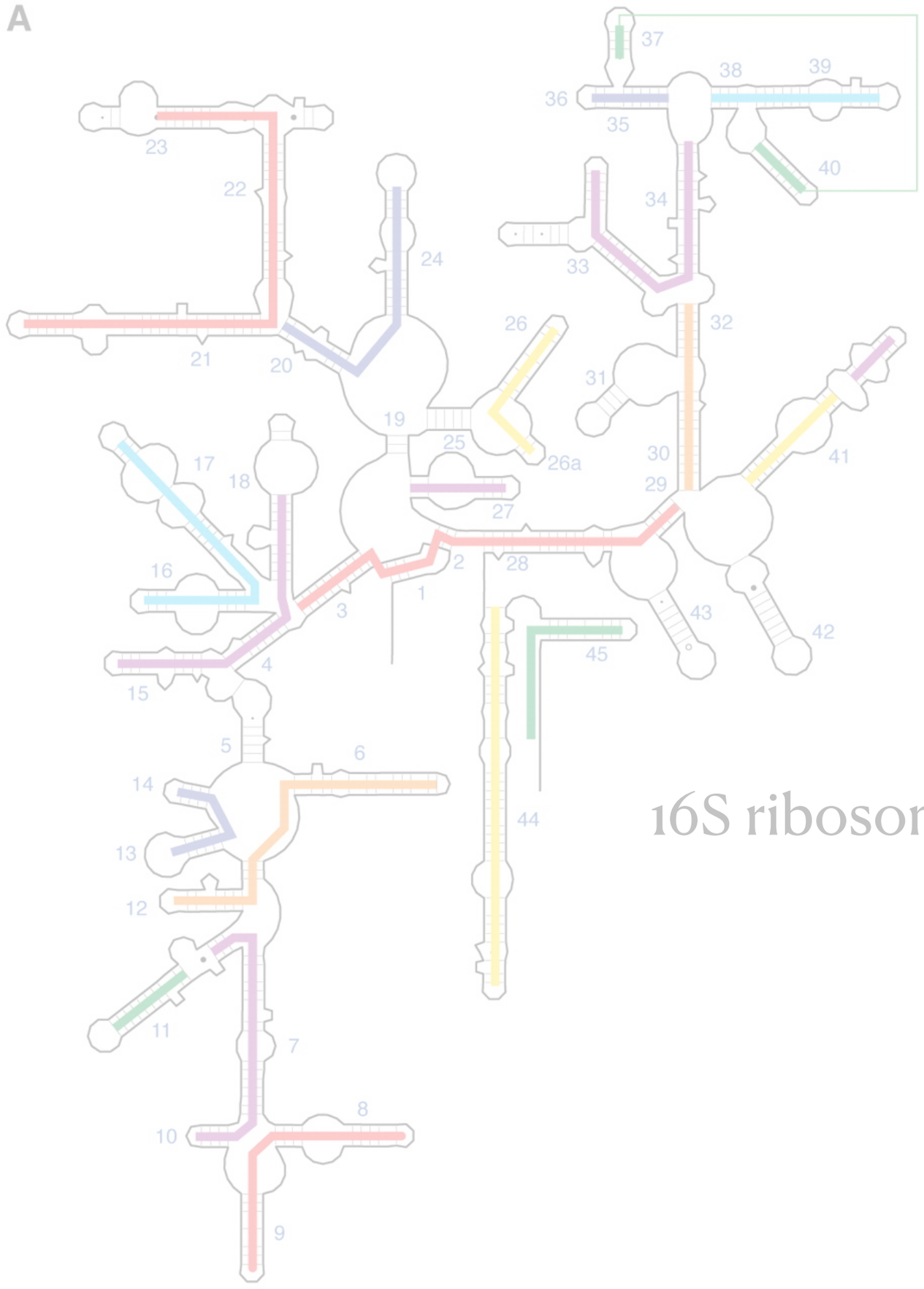
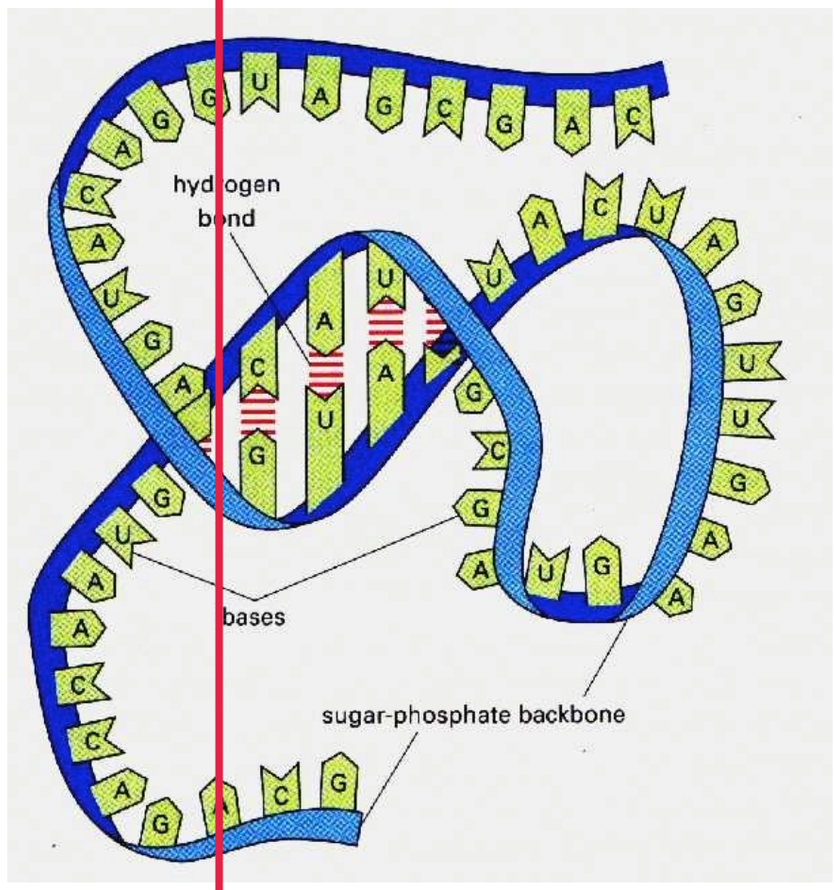
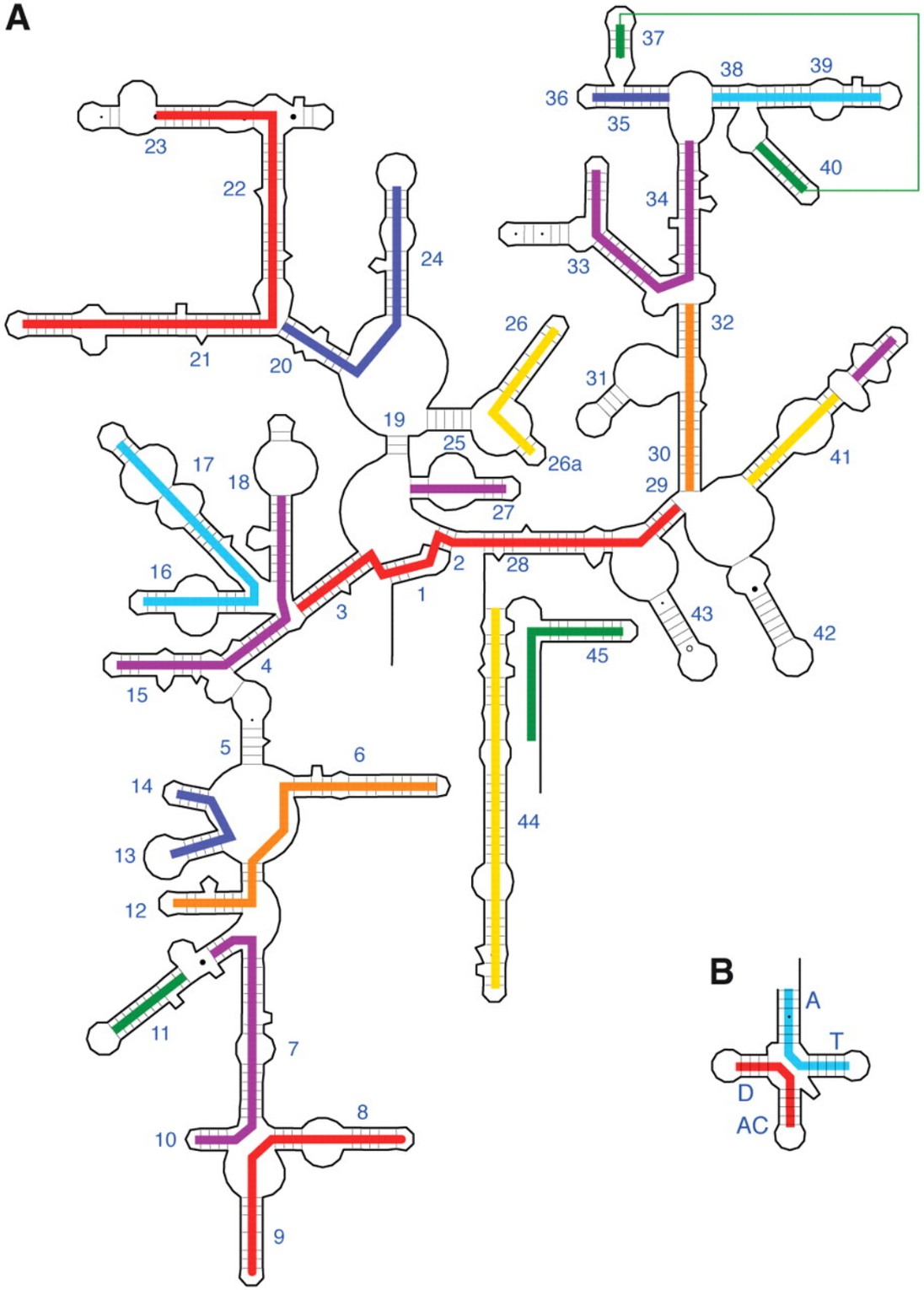




16S ribosomal RNA

A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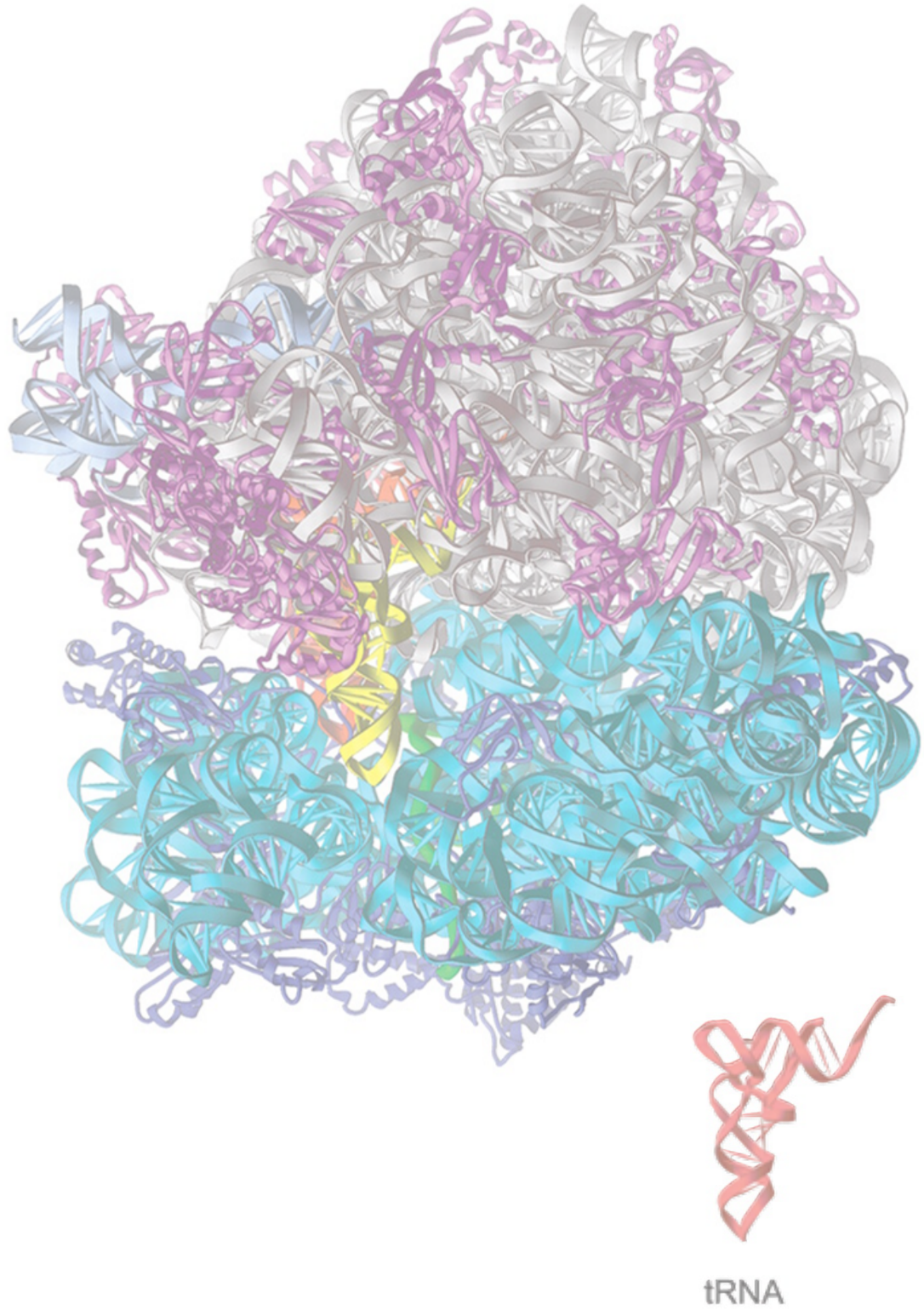
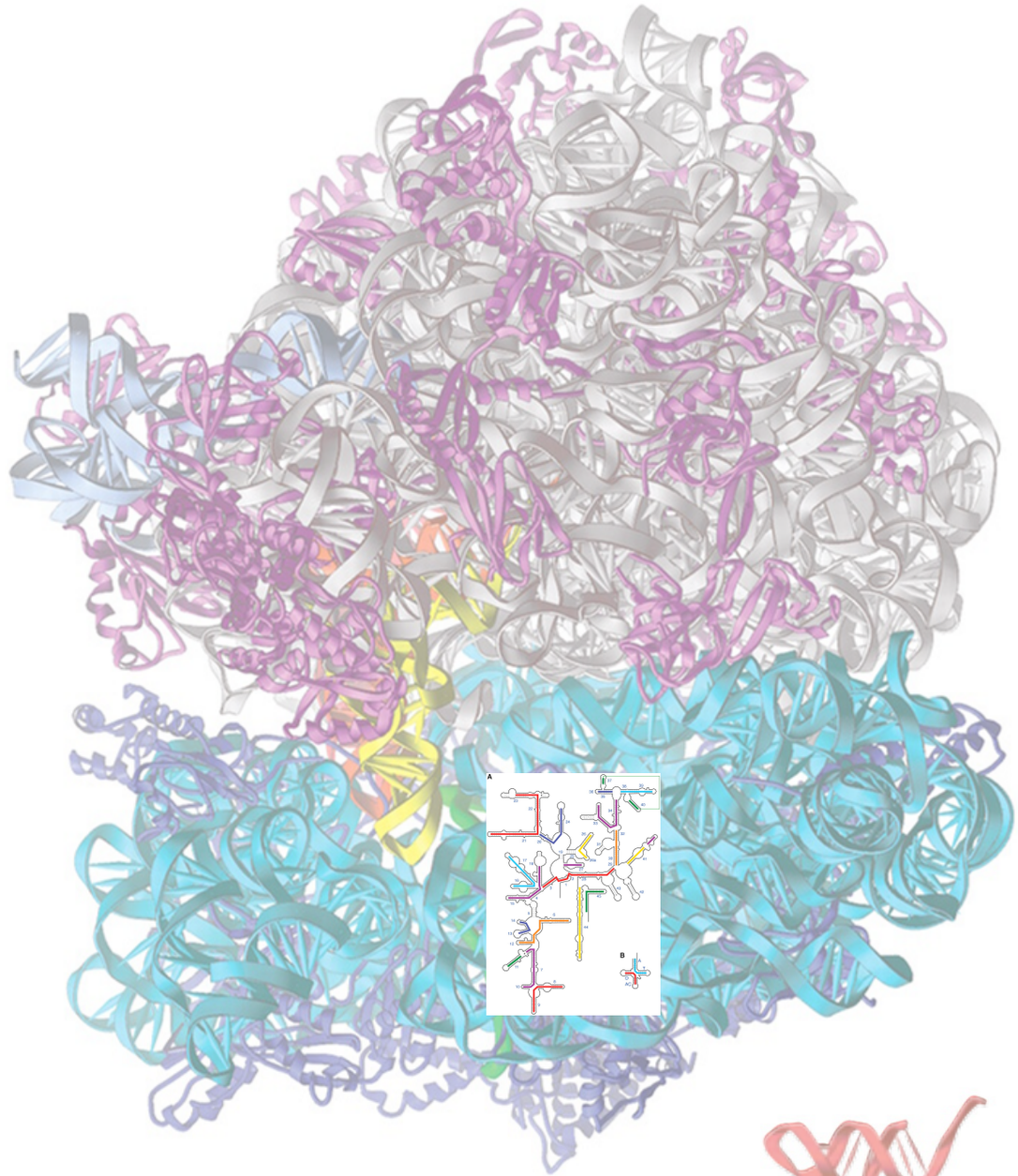
B

A
T
D
AC

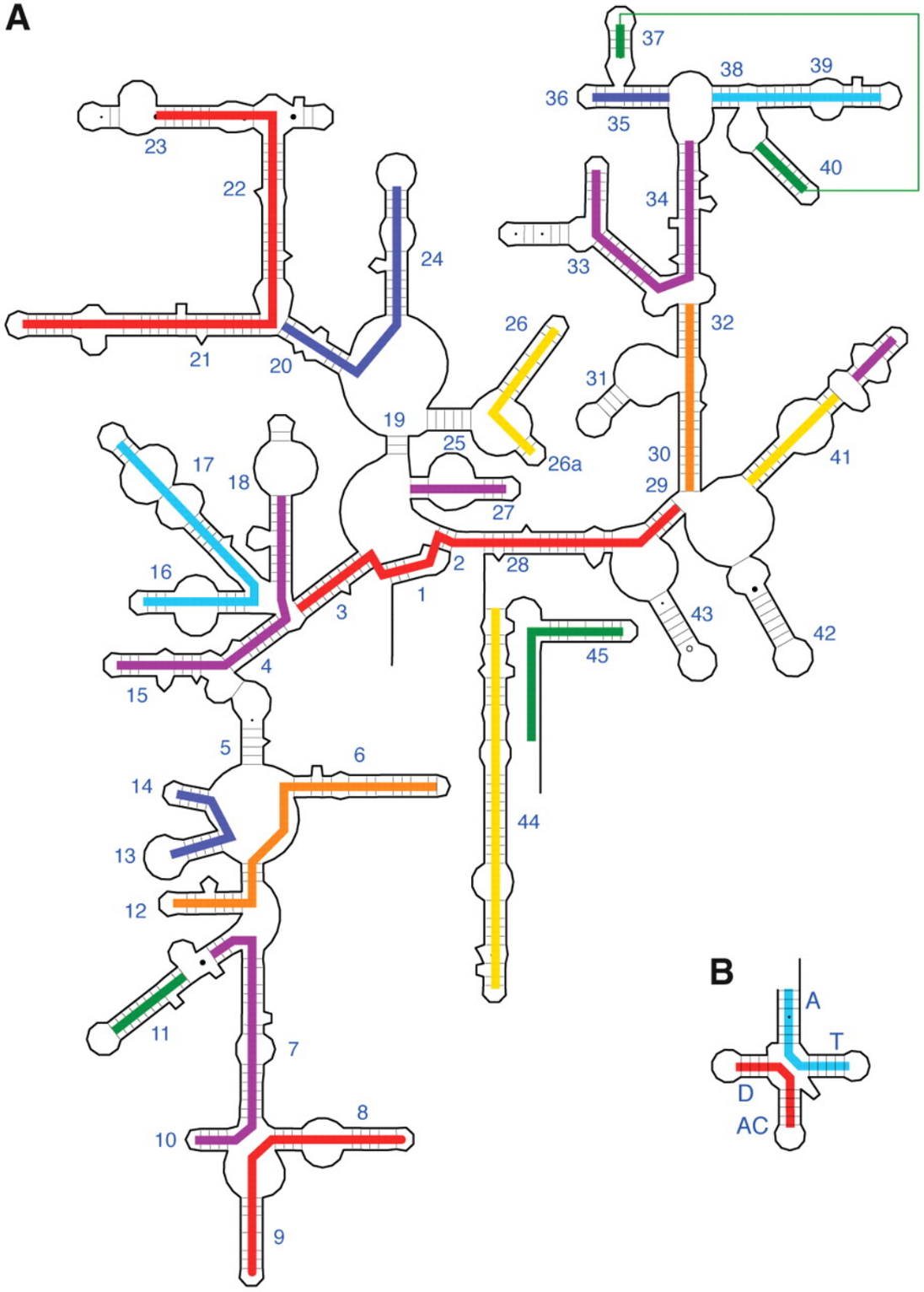


tRNA



tRNA

A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26a
29
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A
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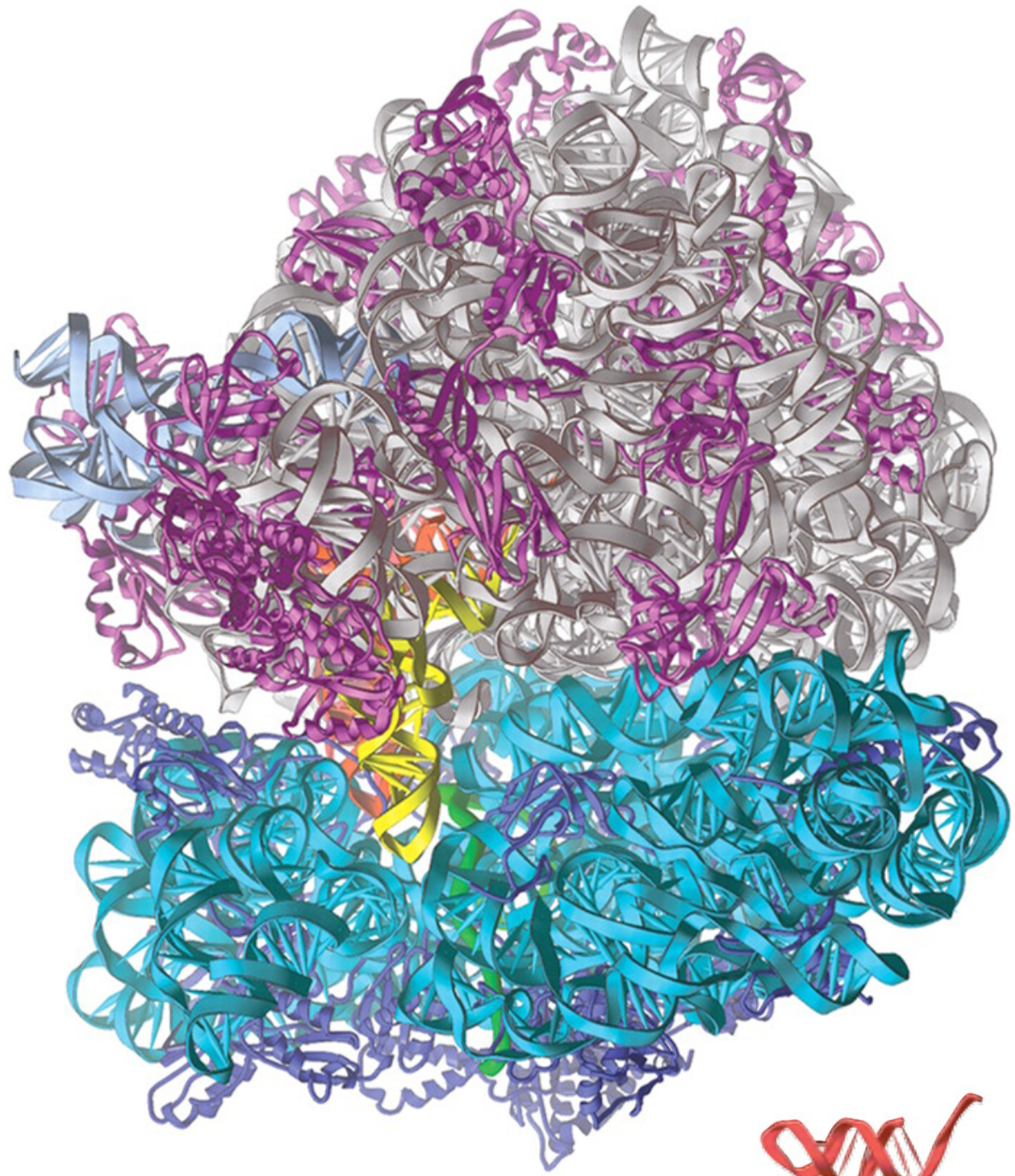
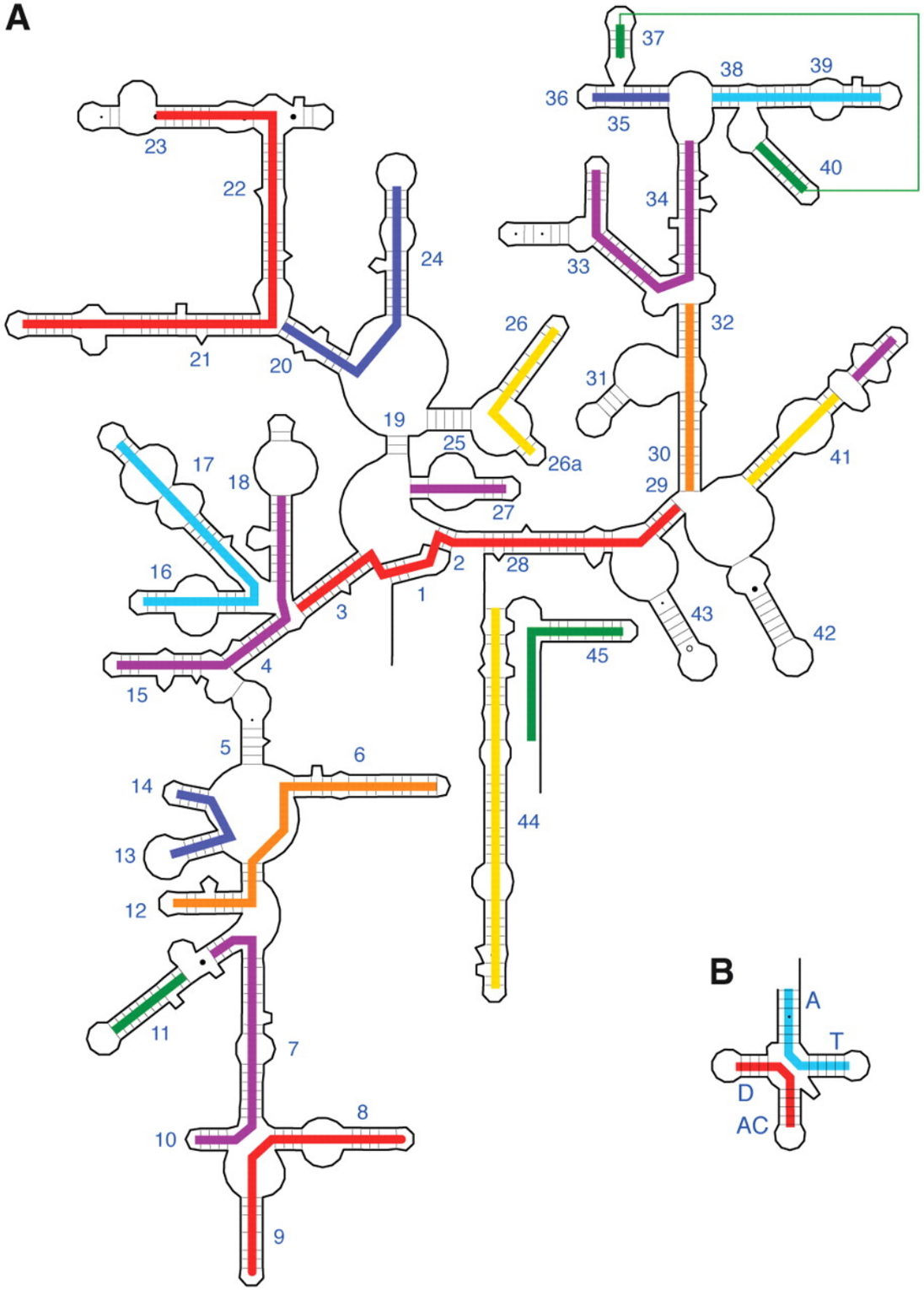
D
AC



tRNA

A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28
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B

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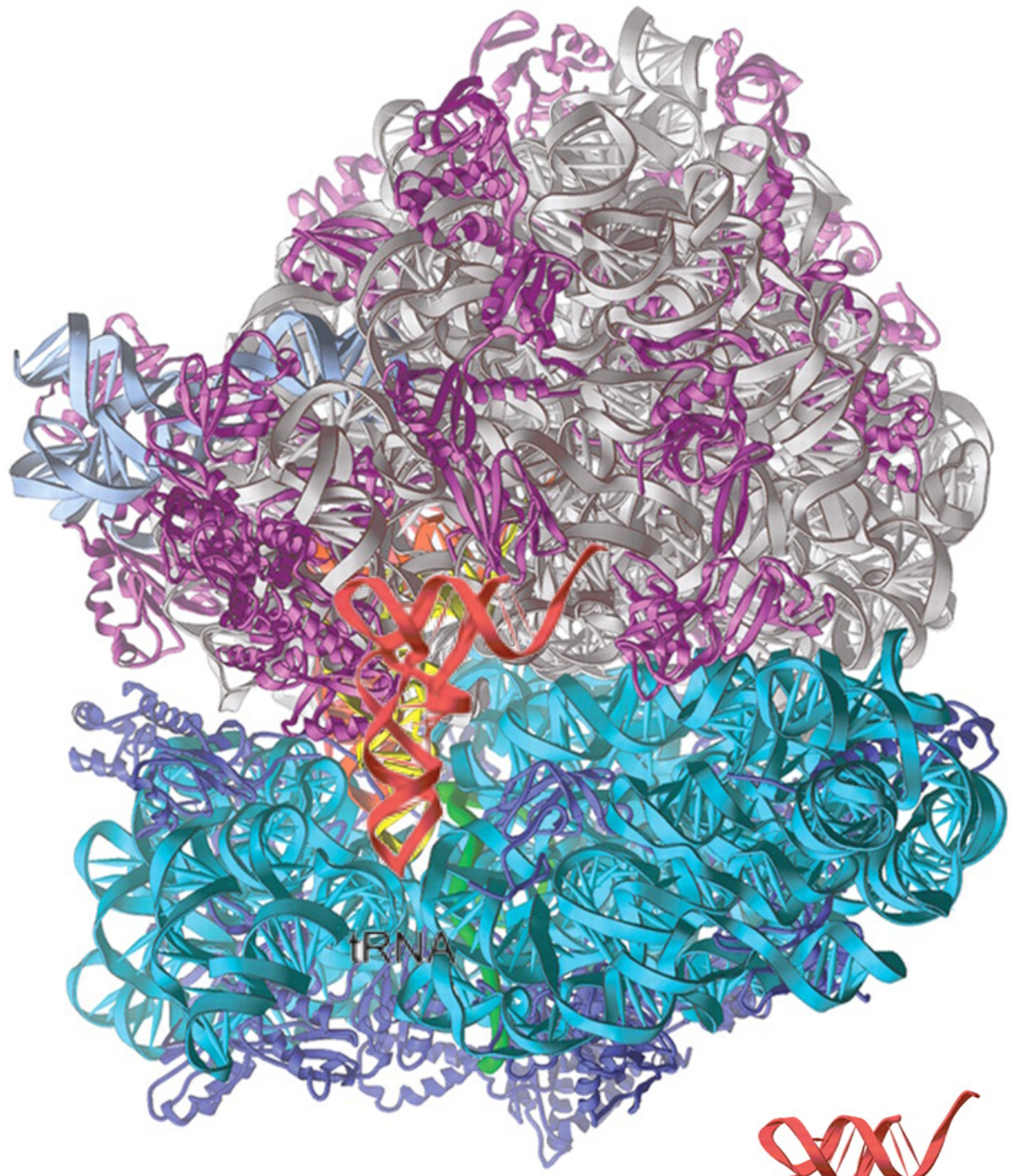
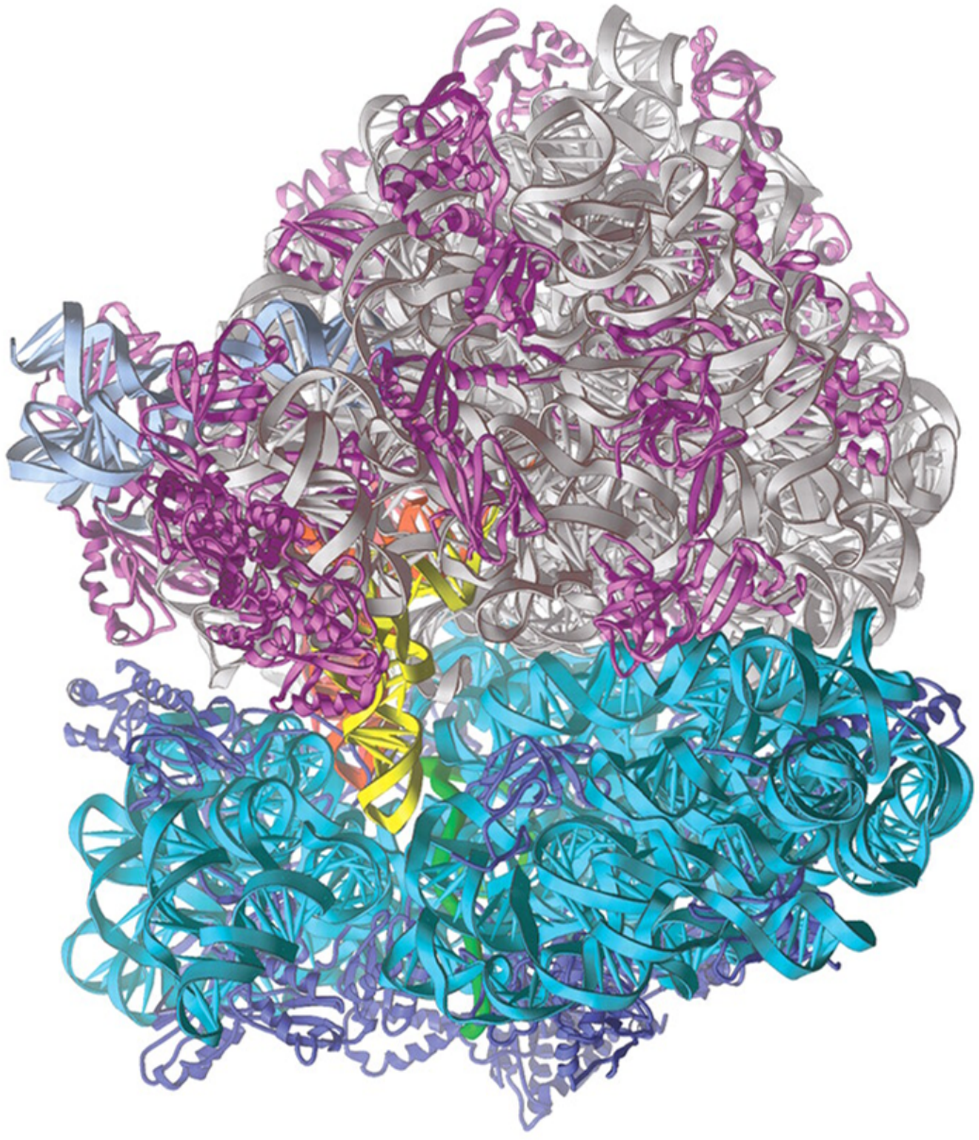
T
D
AC


tRNA

tRNA



Prokaryote rRNA:

23S rRNA,
5S rRNA

&

16S rRNA,

Eukaryote rRNA:

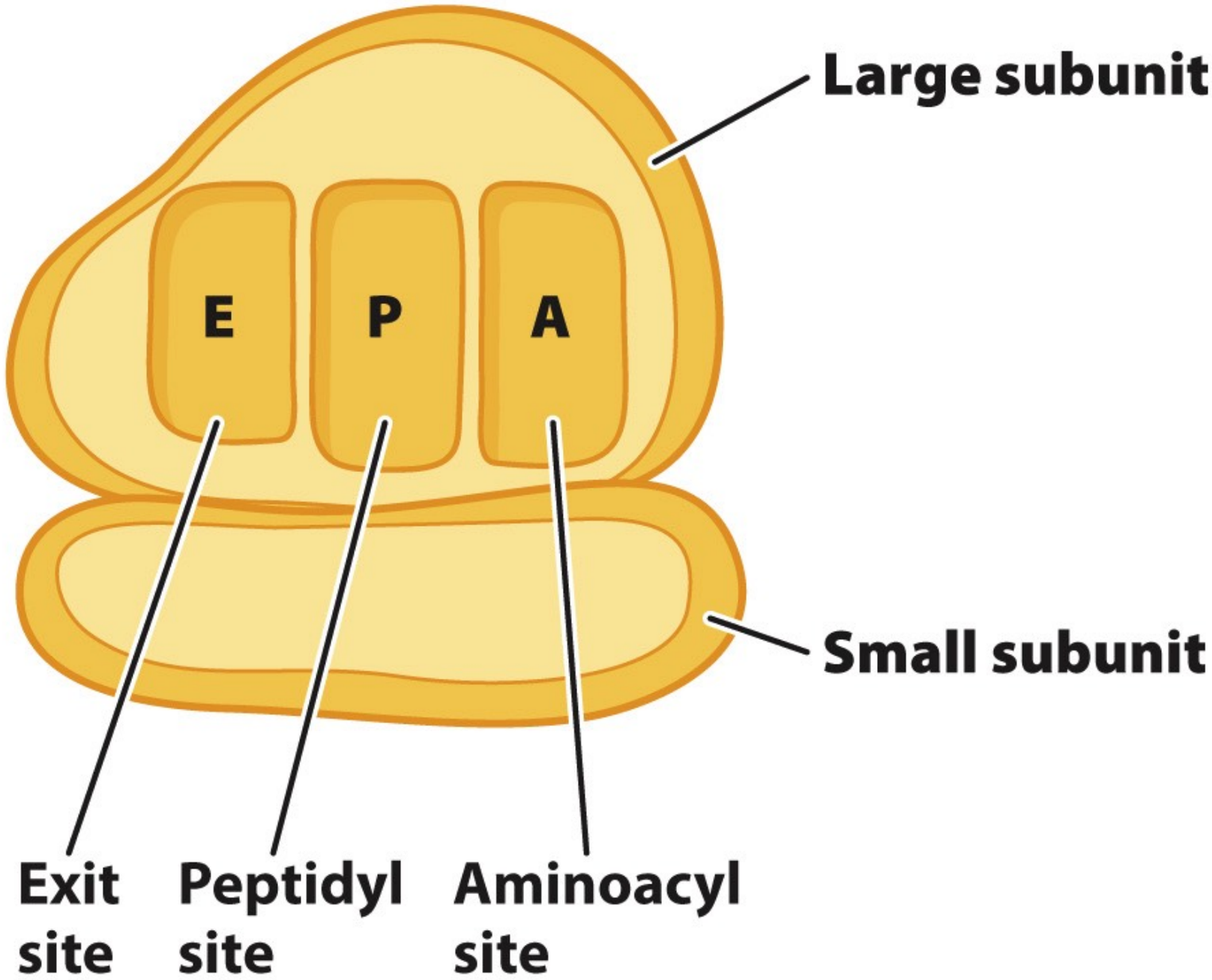
28S rRNA,
5.8S rRNA,
5S rRNA,

&

18S rRNA

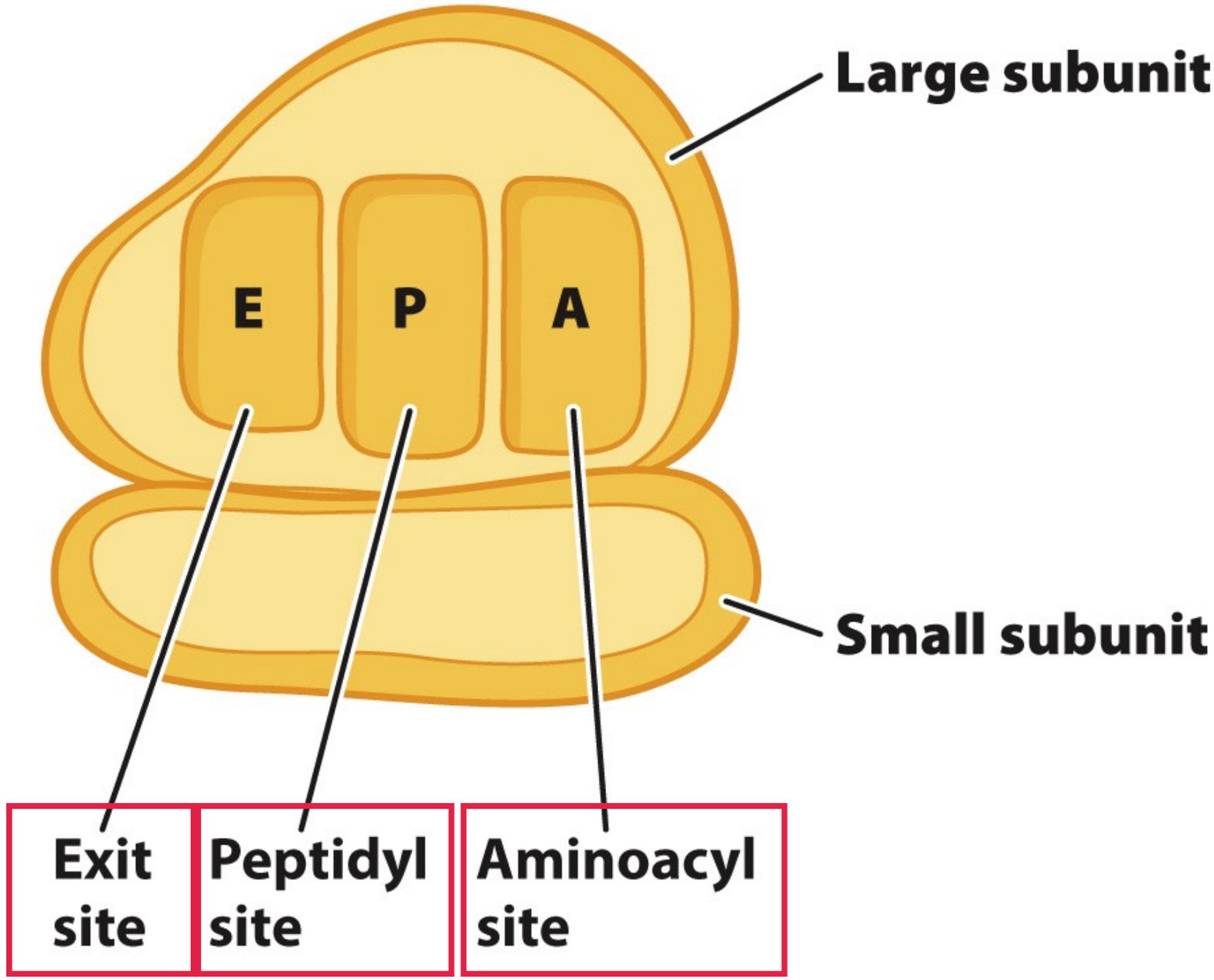
50S

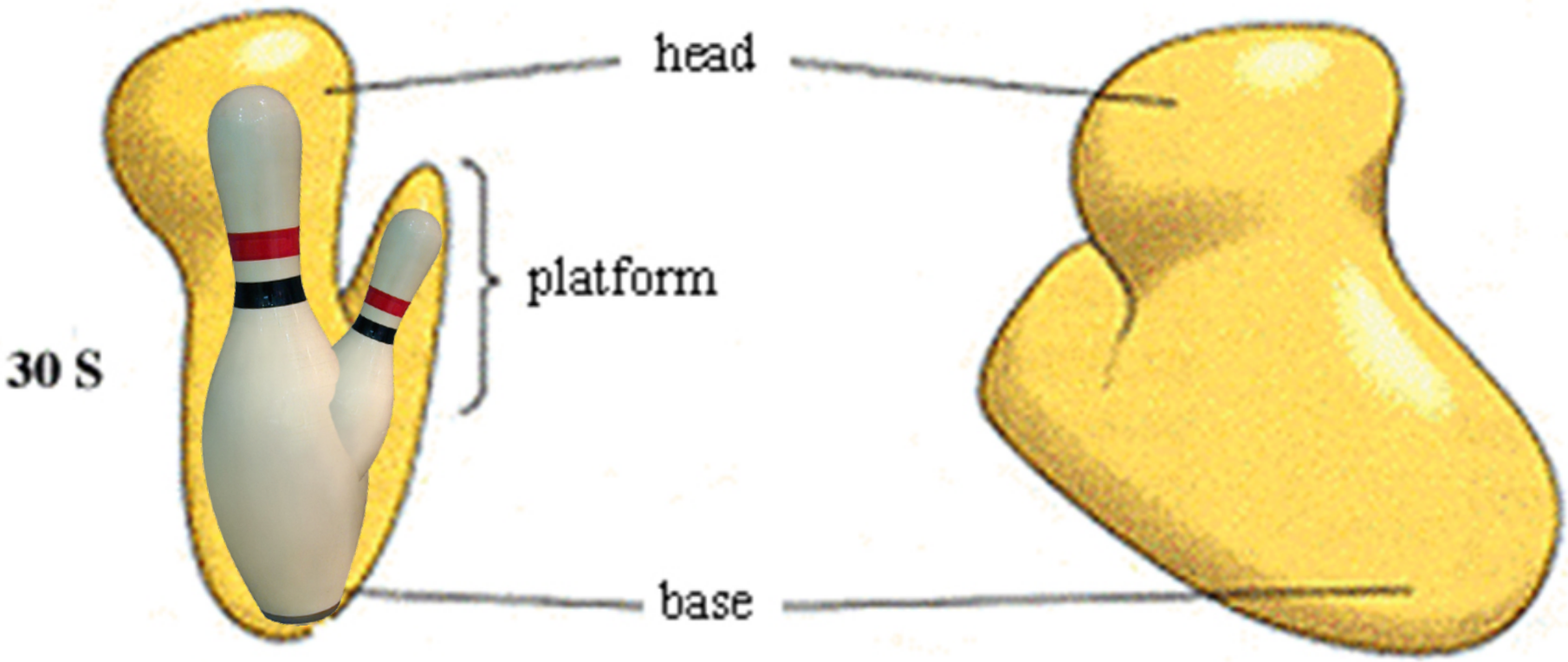
30S


Large subunit
E
P
A
Small subunit
Exit site
Peptidyl site
Aminoacyl site

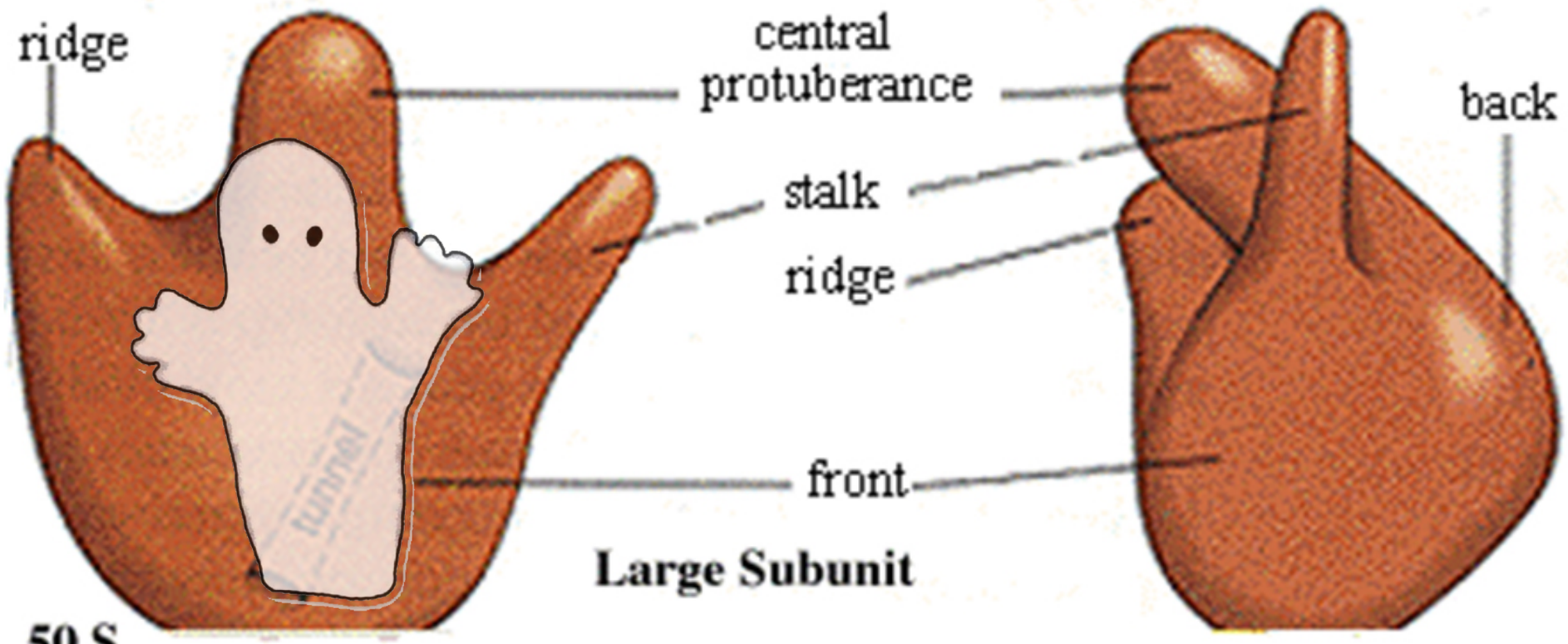
60S

40S


Large subunit
E
P
A
Small subunit
Exit site
Peptidyl site
Aminoacyl site



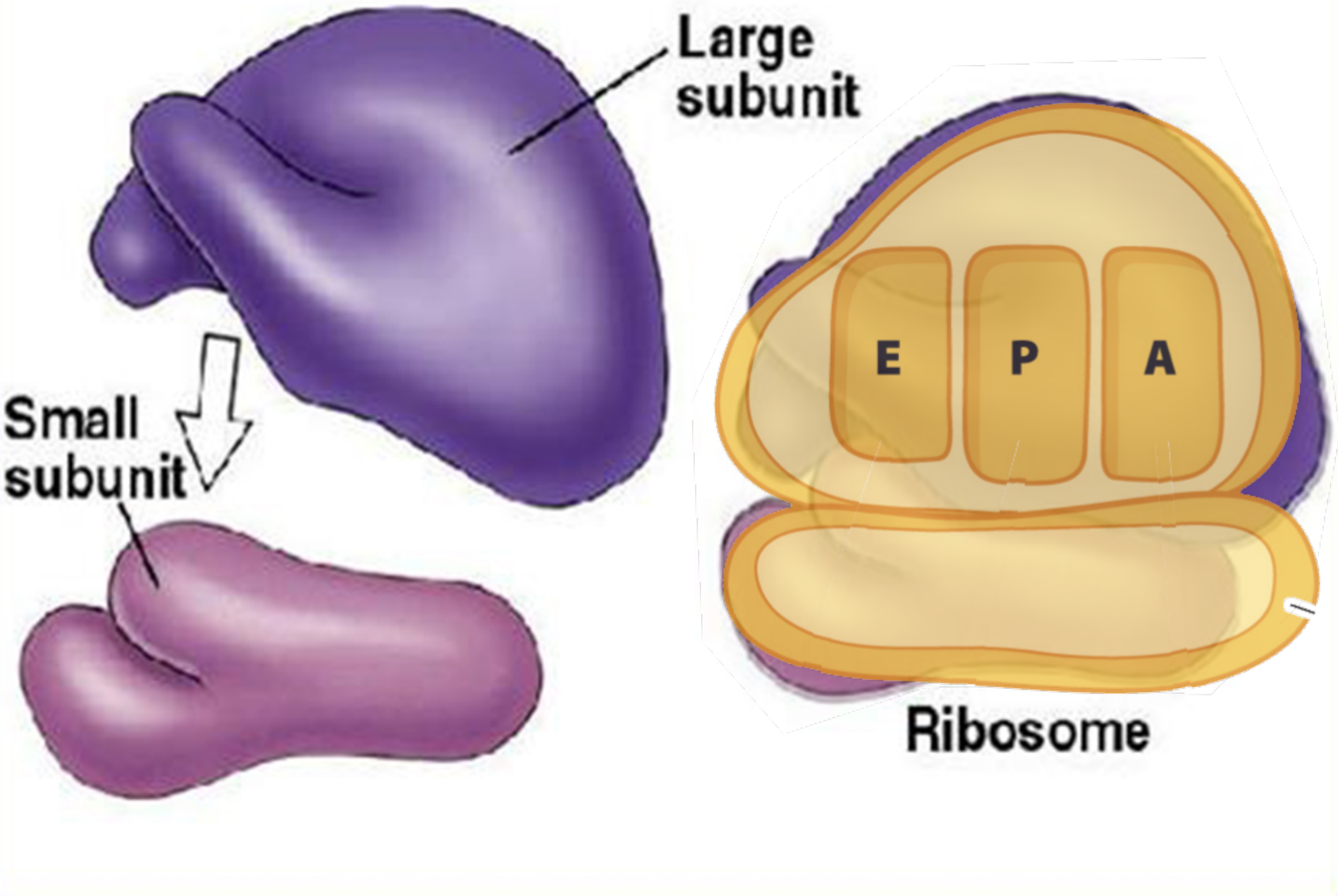
Small Subunit



Large Subunit

Prokaryotic Ribosomes (70 S)

Ribosome



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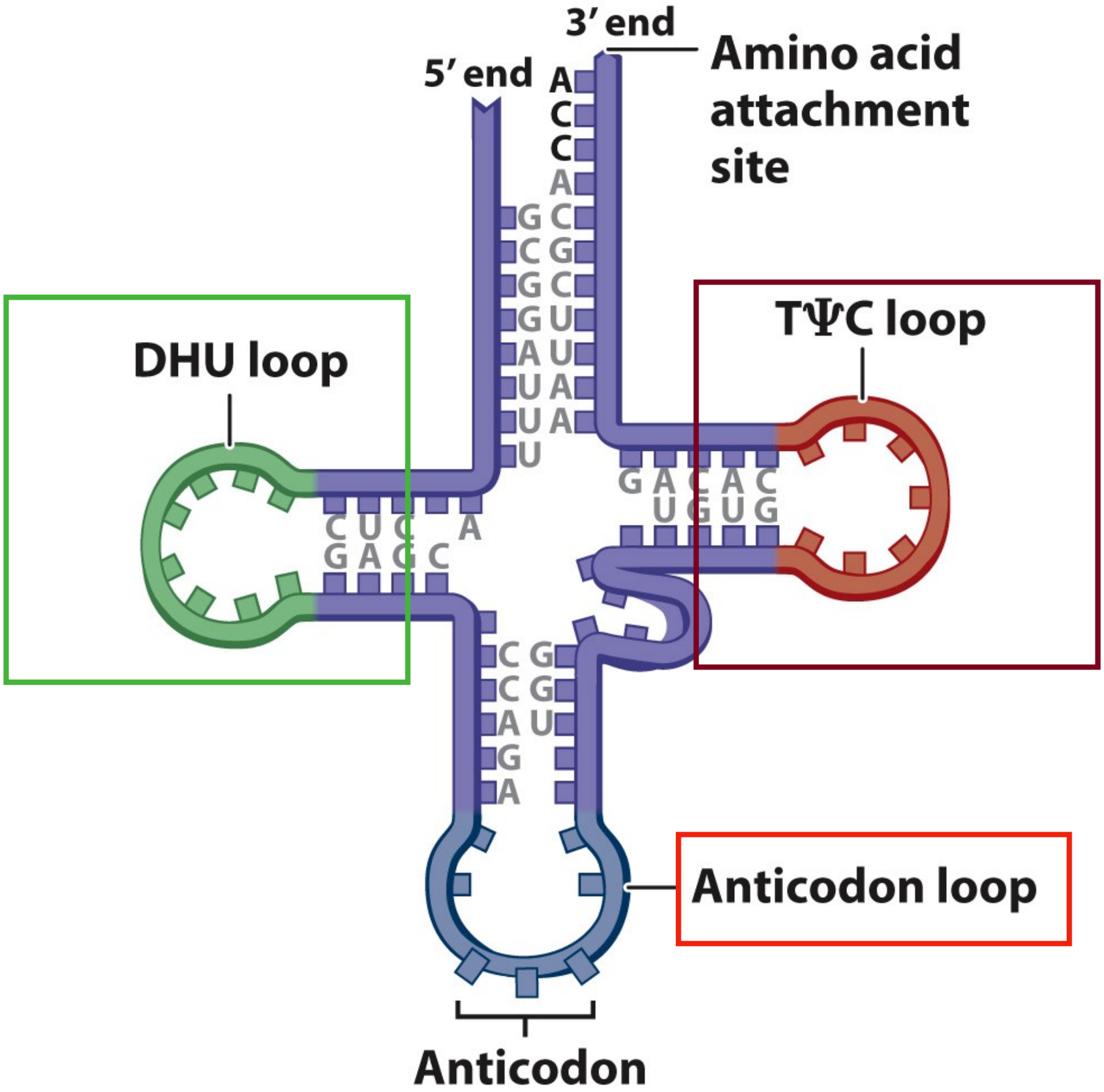
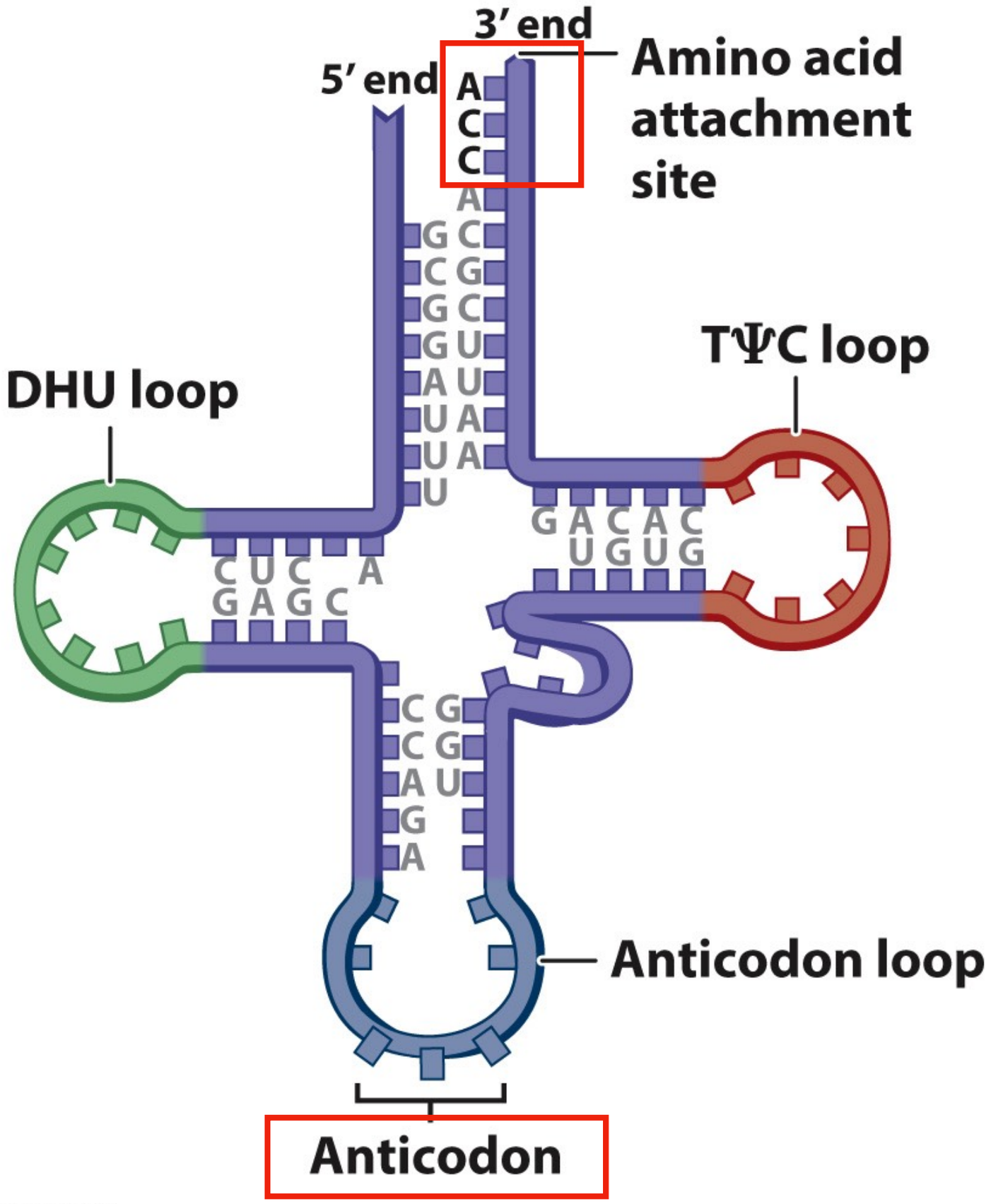


Figure 4.13a
Biology: How Life Works, Second Edition



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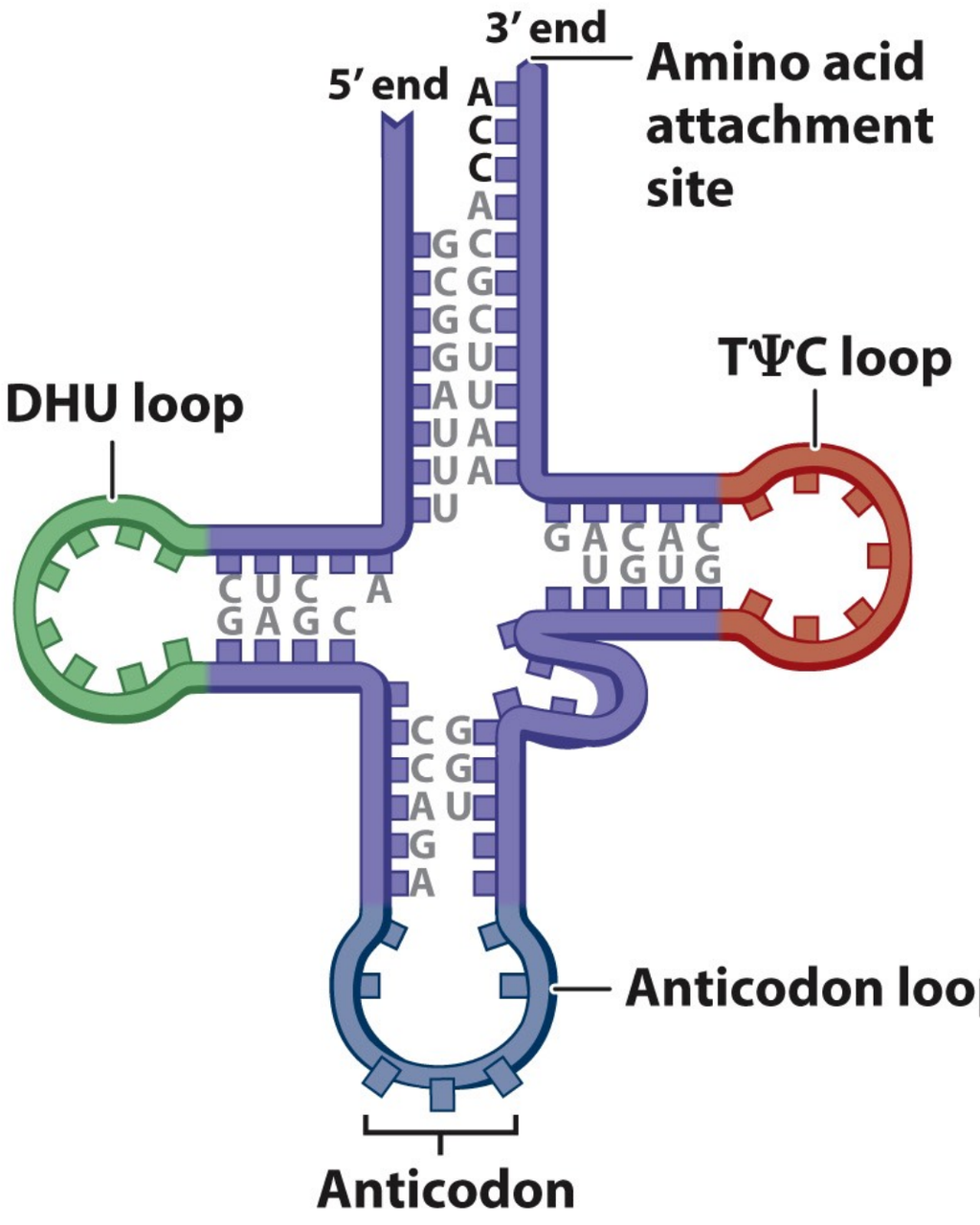
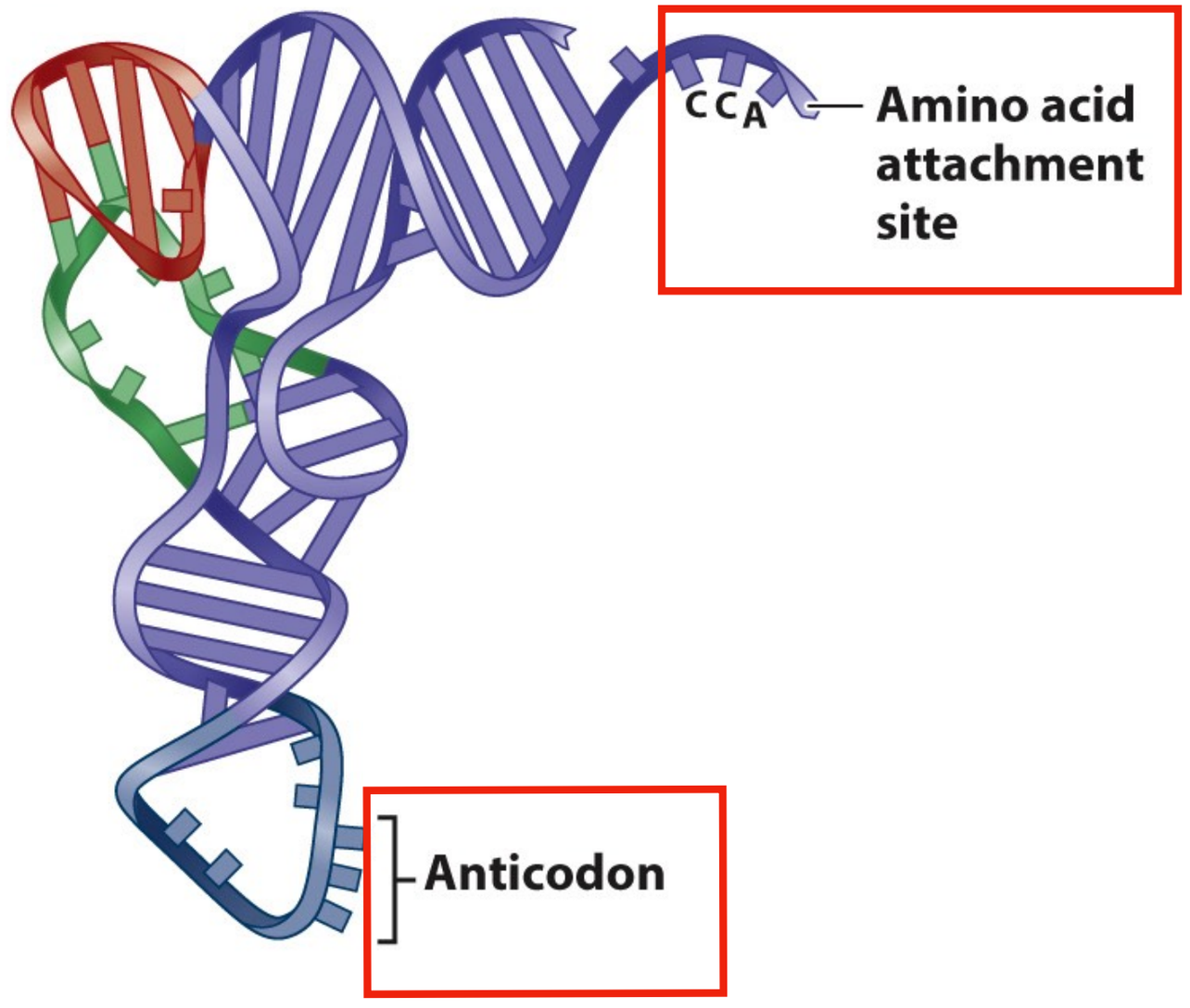
Biology: How Life Works, Second Edition


3′ end
5′ end
Amino acid attachment site
A
C
C
A
G C
C G
G C
G U
A U
U A
U A
U
TΨC loop
DHU loop
G A C A C
U G U G
C U C A
G A G C
C G
C G
A U
G
A
Anticodon loop
Anticodon


b.
C C A
Amino acid attachment site
Anticodon

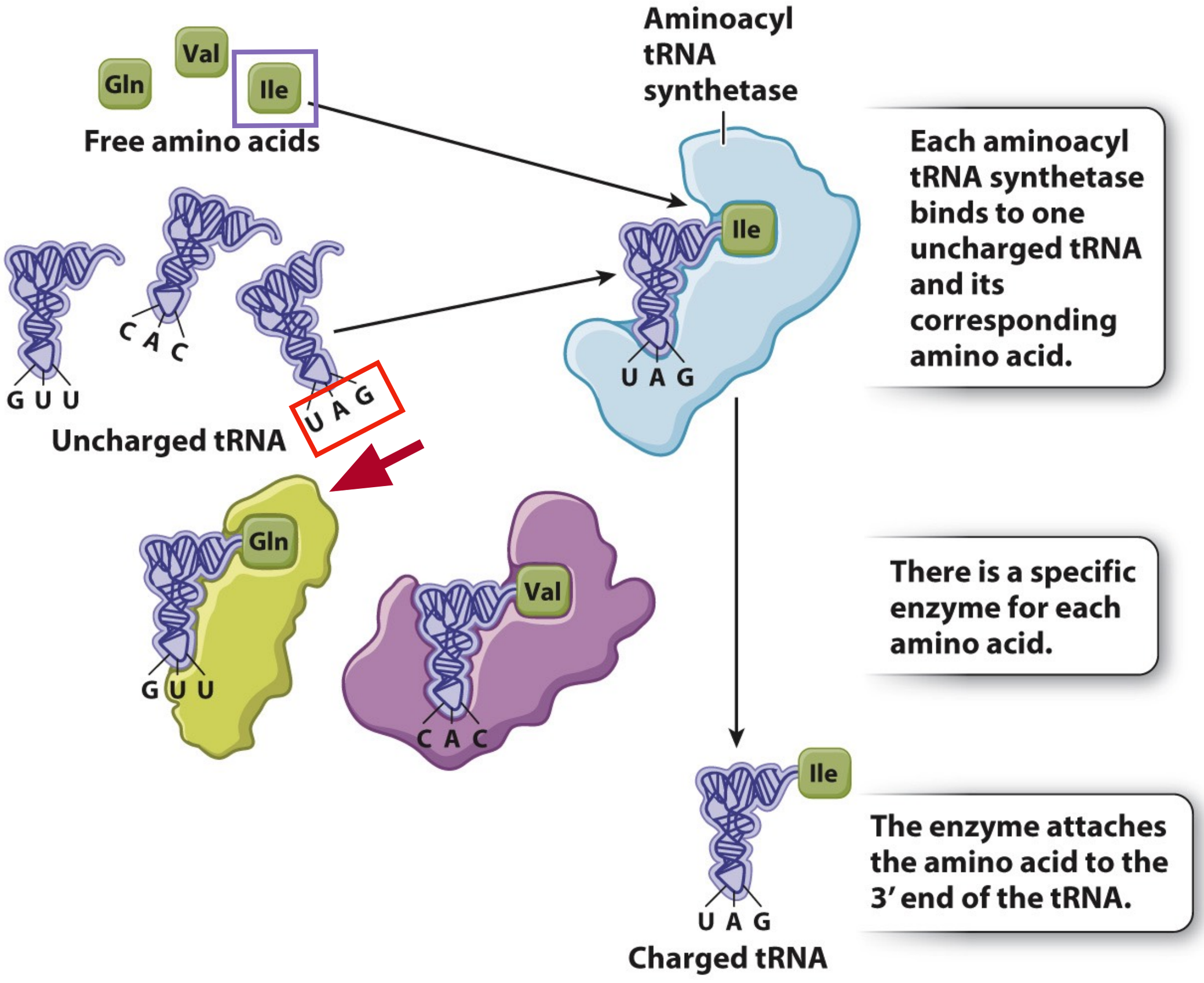


Figure 4.14
Biology: How Life Works, Second Edition

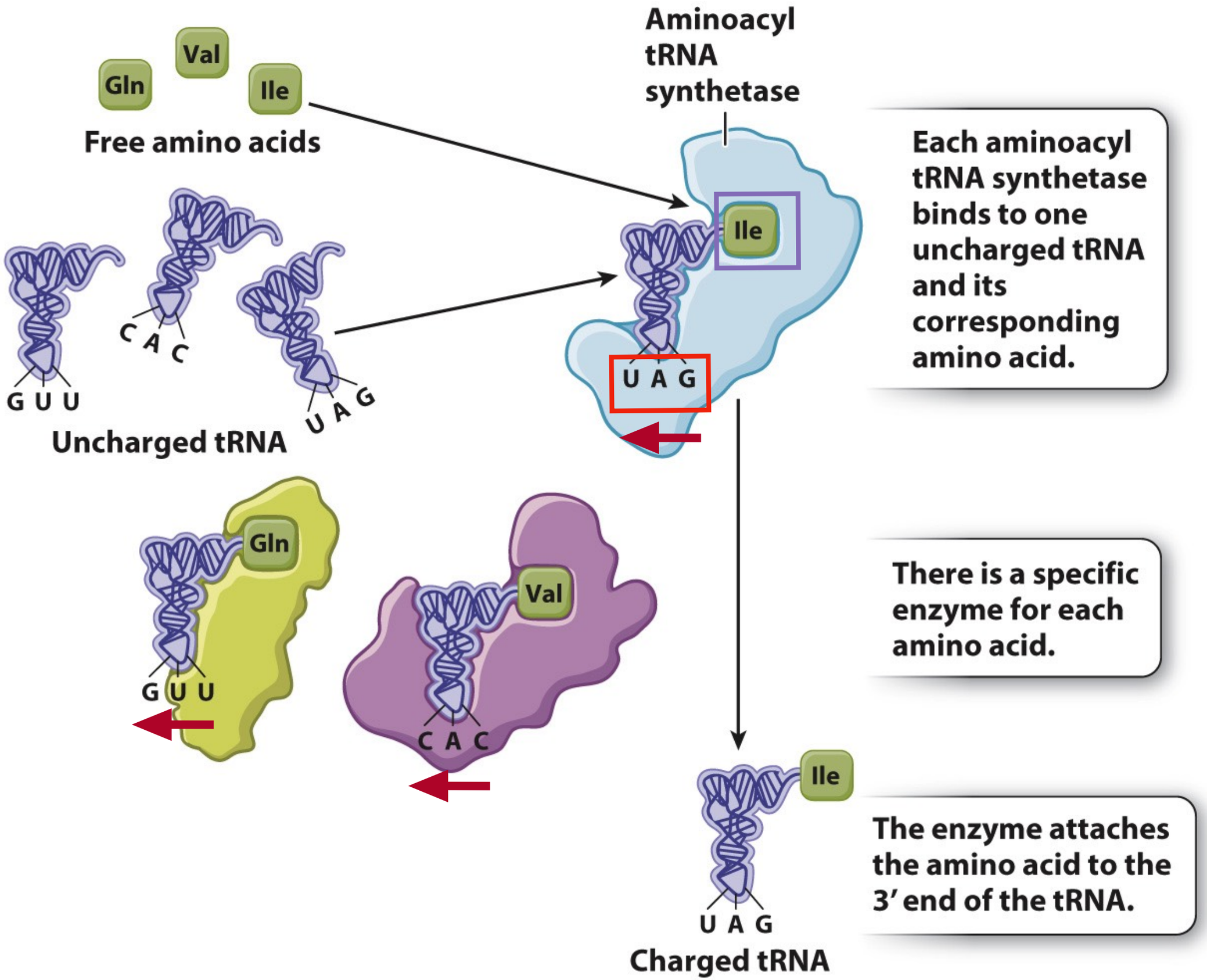
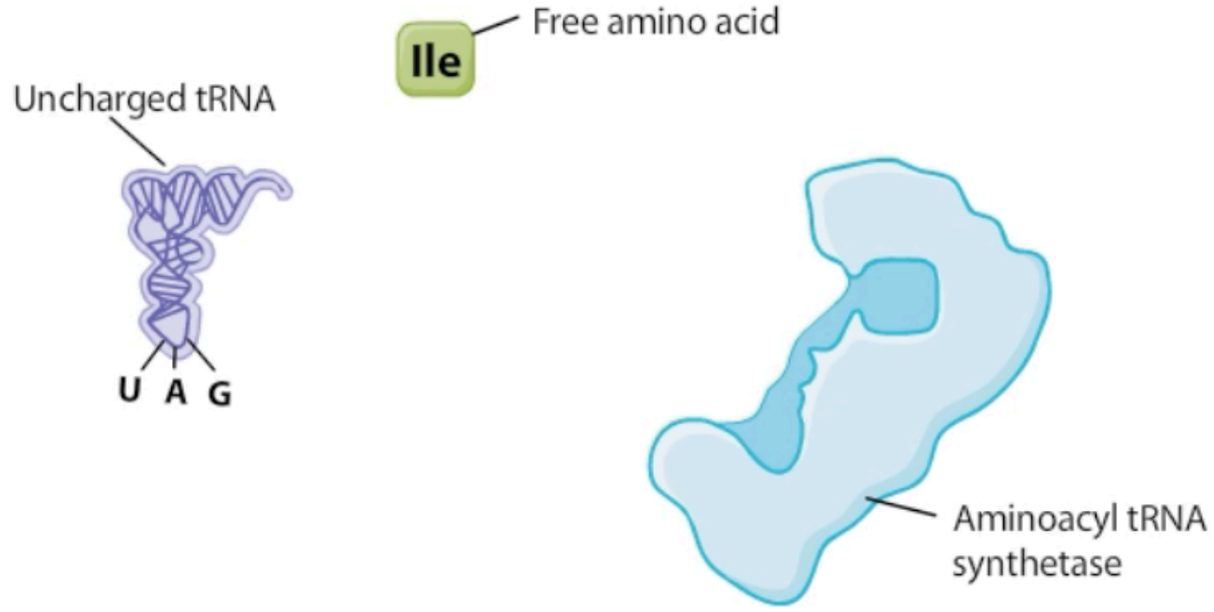
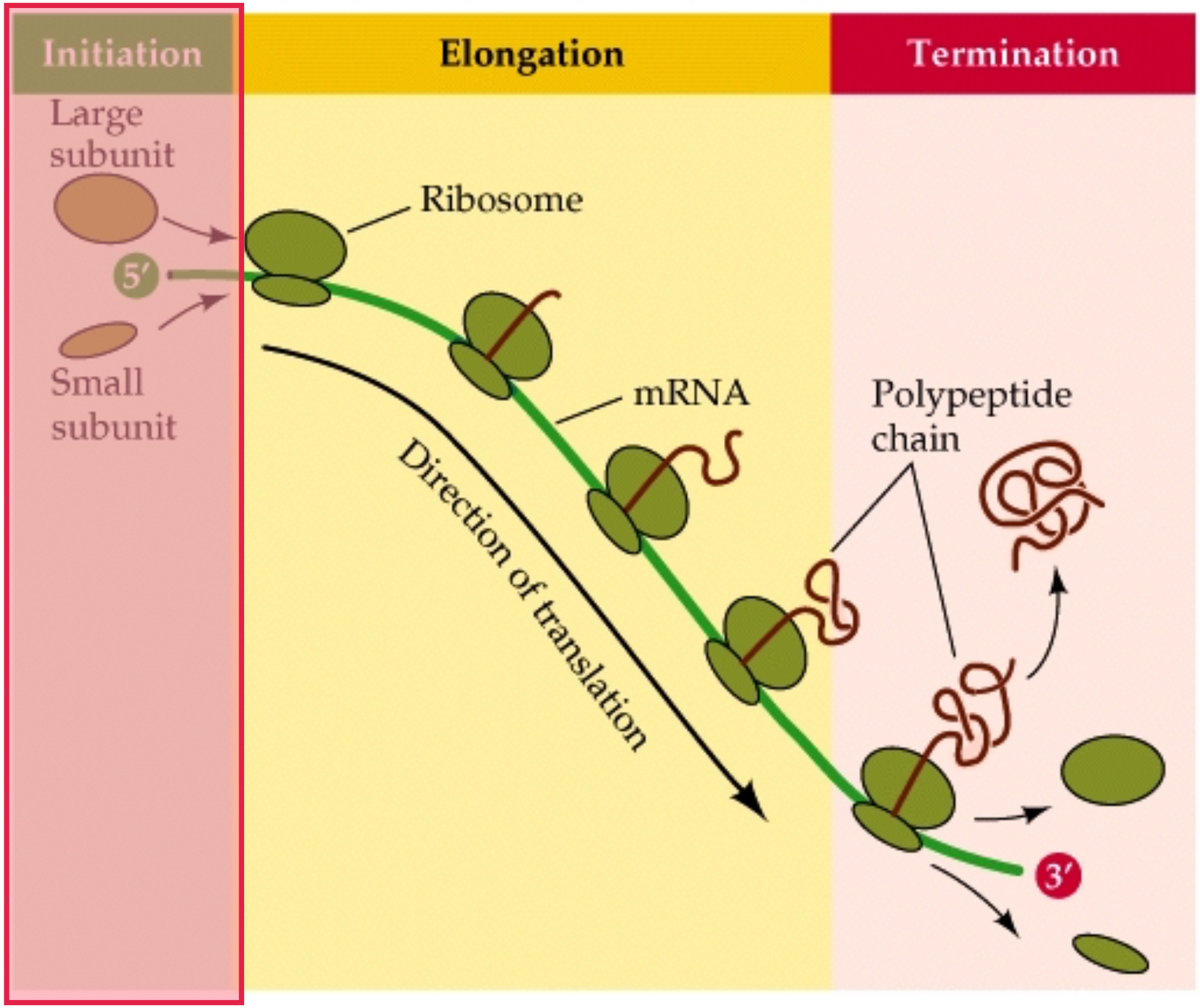


Figure 4.14
Biology: How Life Works, Second Edition

Charging of Transfer RNAs with the Matching Amino Acid



Enzymes known as aminoacyl tRNA synthetases are important in translation. They carry out the actual translation from nucleic acid to amino acid.


Initiation
Elongation
Termination
Large subunit
5′
Small subunit
Ribosome
mRNA
Direction of translation
Polypeptide chain
3′

“Universal” Genetic Code

First letter	Second letter: U	Second letter: C	Second letter: A	Second letter: G	Third letter
U	UUU, UUC: Phenylalanine	UCU, UCC, UCA, UCG: Serine	UAU, UAC: Tyrosine	UGU, UGC: Cysteine	U C A G
	UUA, UUG: Leucine		UAA: Stop codon; UAG: Stop codon	UGA: Stop codon; UGG: Tryptophan	
C	CUU, CUC, CUA, CUG: Leucine	CCU, CCC, CCA, CCG: Proline	CAU, CAC: Histidine	CGU, CGC, CGA, CGG: Arginine	U C A G
			CAA, CAG: Glutamine		
A	AUU, AUC, AUA: Isoleucine	ACU, ACC, ACA, ACG: Threonine	AAU, AAC: Asparagine	AGU, AGC: Serine	U C A G
	AUG: Methionine; start codon		AAA, AAG: Lysine	AGA, AGG: Arginine	
G	GUU, GUC, GUA, GUG: Valine	GCU, GCC, GCA, GCG: Alanine	GAU, GAC: Aspartic acid	GGU, GGC, GGA, GGG: Glycine	U C A G
			GAA, GAG: Glutamic acid		

AUG, which codes for the amino acid **methionine**, is called the ***start*** **codon**, which initiates the translational process.

Three of the possible codons are *stop* codons (**UAA**, **UAG**, and **UGA**), which direct the ribosomes to STOP reading the mRNA; that is, they end translation.

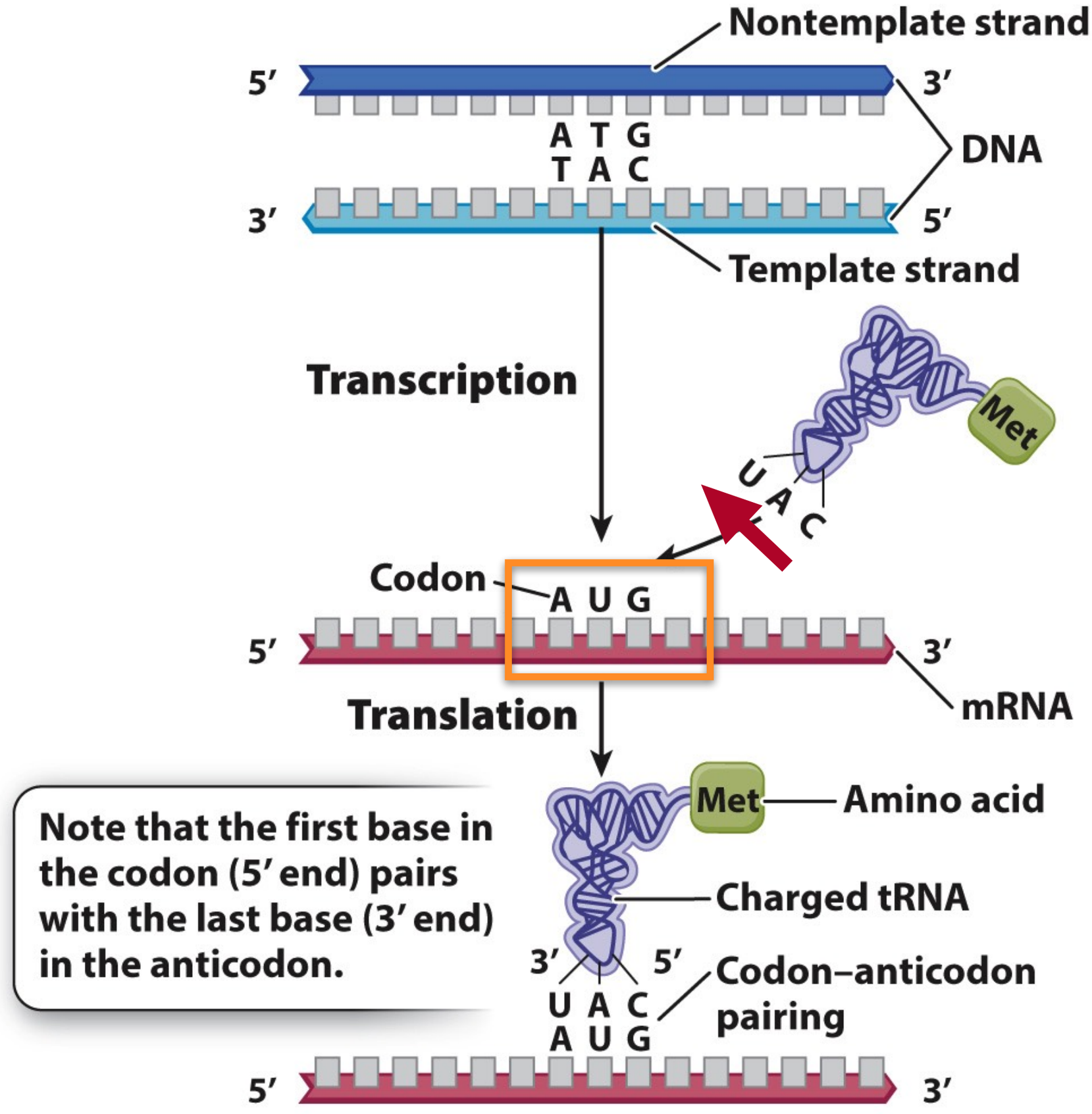


Figure 4.15
Biology: How Life Works, Second Edition

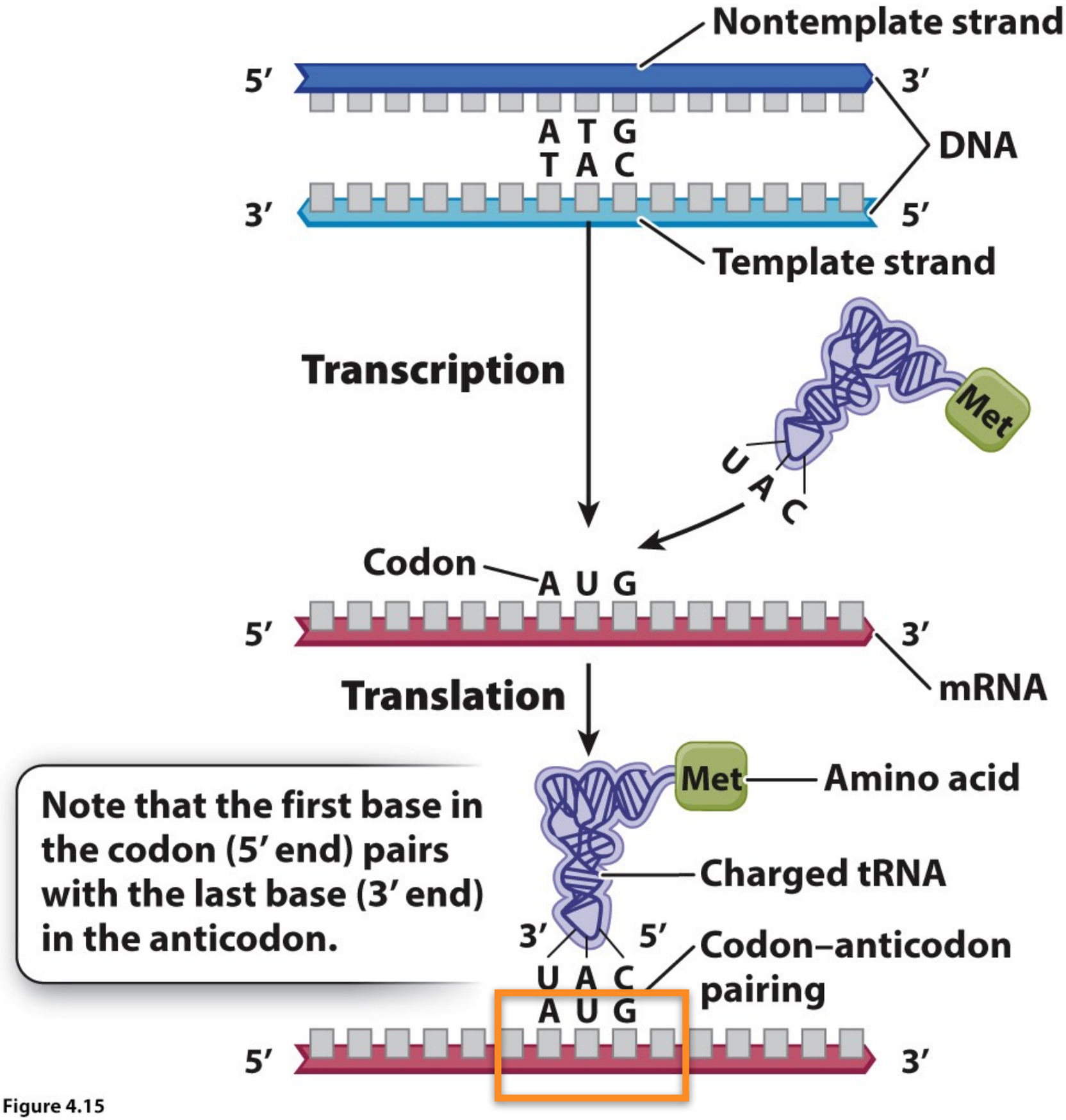


Figure 4.15
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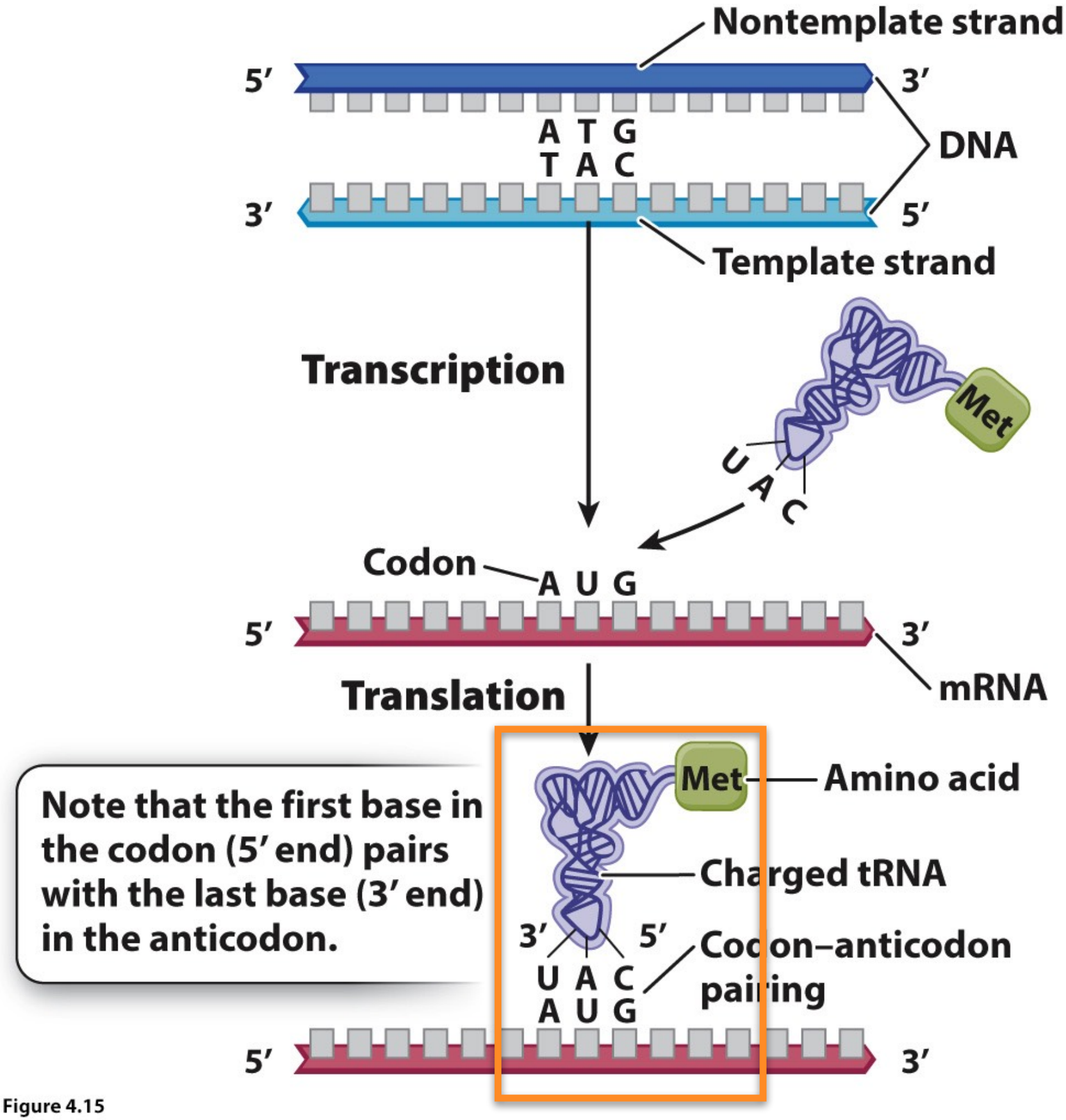

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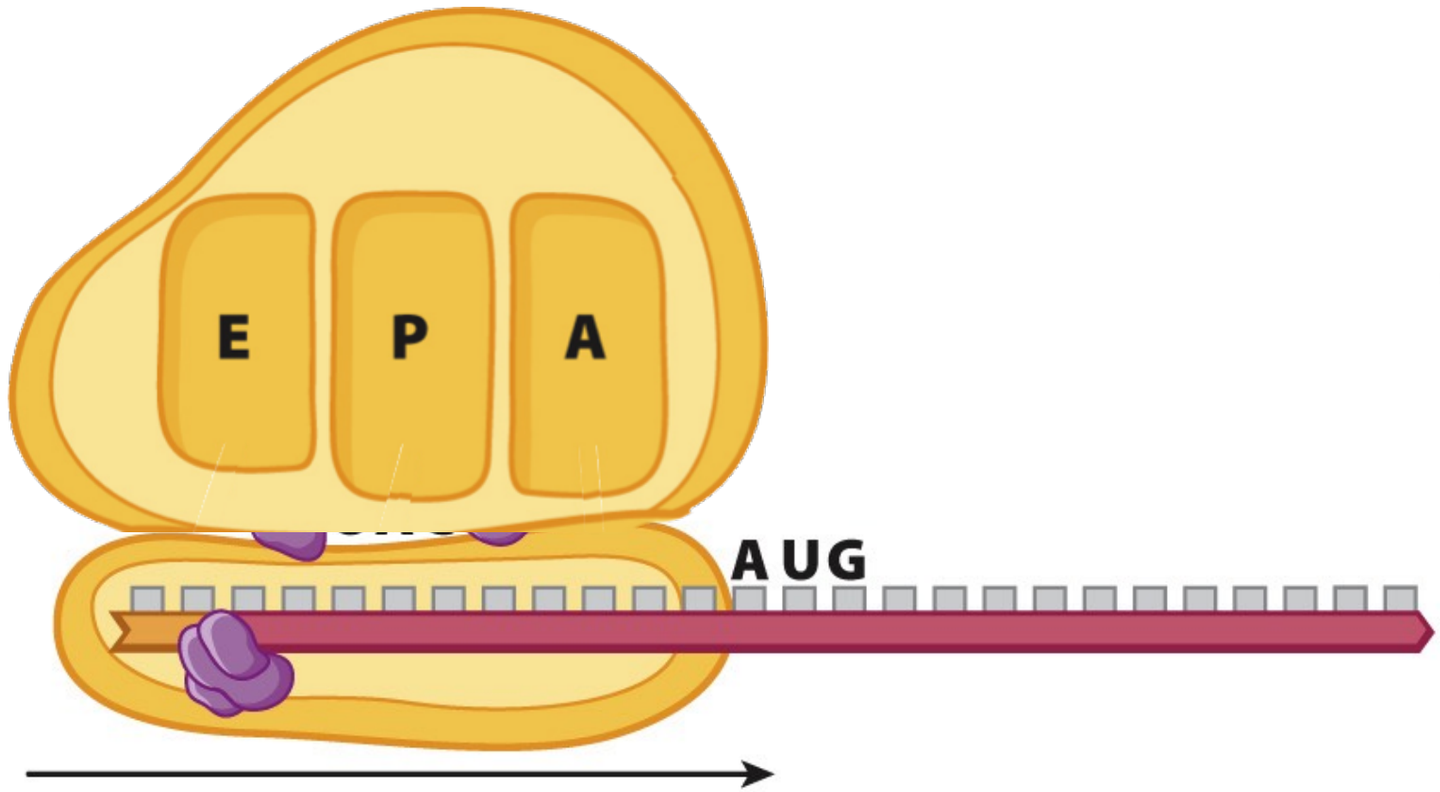
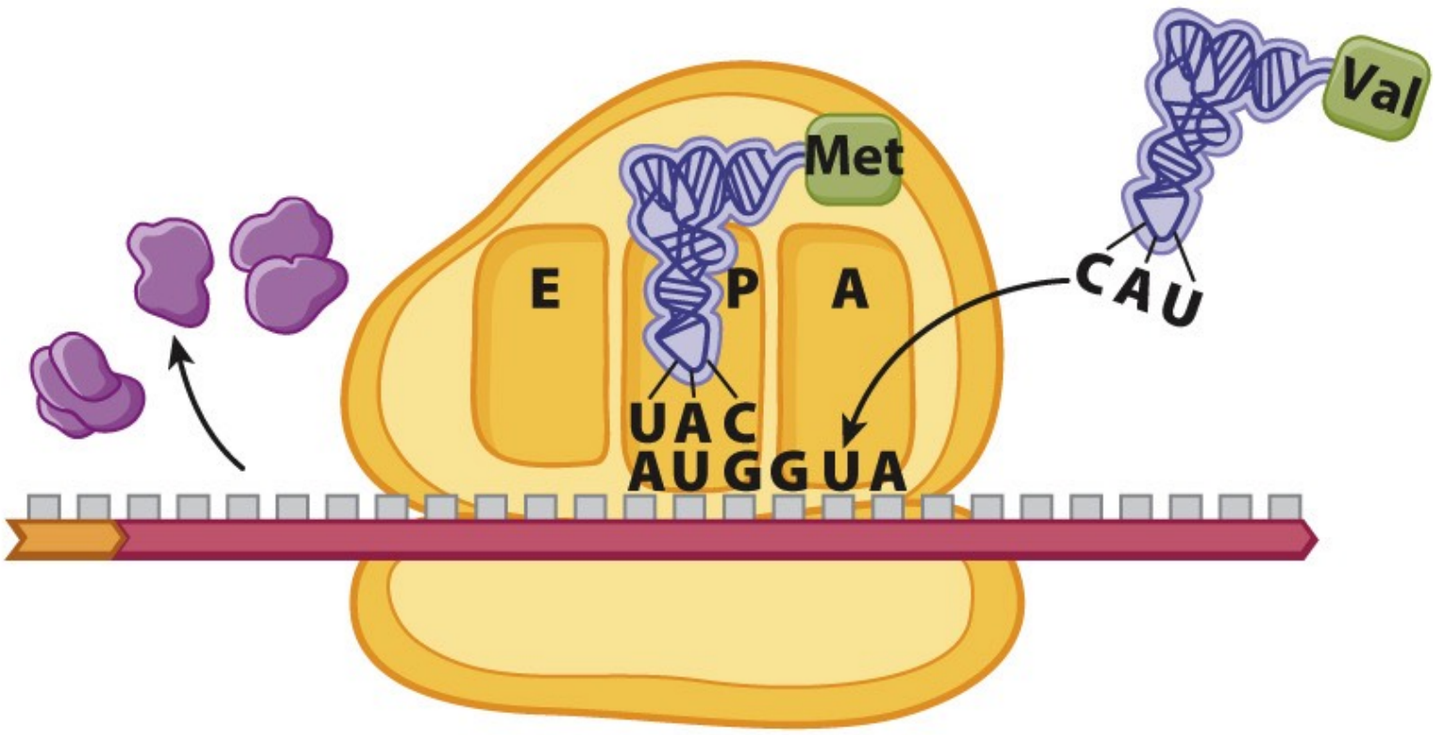
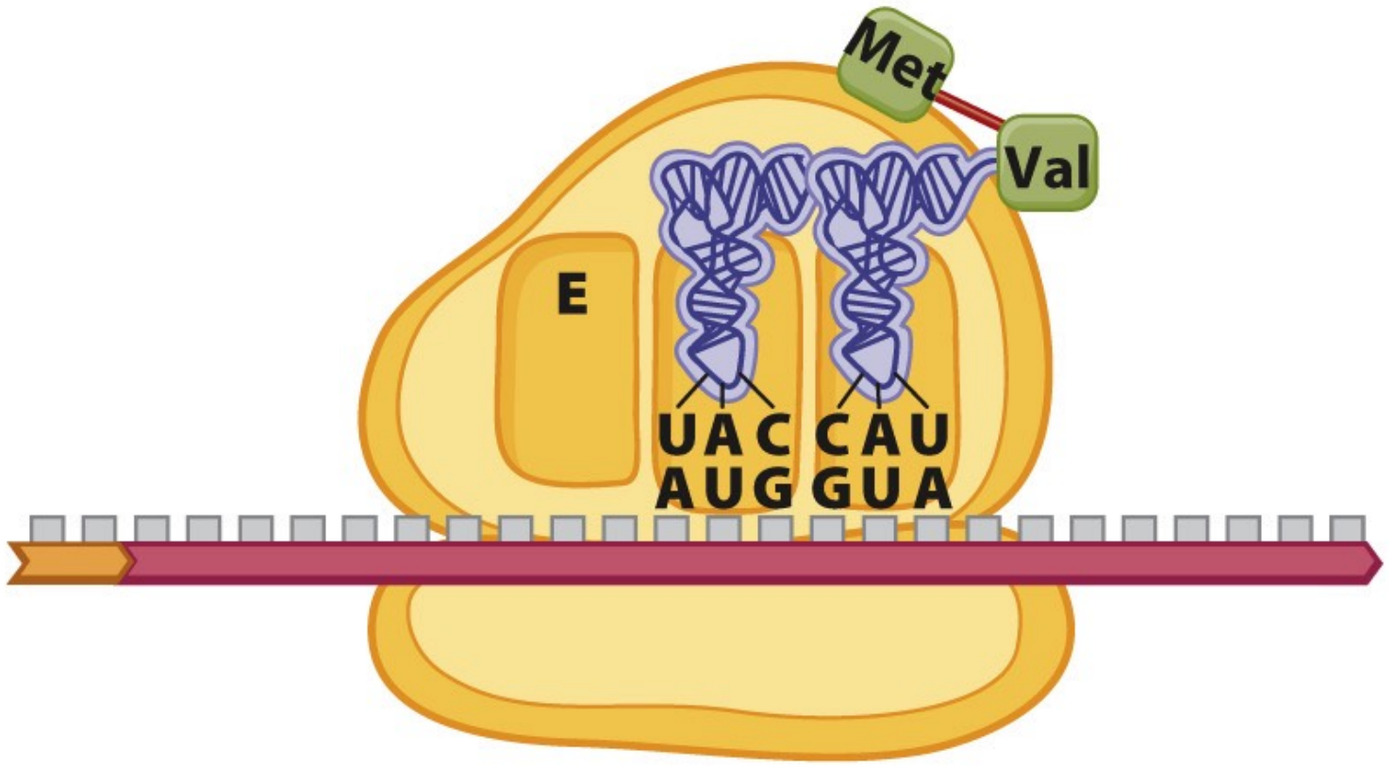


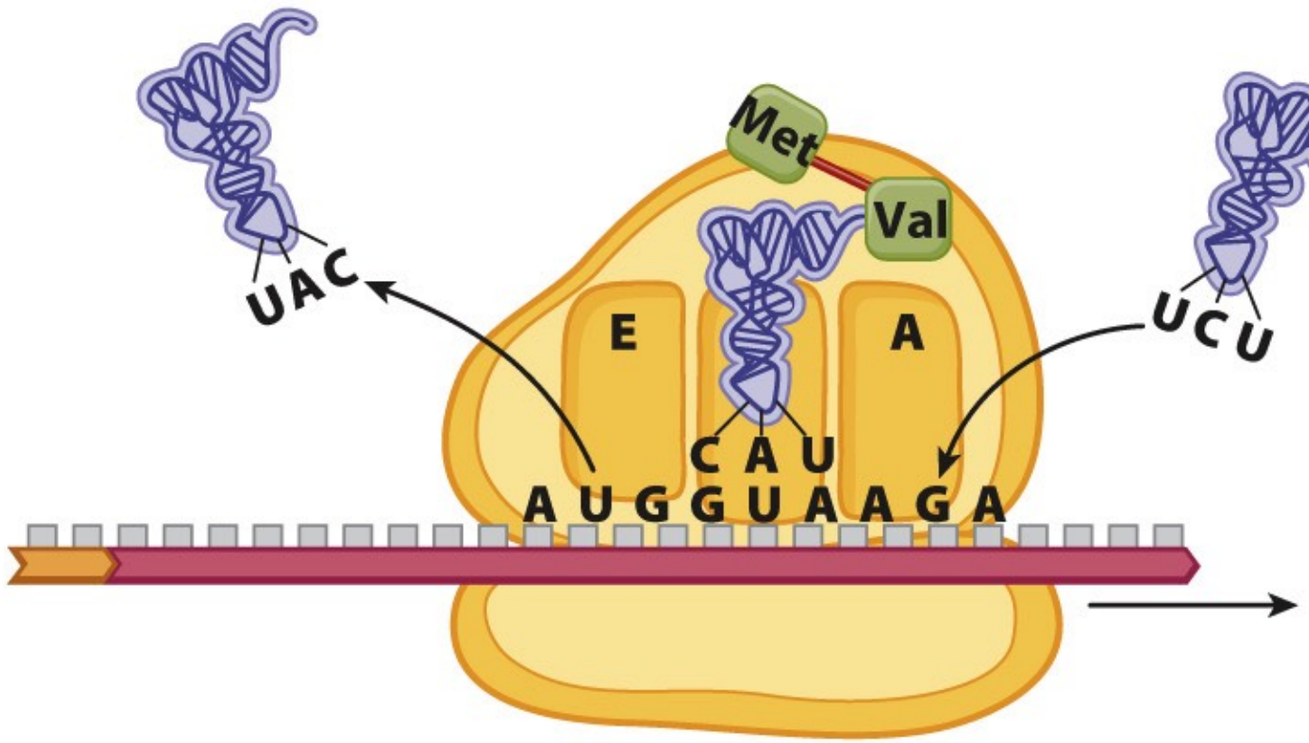
Initiation factors recruit the small ribosomal subunit and tRNAMet and scan the mRNA for an AUG codon.



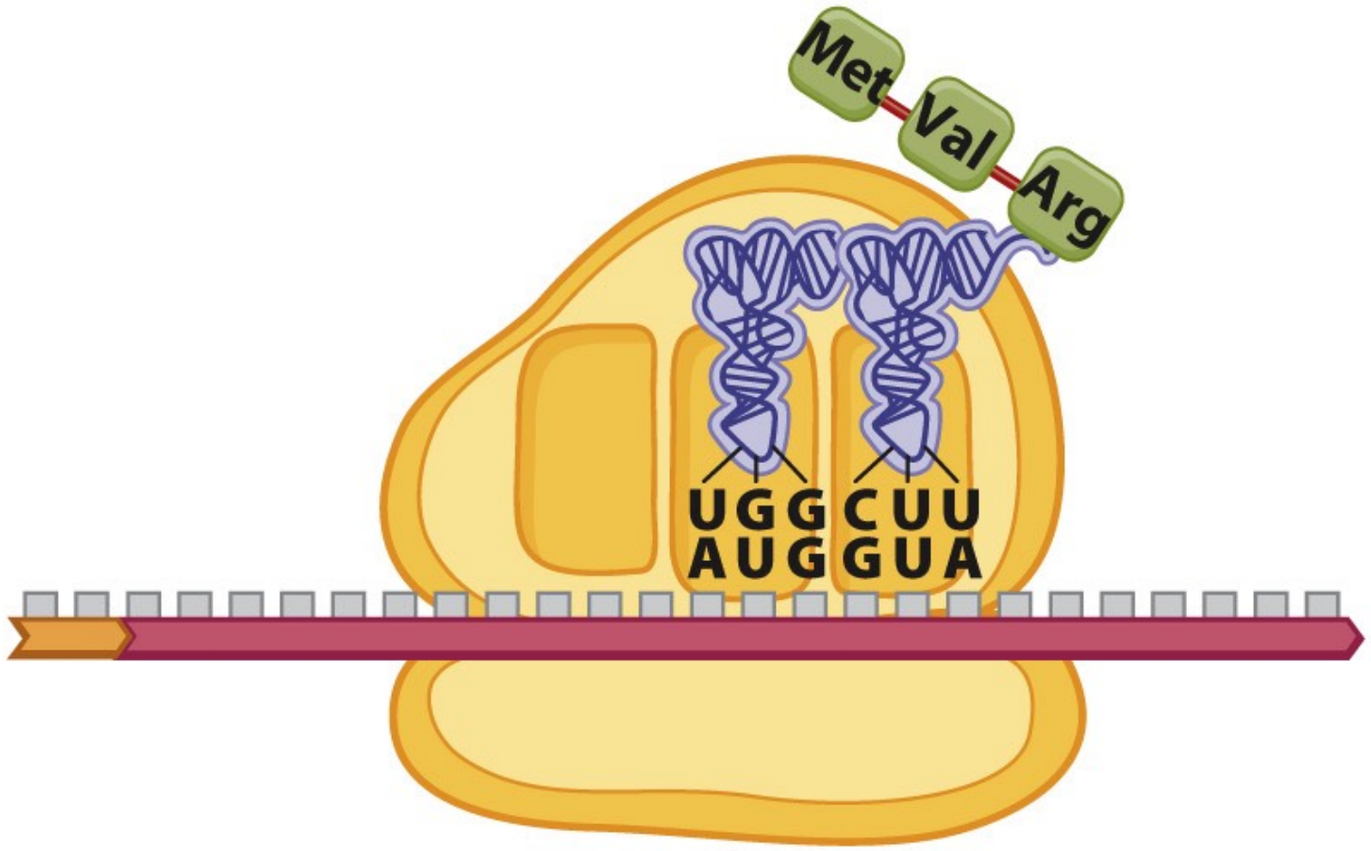
When the complex reaches an AUG, the large ribosomal subunit joins, the initiation factors are released, and a tRNA complementary to the next codon binds to the A site.



A reaction transfers the Met to the amino acid on the tRNA in the A site, forming a peptide bond.

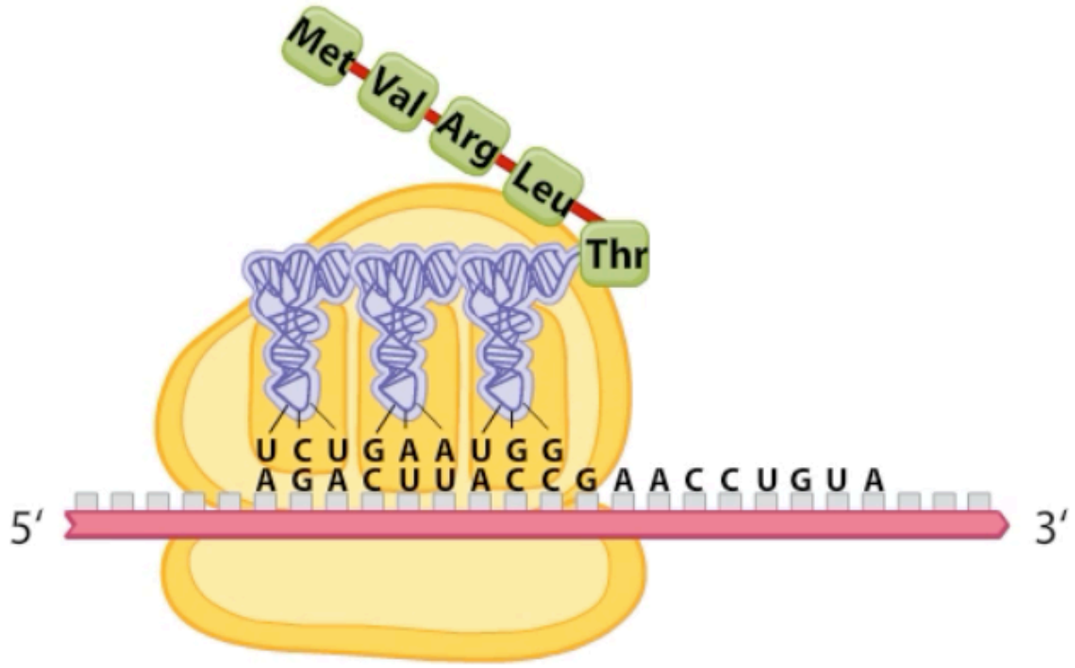


The ribosome moves down one codon, which puts the amino acid carrying the polypeptide into the P site and the now-uncharged tRNA into the E site, where it is ejected. A new tRNA complementary to the next codon binds to the A site.

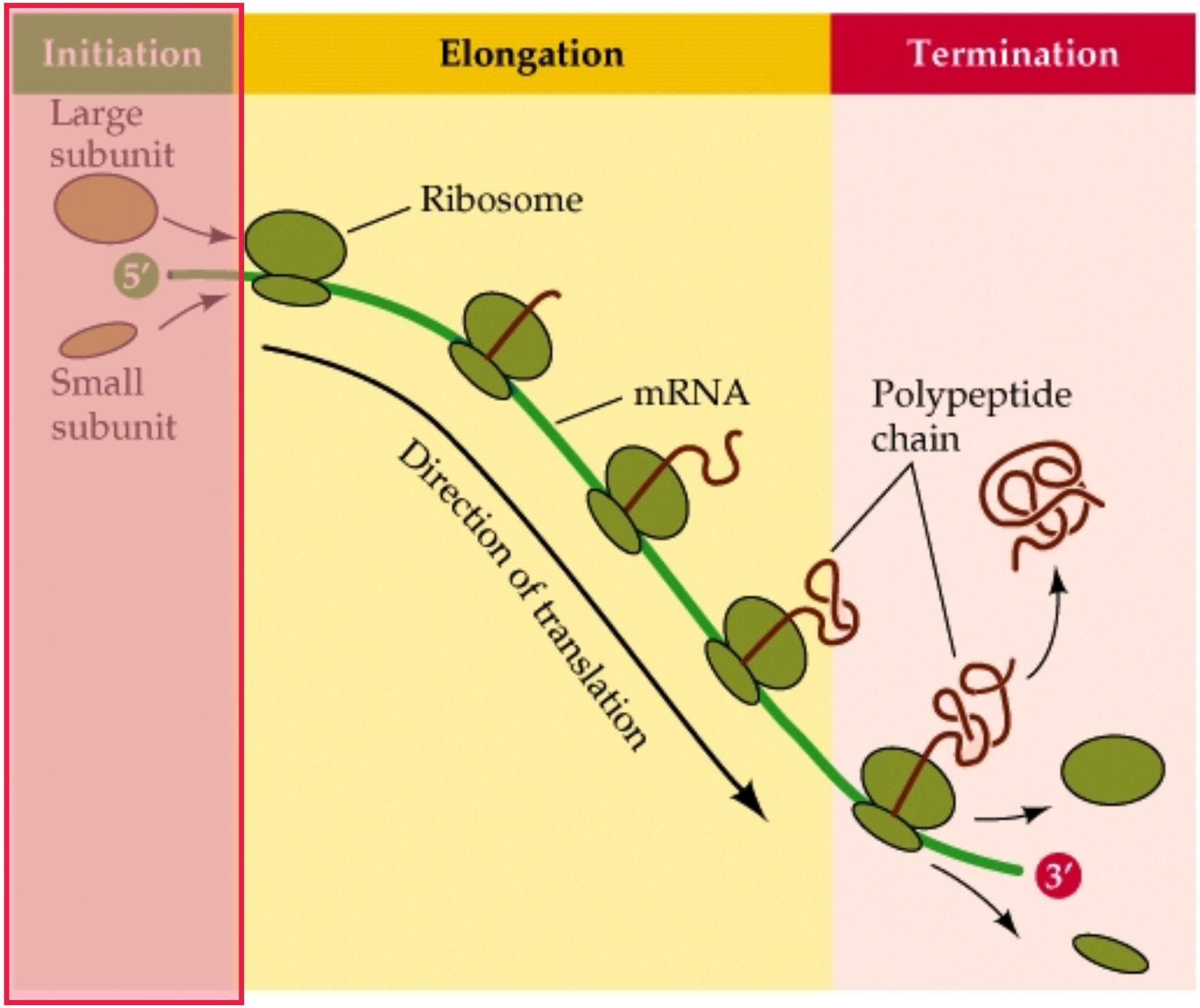


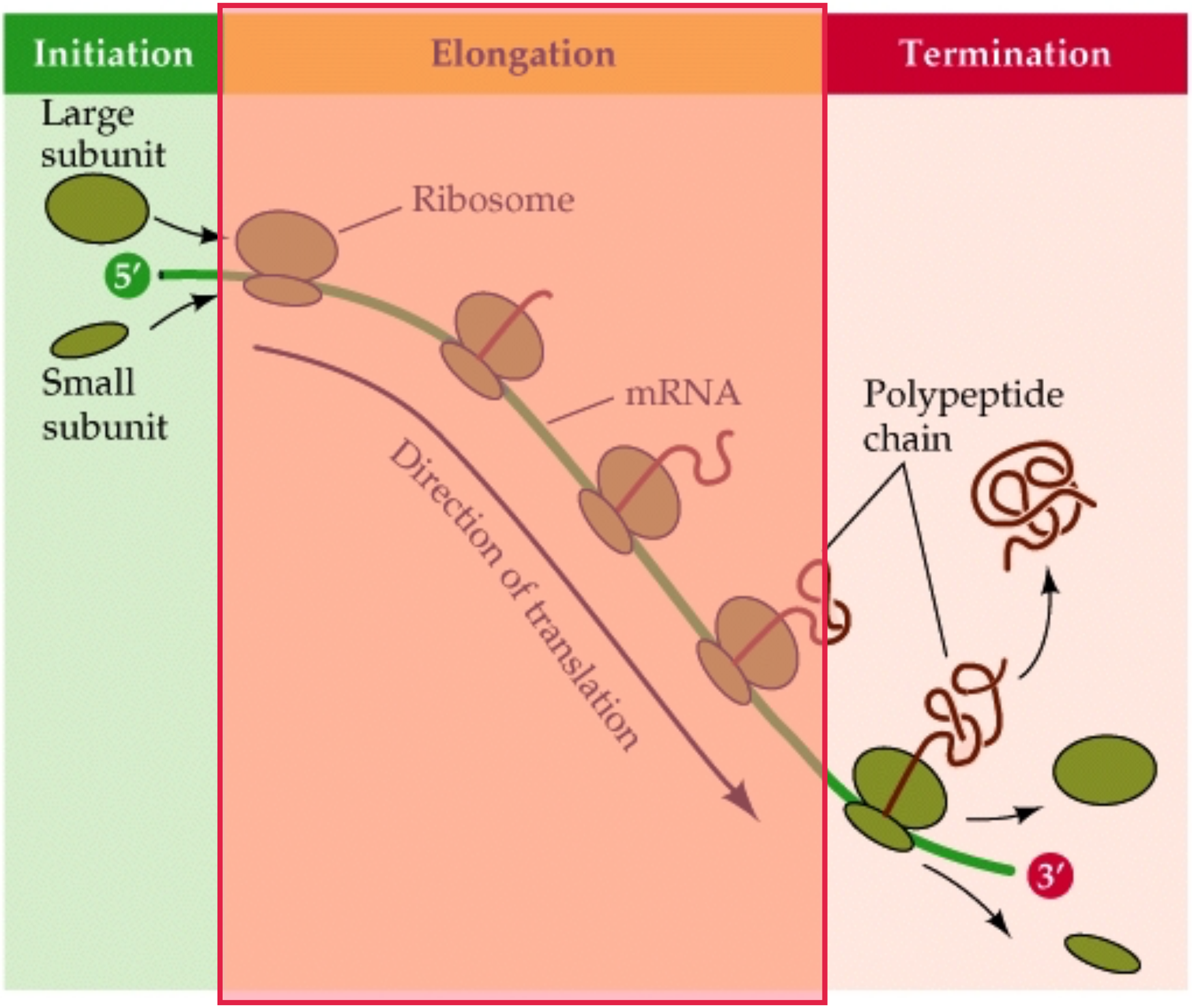
The polypeptide transfers to the amino acid on the tRNA in the A site. The polypeptide is elongated by repeating steps (d) and (e).

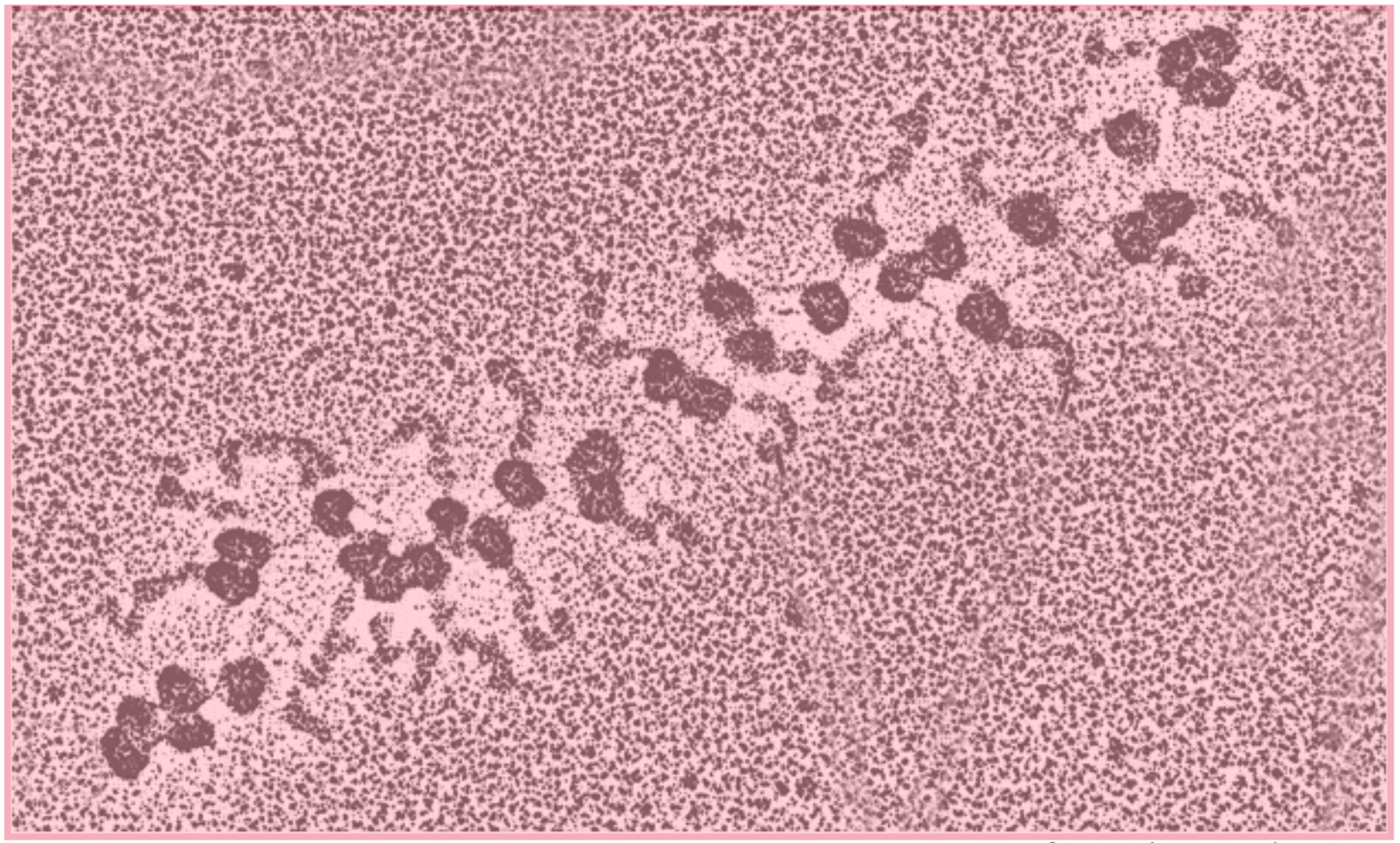
Translation Elongation



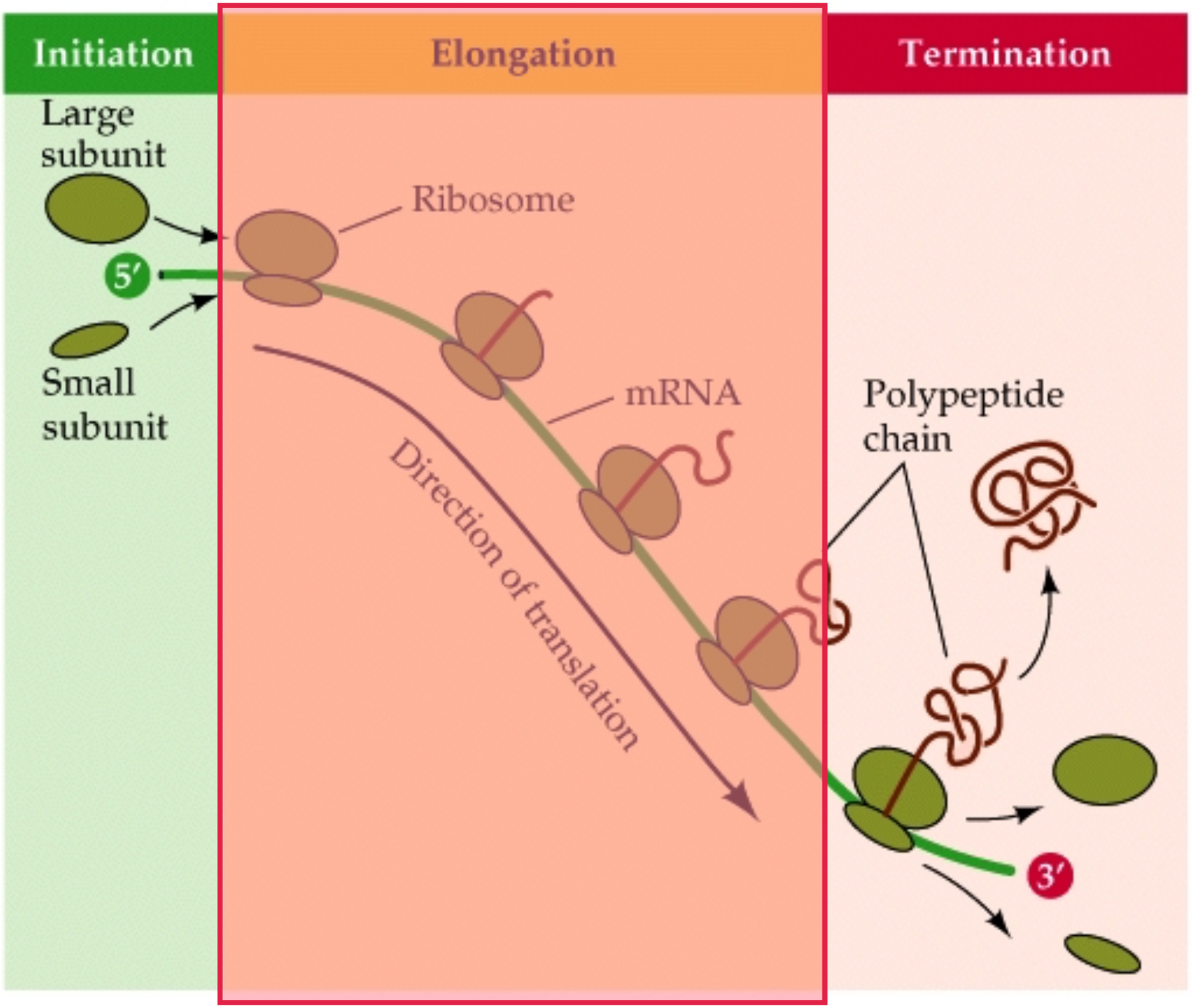
Translation of the sequence of codons in messenger RNA into the sequence of amino acids in a polypeptide chain is an orderly process repeated over and over again.

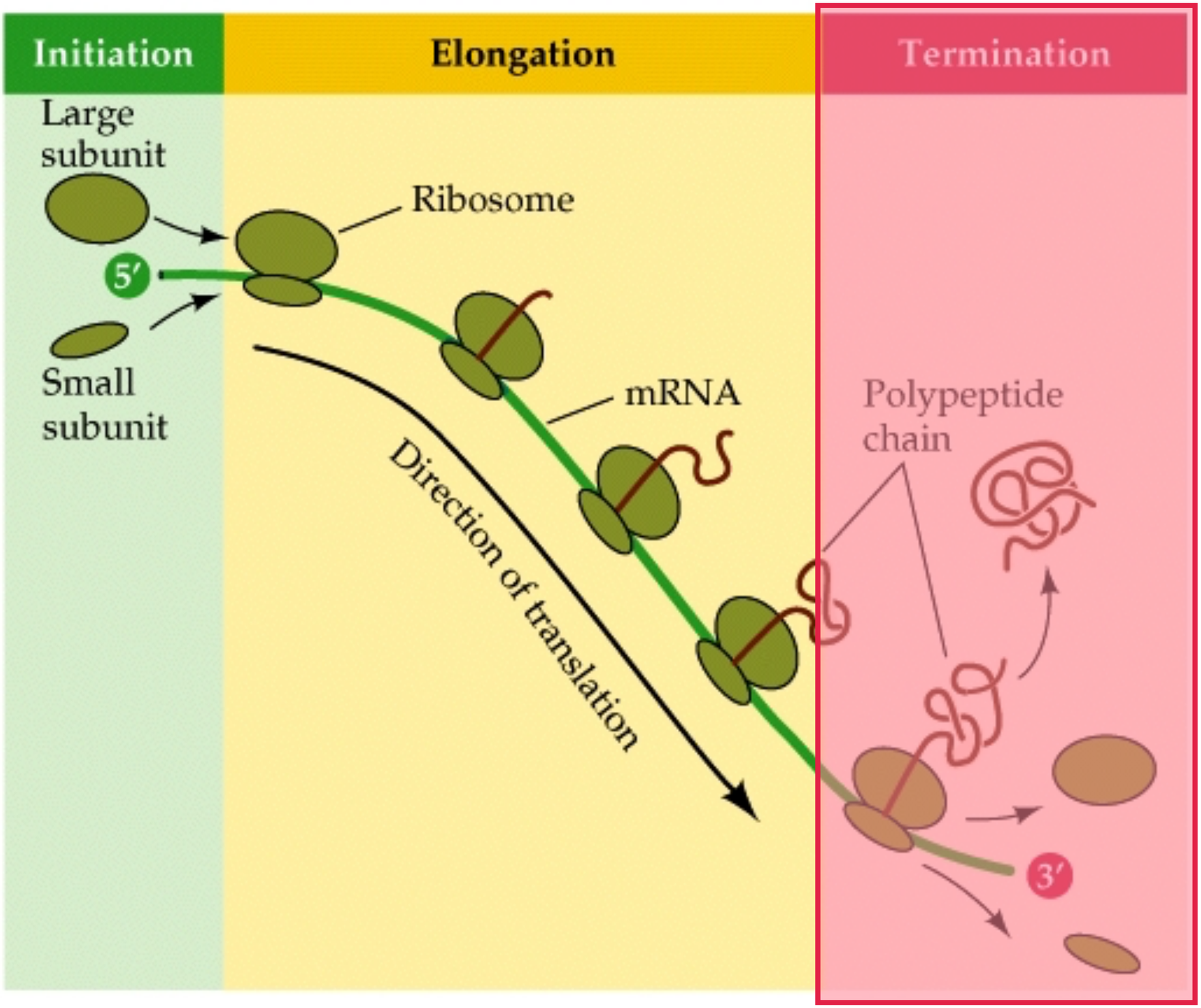

Initiation
Elongation
Termination
Large subunit
5′
Small subunit
Ribosome
mRNA
Direction of translation
Polypeptide chain
3′

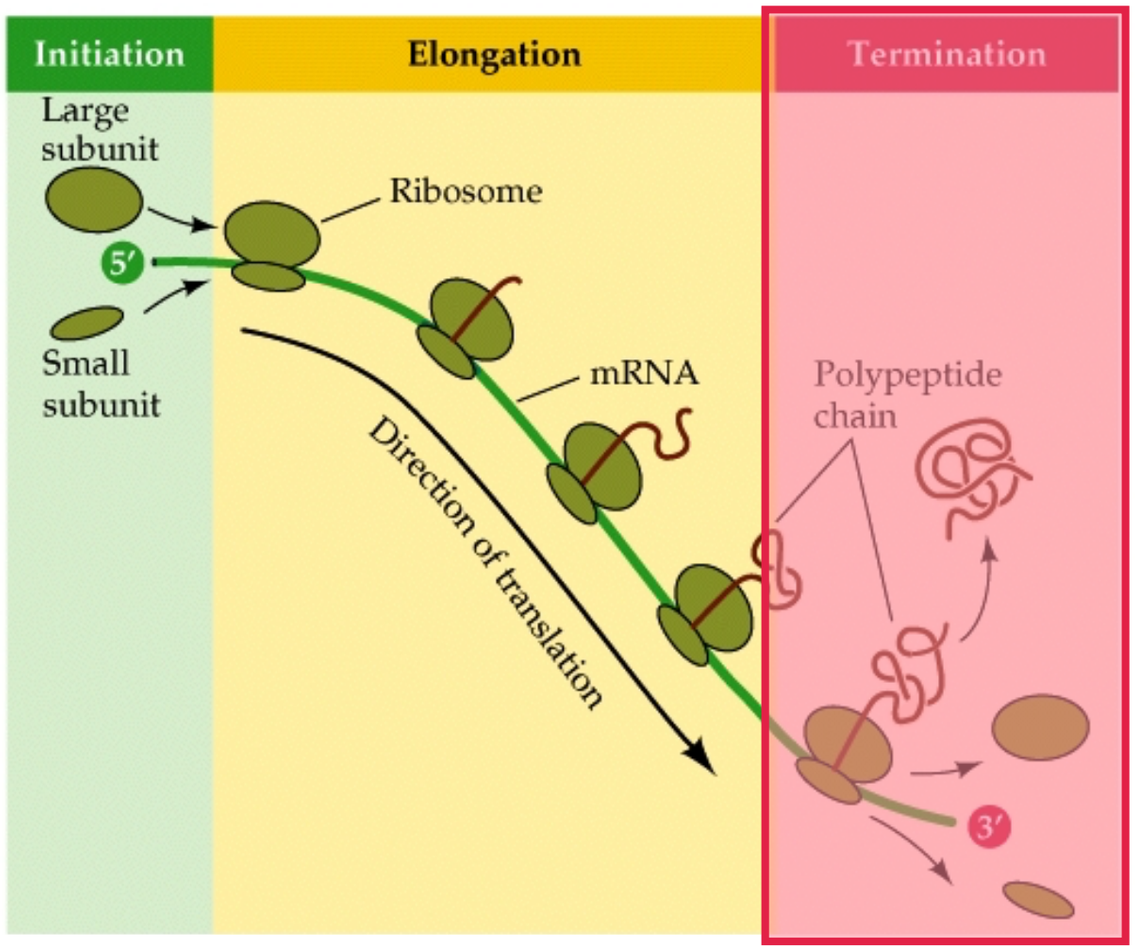

Initiation
Elongation
Termination
Large subunit
5′
Small subunit
Ribosome
mRNA
Direction of translation
Polypeptide chain
3′



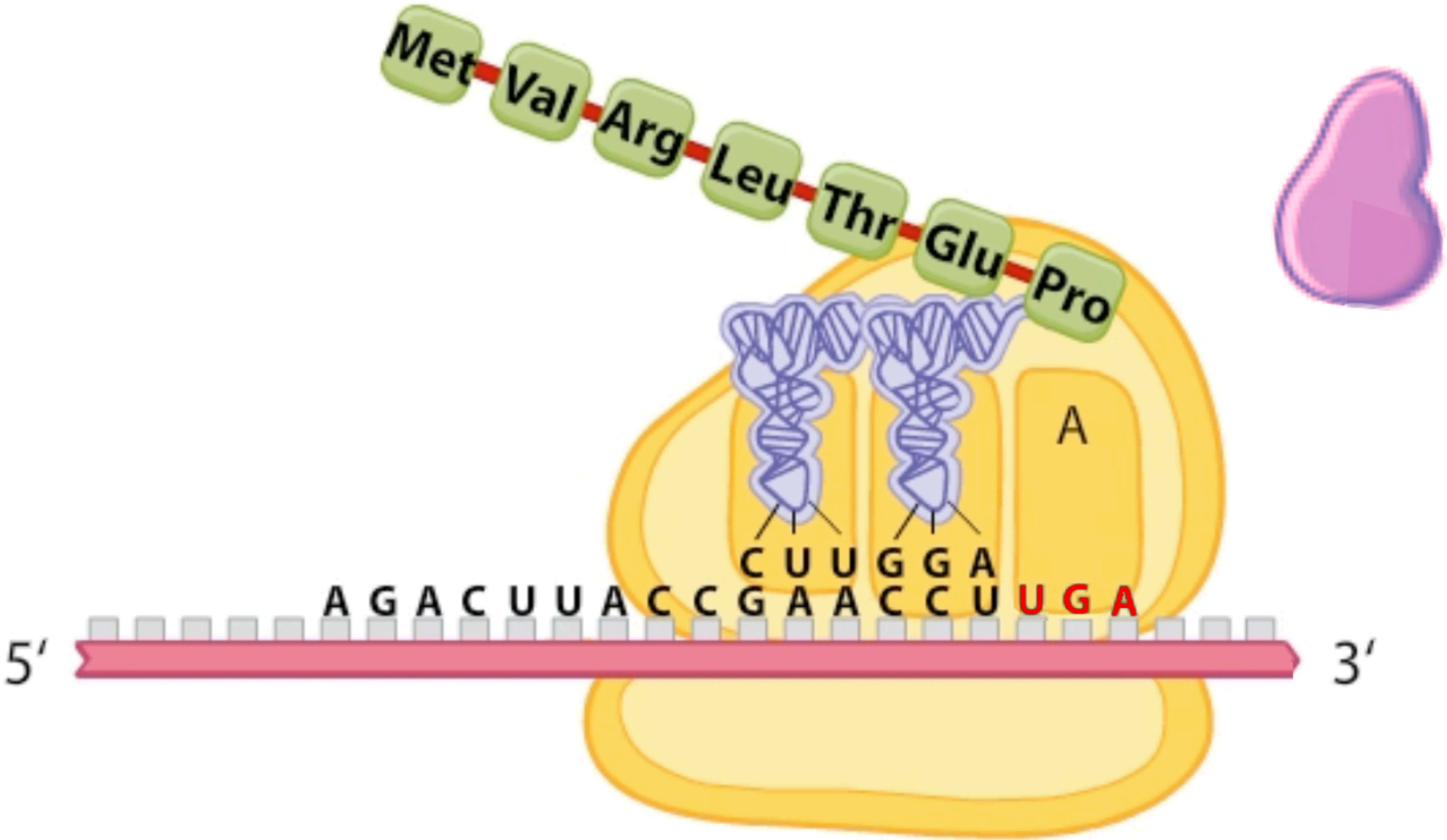
Courtesy of J. E. Edström and EMBO J.

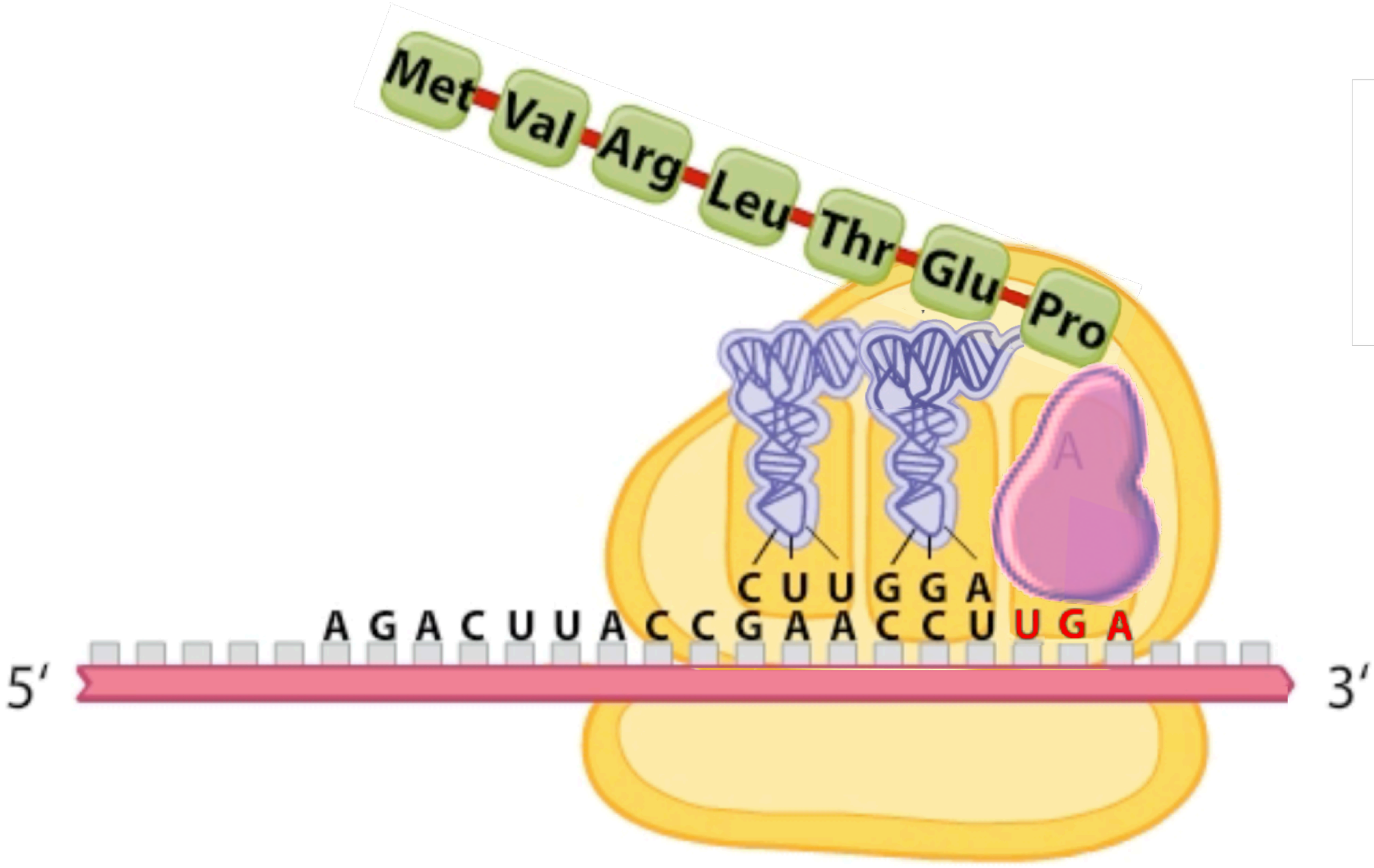

Initiation
Elongation
Termination
Large subunit
5′
Small subunit
Ribosome
mRNA
Direction of translation
Polypeptide chain
3′

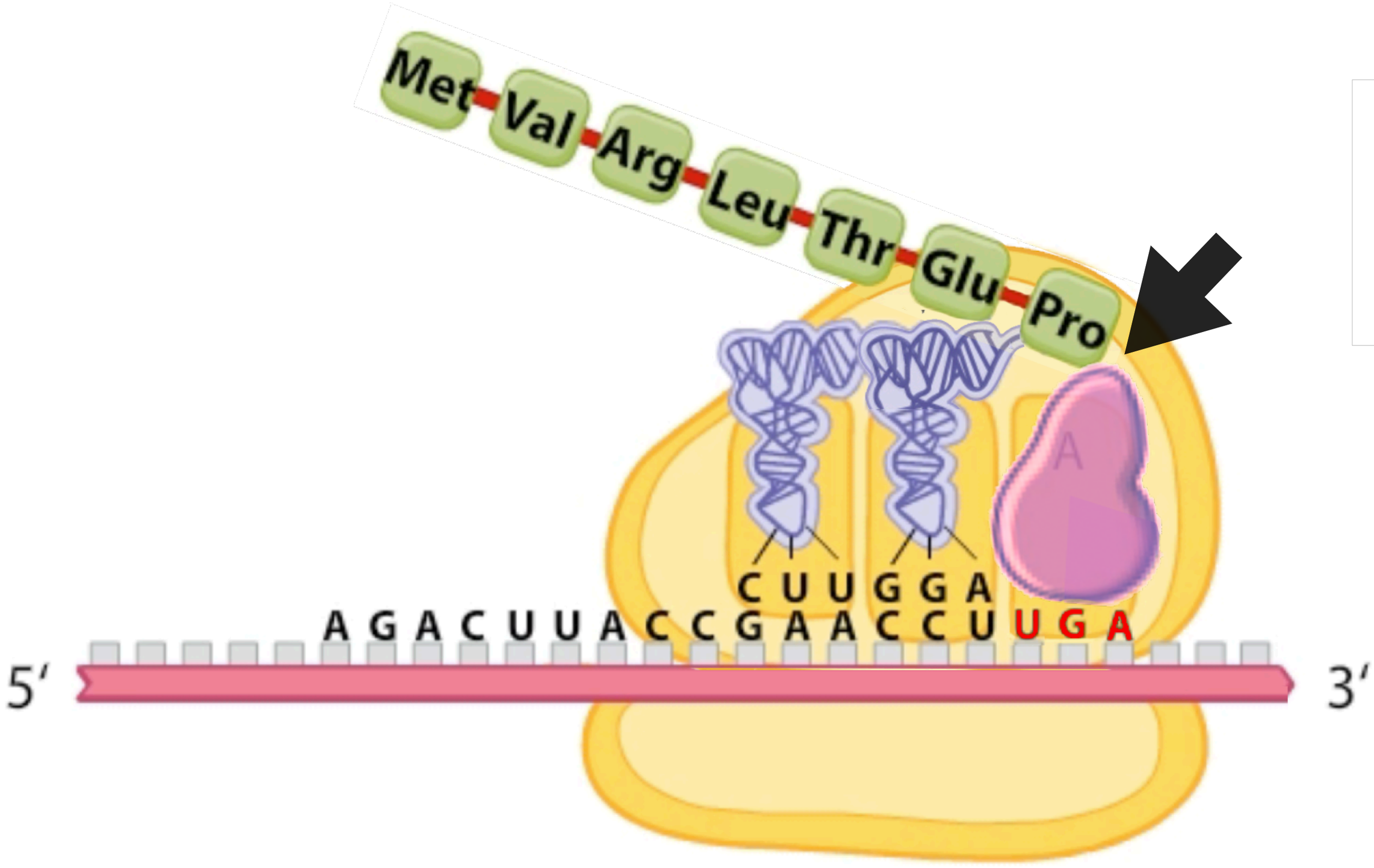

Initiation
Elongation
Termination
Large subunit
Ribosome
5′
Small subunit
mRNA
Polypeptide chain
Direction of translation
3′



Release factors


Met
Val
Arg
Leu
Thr
Glu
Pro
A
C U U G G A
A G A C U U A C C G A A C C U U G A
5′
3′


Met
Val
Arg
Leu
Thr
Glu
Pro
A
C U U G G A
A G A C U U A C C G A A C C U U G A
5′
3′


Met
Val
Arg
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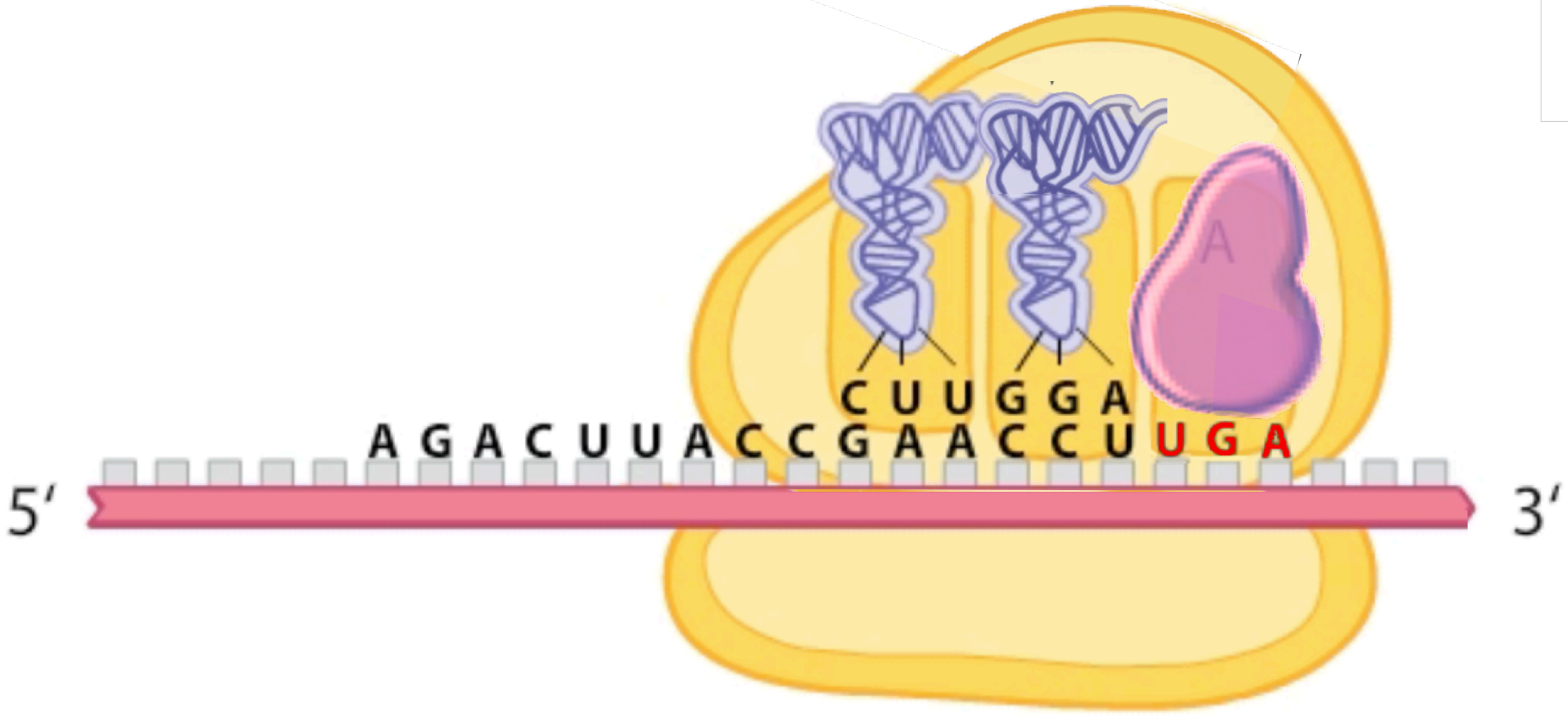
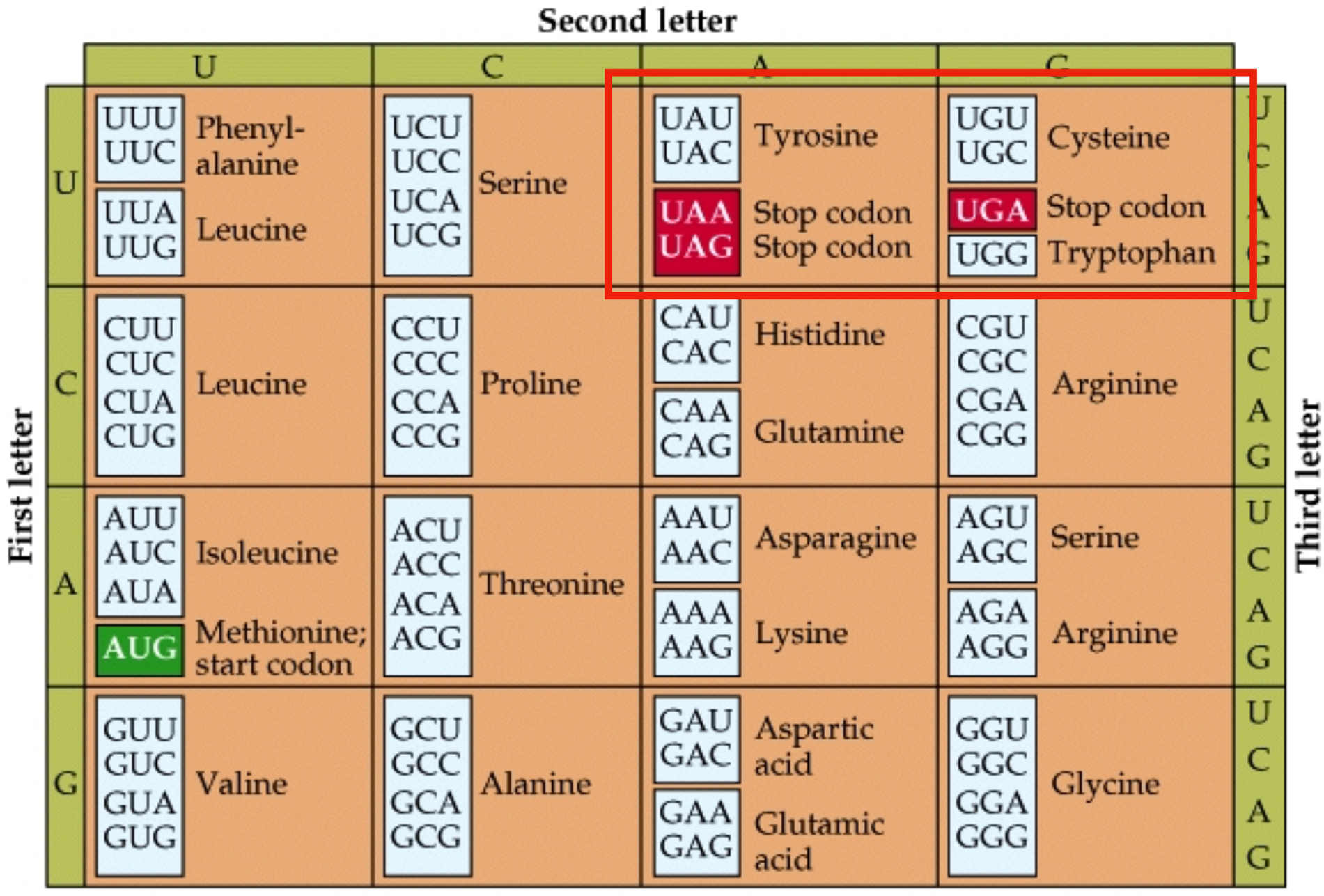
Thr
Glu
Pro
A
C U U G G A
A G A C U U A C C G A A C C U U G A
5′
3′

Leu Thr Glu Pro



“Universal” Genetic Code

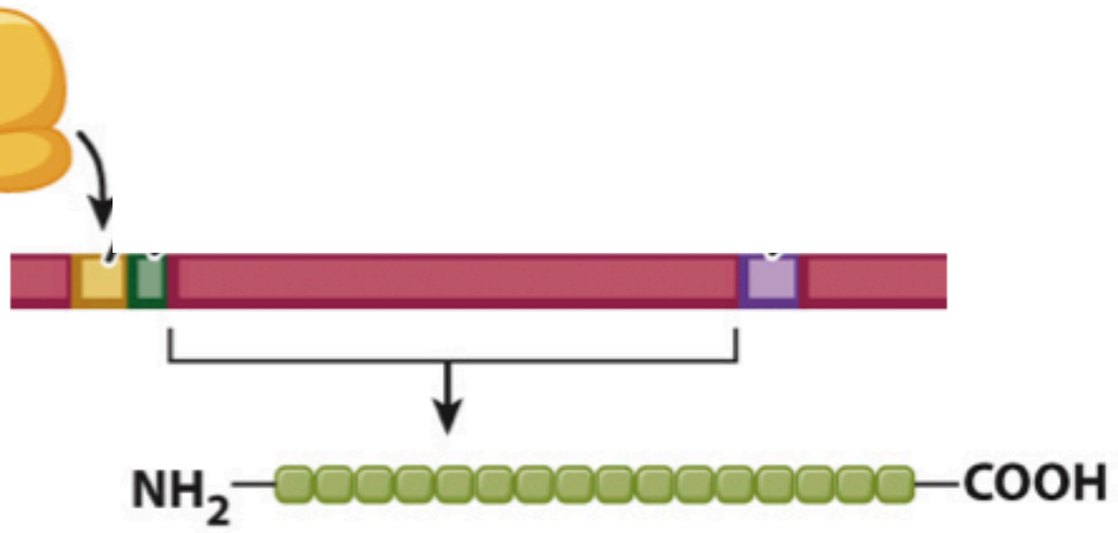


AUG, which codes for the amino acid **methionine**, is called the ***start* codon**, which initiates the translational process.

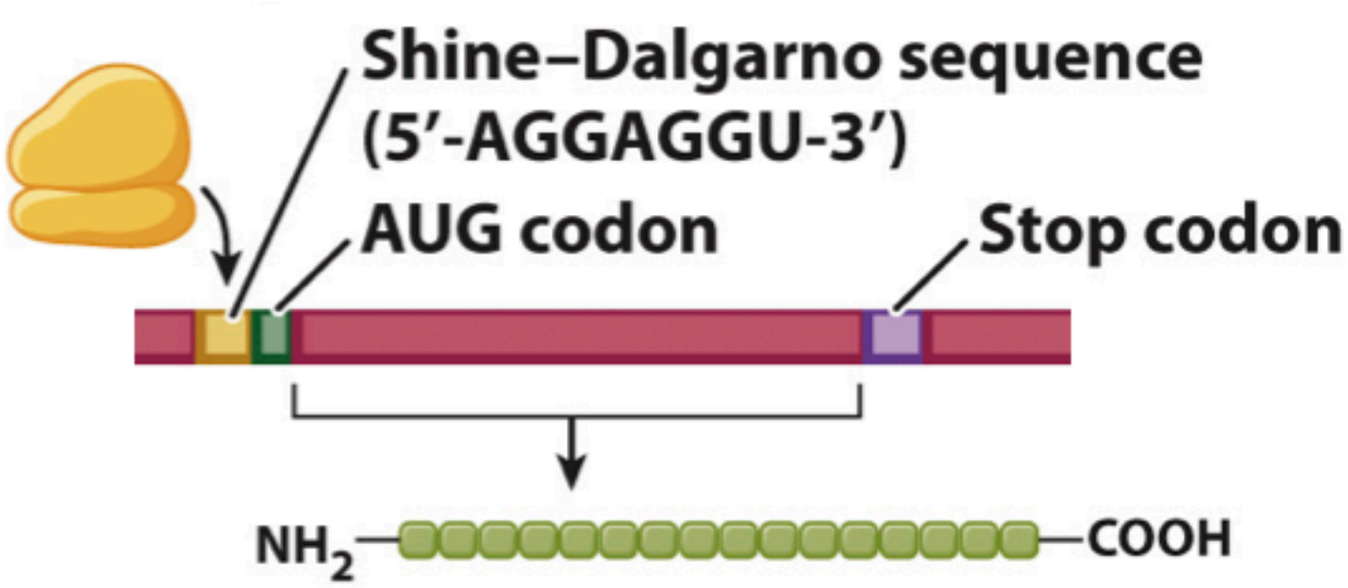
Three of the possible codons are *stop* codons (**UAA**, **UAG**, and **UGA**), which direct the ribosomes to STOP reading the mRNA; that is, they end translation.

Initiation in prokaryotes is at any Shine–Dalgarno sequence; the mRNA can therefore be a polycistronic mRNA that codes for several polypeptides.

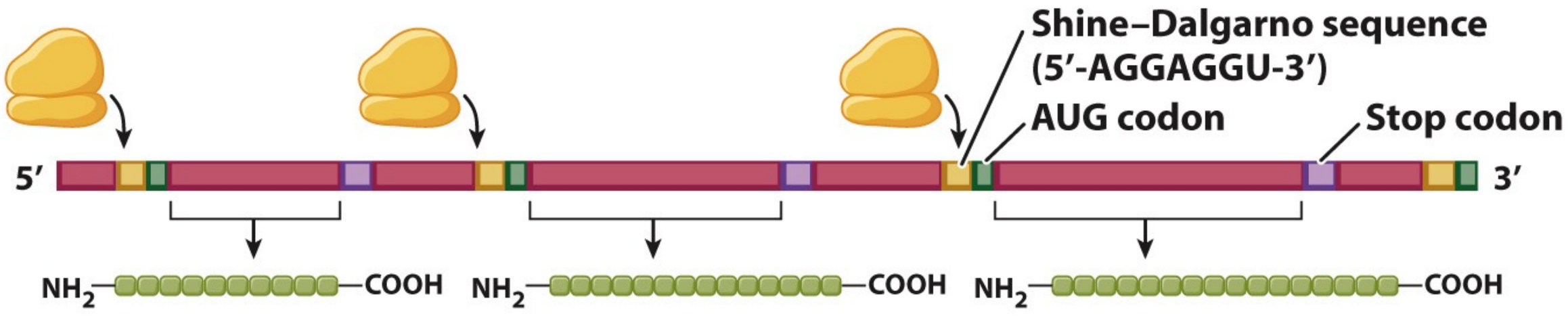
Monocistronic mRNA



Monocistronic mRNA

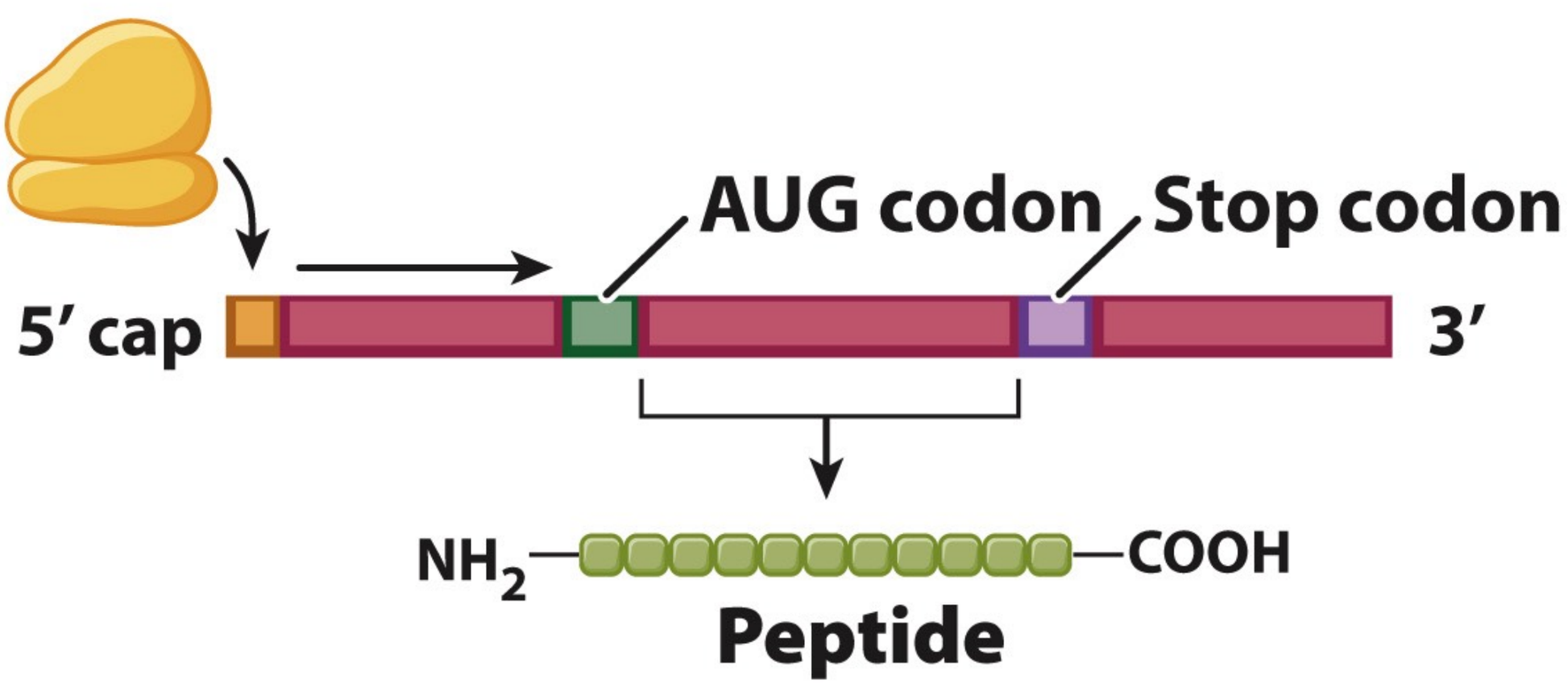


Polycistronic mRNA



Monocistronic mRNA

Initiation in eukaryotes is at the 5′ cap, and the first AUG is the start codon.



Transcription
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RNA processing
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Transport
mRNA travels through nuclear pores into the cytoplasm.

Translation
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Nucleolus

tRNA

DNA

Gene

RNA polymerase

Primary transcript (RNA)

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5′ cap

Exon

Intron

AAAAA

Spliceosome

Intron lariat

RNA transcription begins at a promoter region and continues until a terminator sequence is encountered.

RNA transcript

RNA–DNA duplex

Template DNA

Promoter region

Terminator sequence

5′

3′

Gene

Polymerase movement

Nucleus

Growing polypeptide chain

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tRNA

E site

P site

A site

Thr

Glu

Incoming tRNA charged with amino acid

Anticodon

Ribosome

A G A A C C G A A

U G G

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5′

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mRNA

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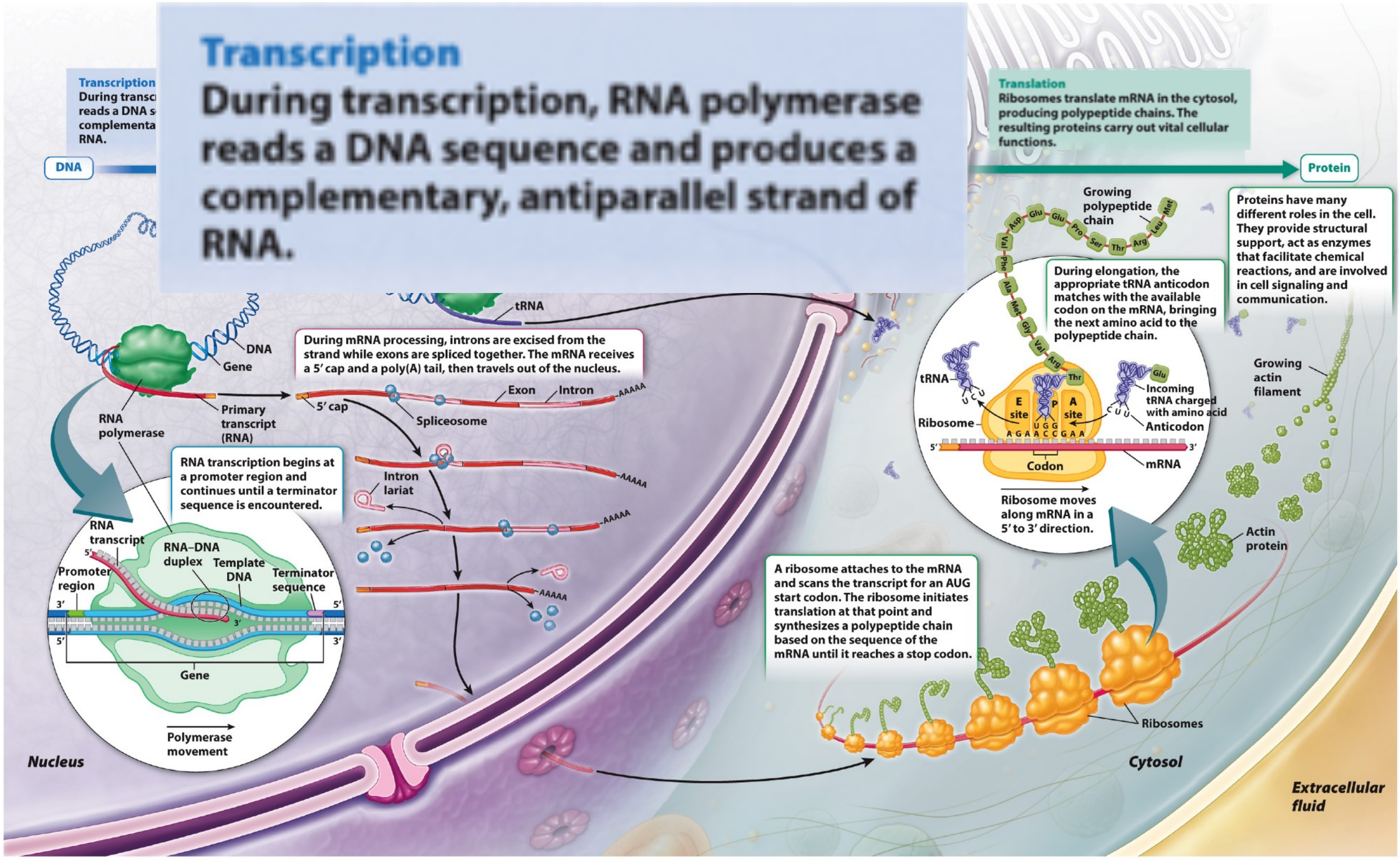

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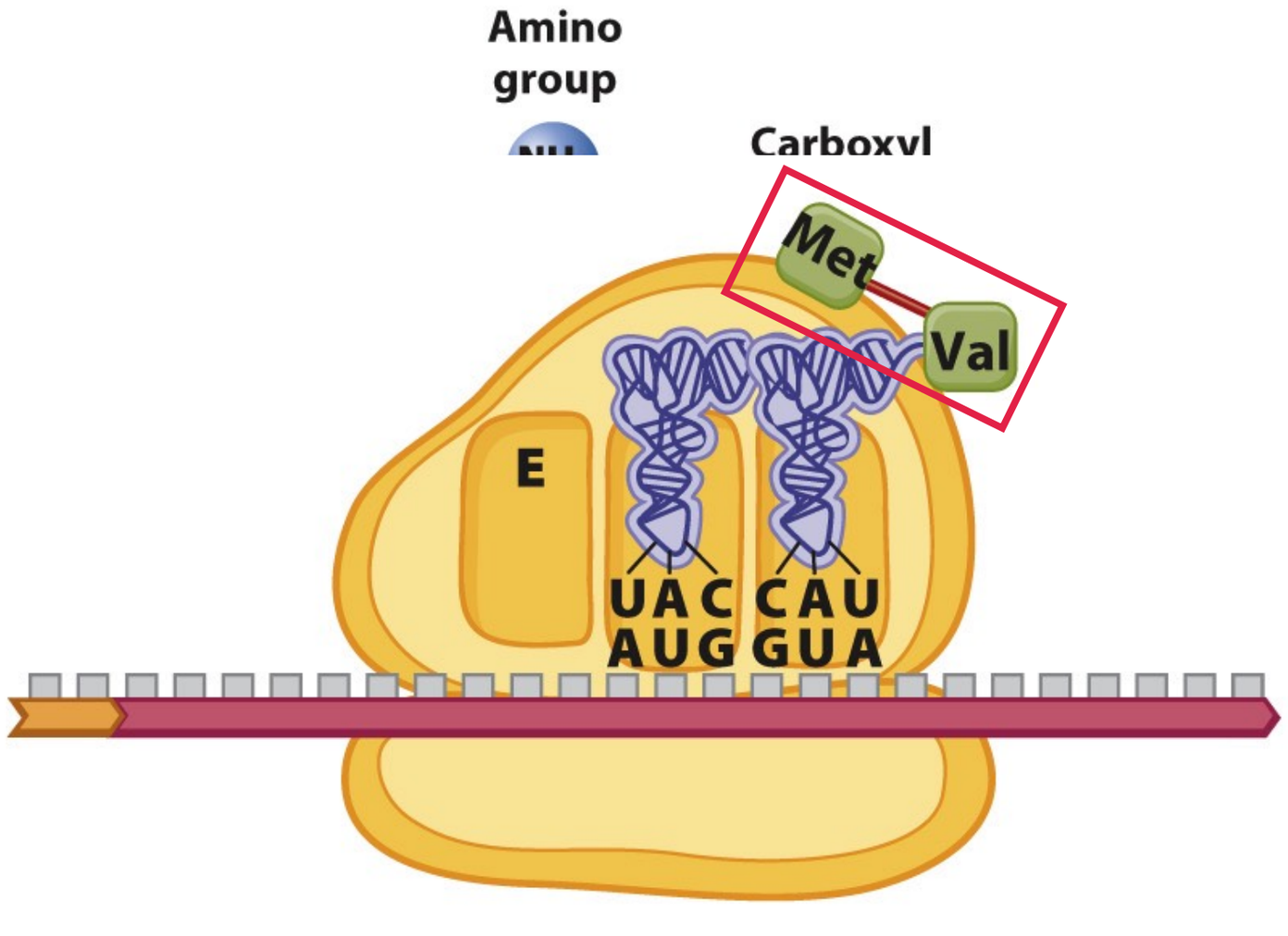
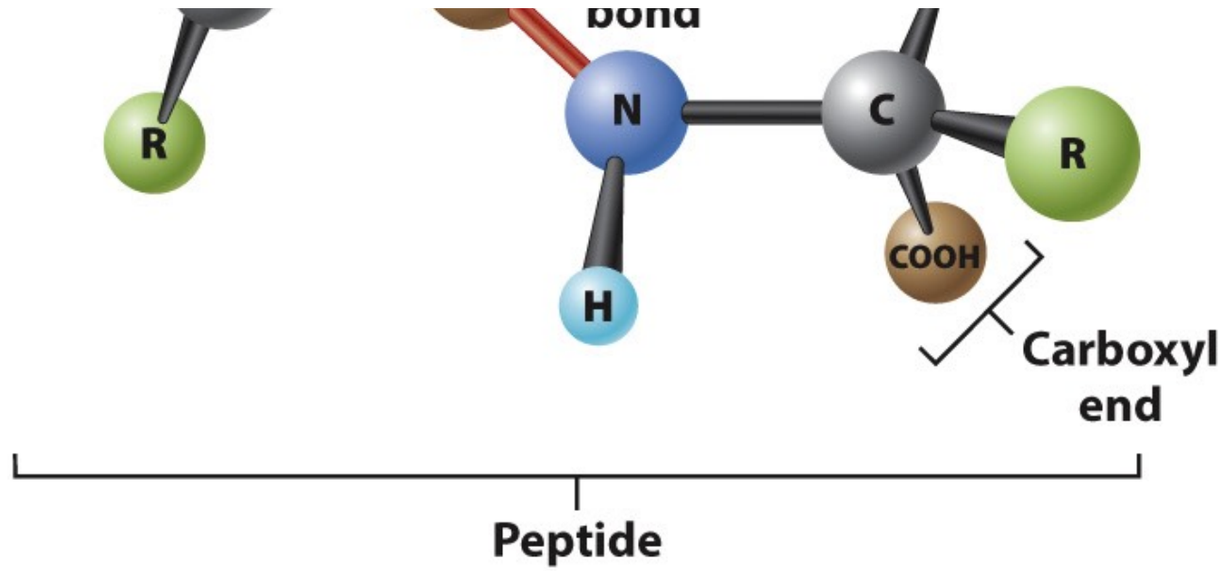
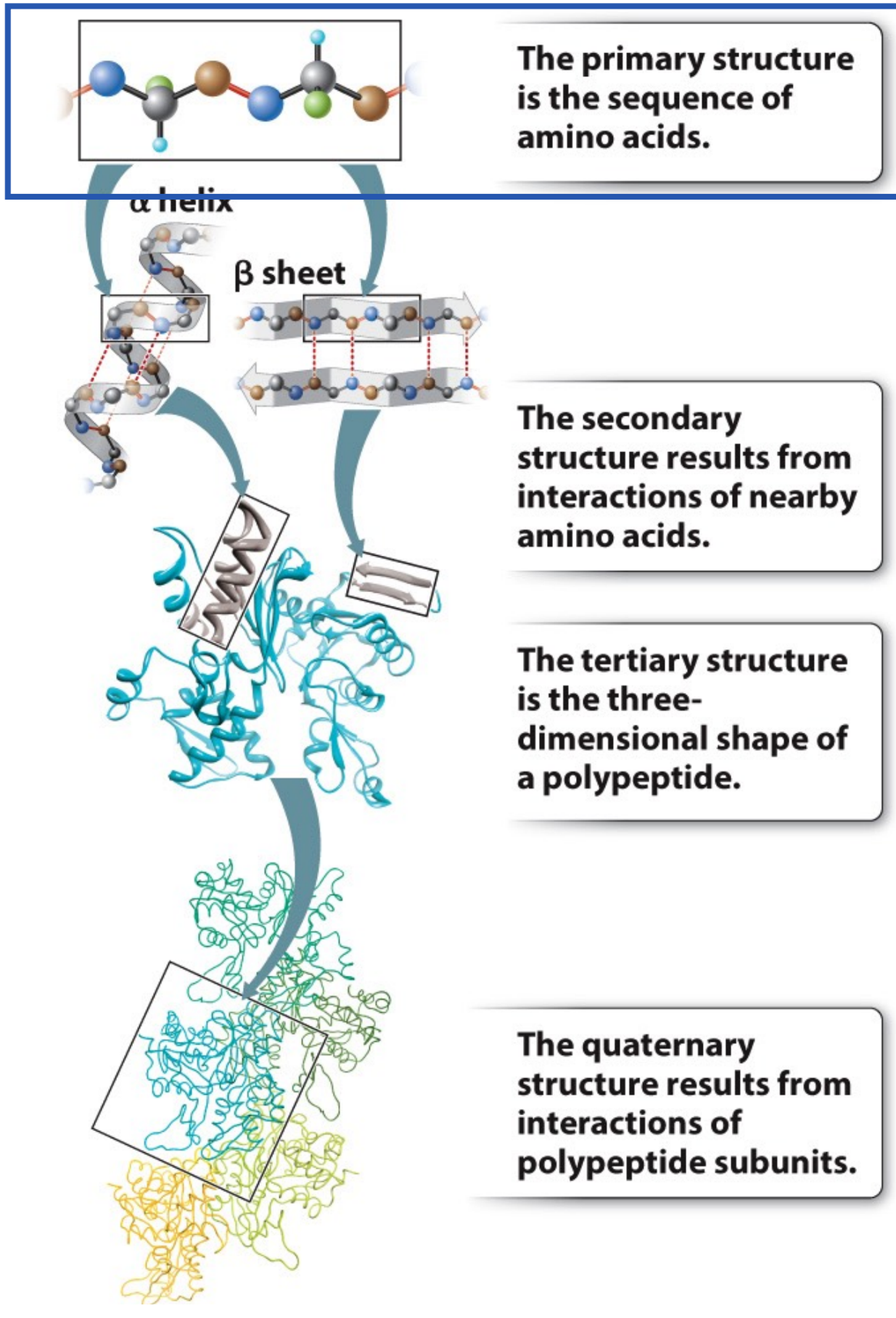


A reaction transfers the Met to the amino acid on the tRNA in the A site, forming a peptide bond.



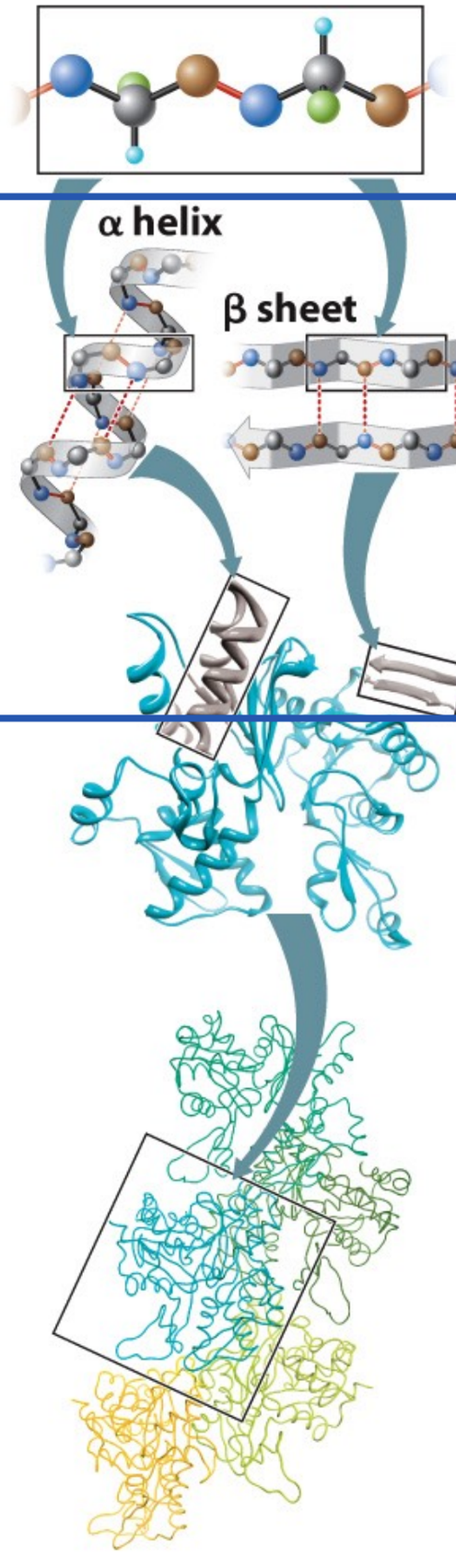


The primary structure is the sequence of amino acids.

The secondary structure results from interactions of nearby amino acids.

The tertiary structure is the three-dimensional shape of a polypeptide.

The quaternary structure results from interactions of polypeptide subunits.



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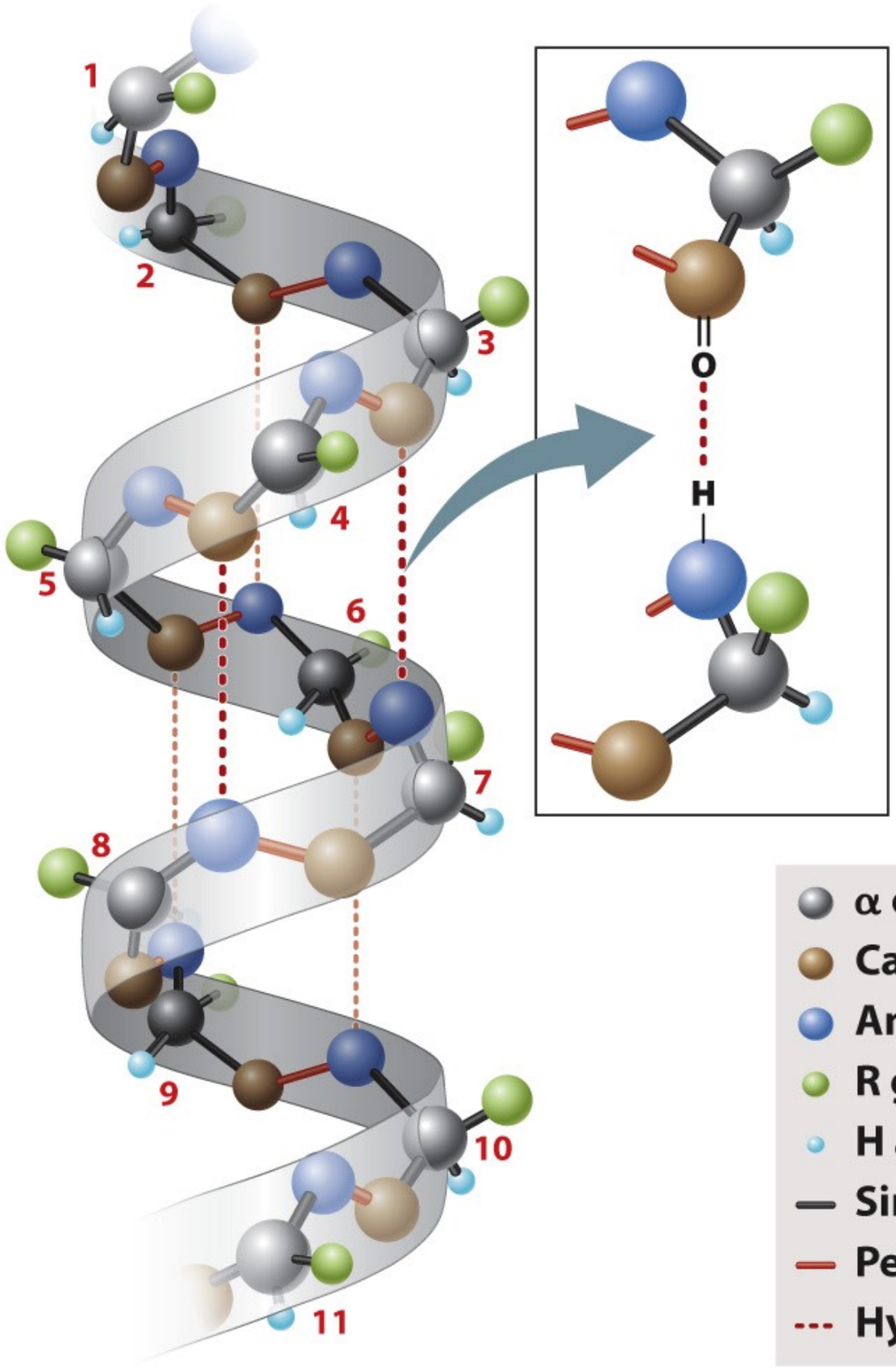
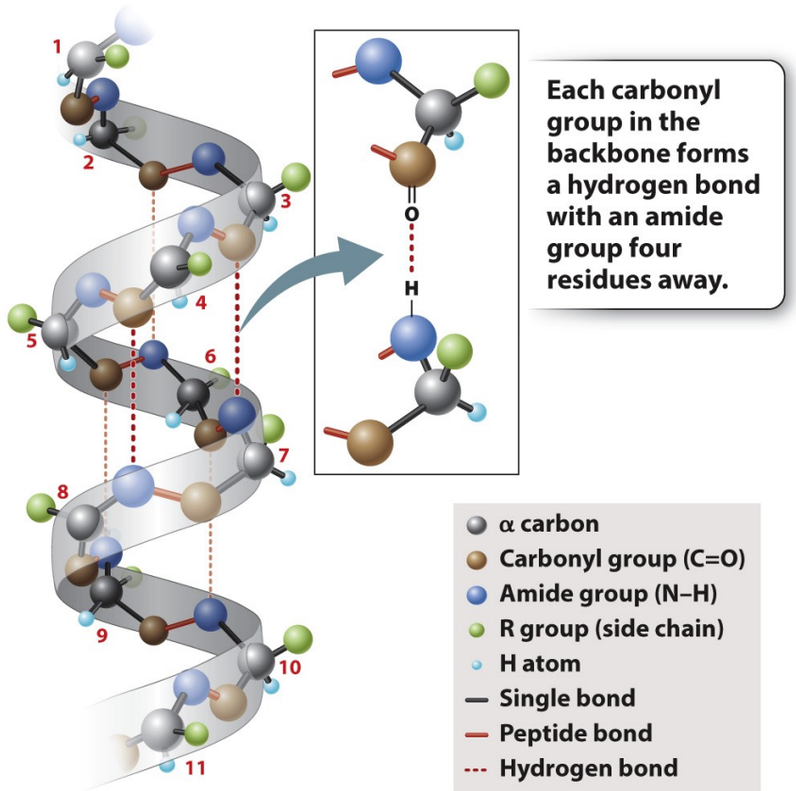


Each carbonyl group in the backbone forms a hydrogen bond with an amide group four residues away.

- α carbon
- Carbonyl group (C=O)
- Amide group (N–H)
- R group (side chain)
- H atom
- Single bond
- Peptide bond
- Hydrogen bond



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R group (side chain)
H atom
Single bond
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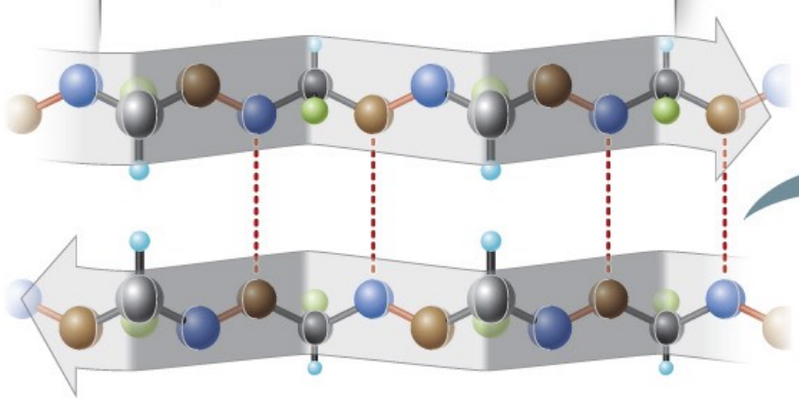
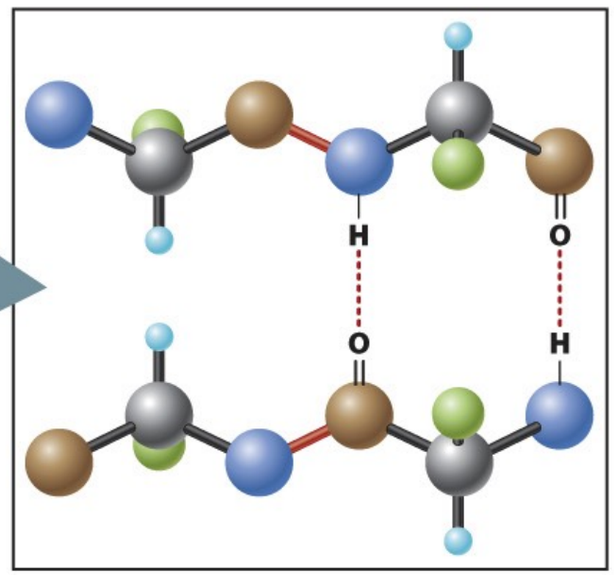
Hydrogen bond

Adjacent strands can run in the same direction (parallel), or in opposite directions (antiparallel), as shown here.



Hydrogen bonds form between carbonyl groups in one polypeptide and amide groups in a different part of the polypeptide.



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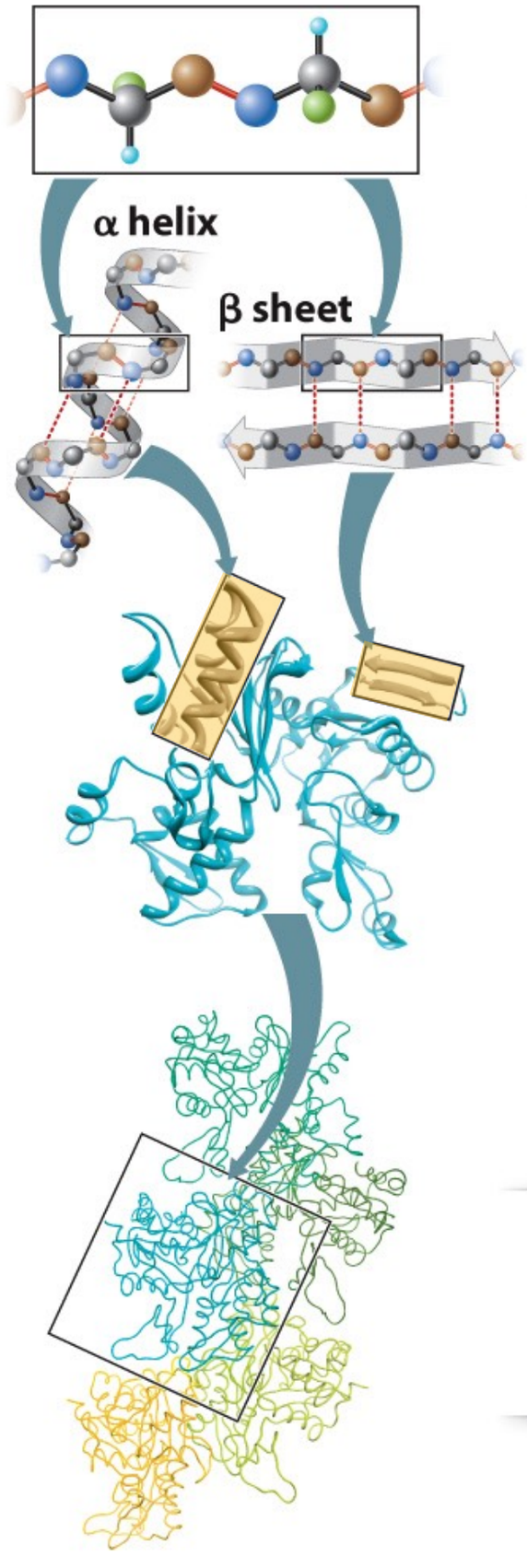

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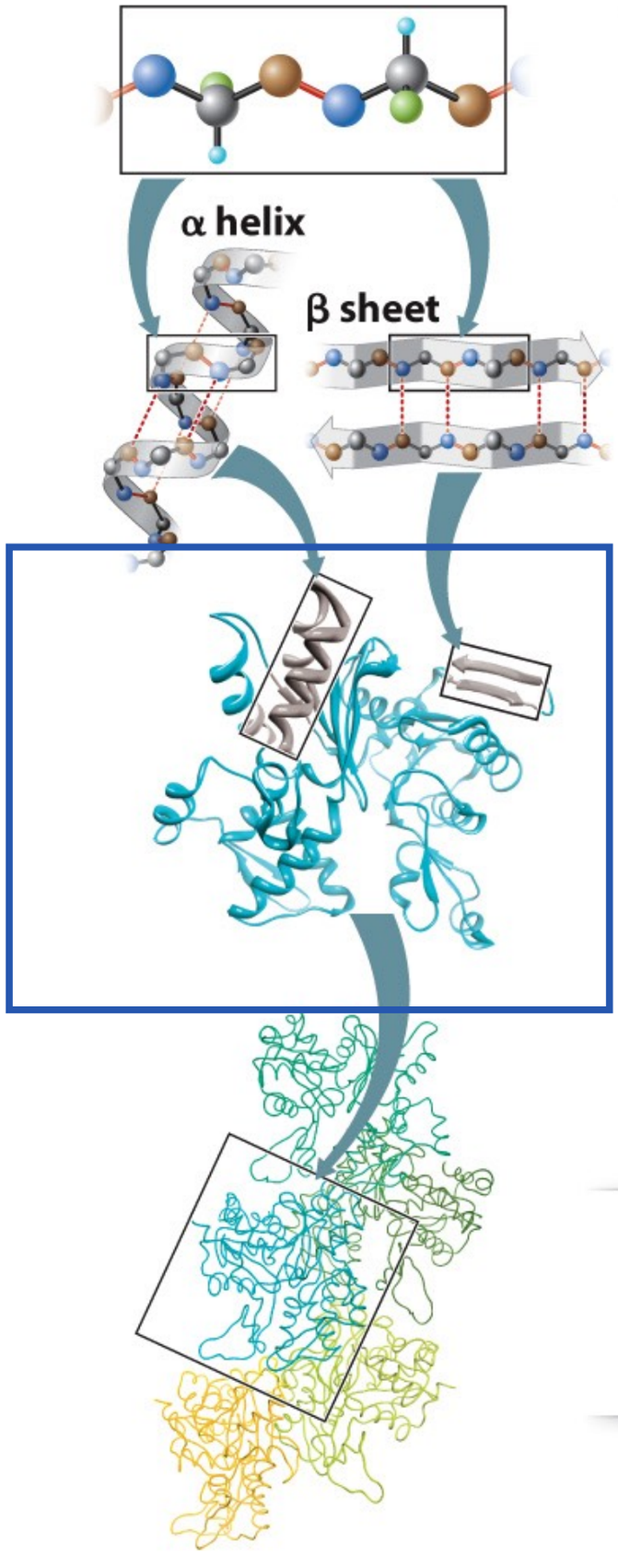

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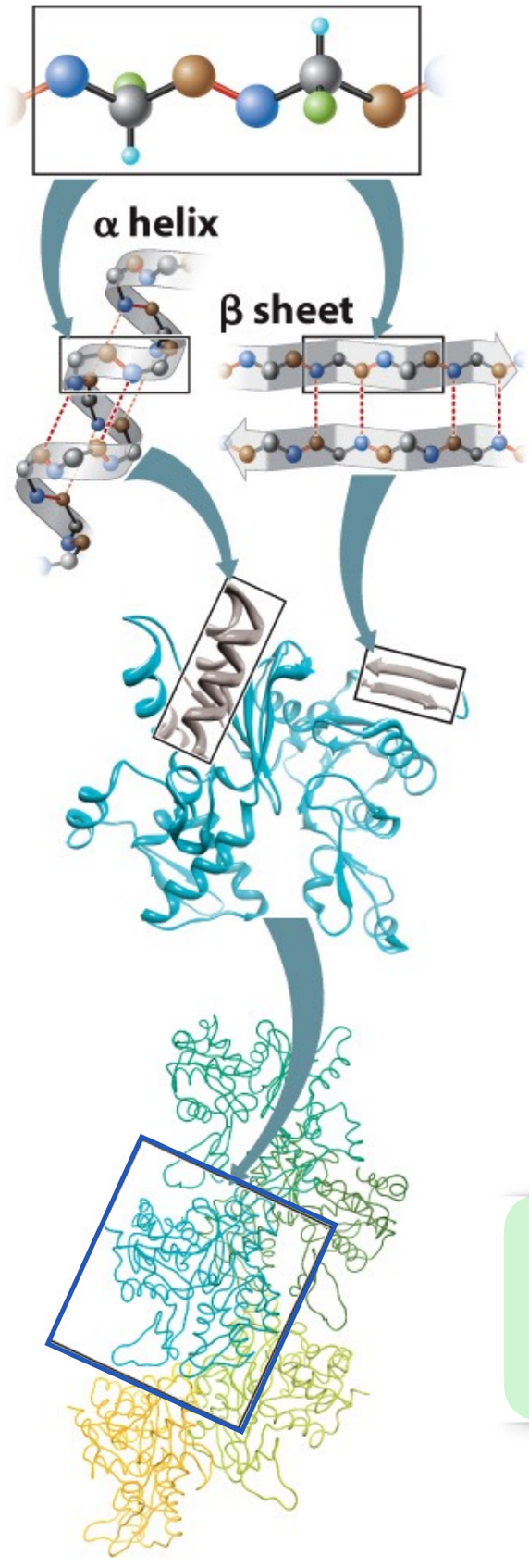

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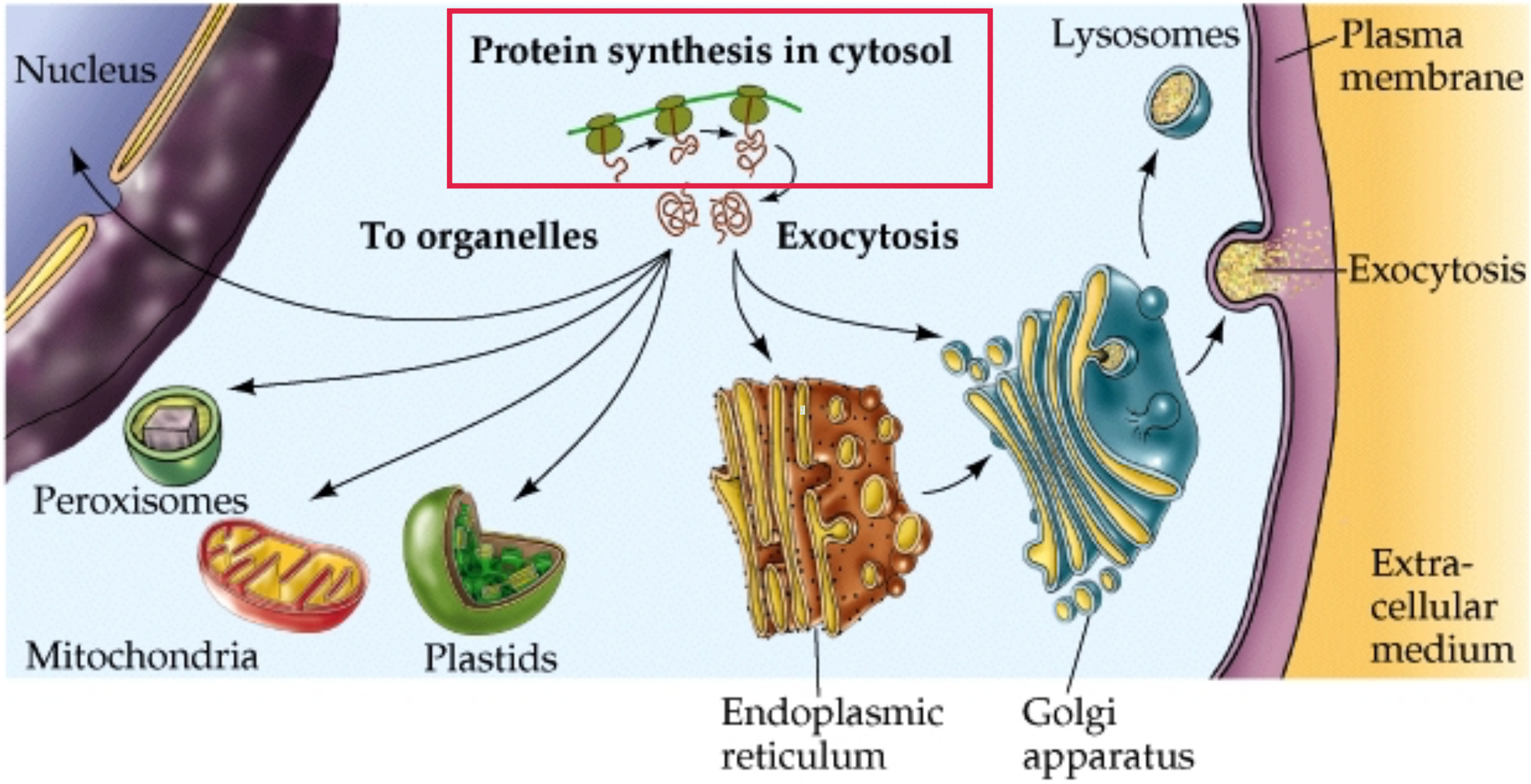
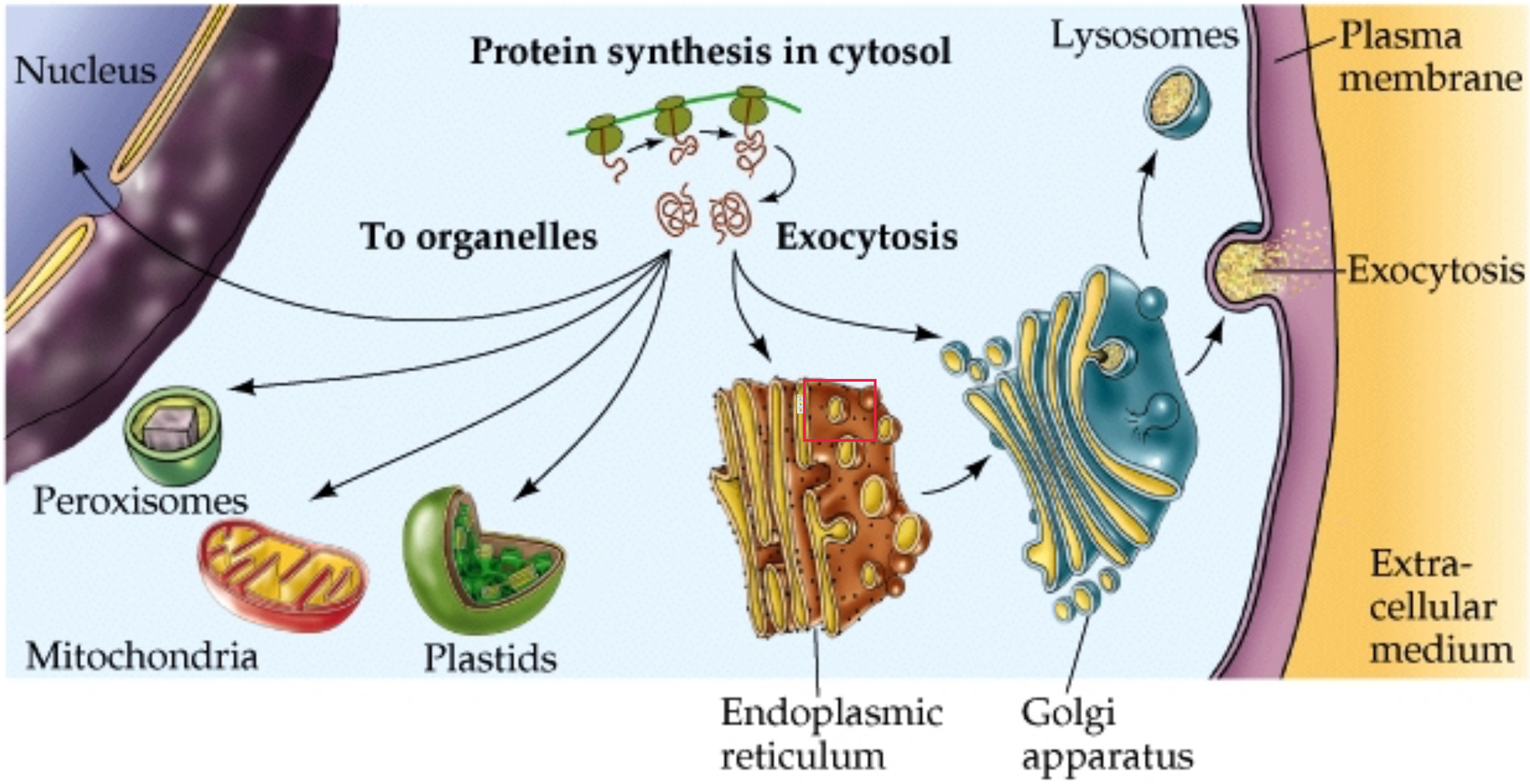
Figure 4.4
Biology: How Life Works, Second Edition


Protein synthesis in cytosol
Nucleus
To organelles
Exocytosis
Lysosomes
Plasma membrane
Exocytosis
Peroxisomes
Mitochondria
Plastids
Endoplasmic reticulum
Golgi apparatus
Extra-cellular medium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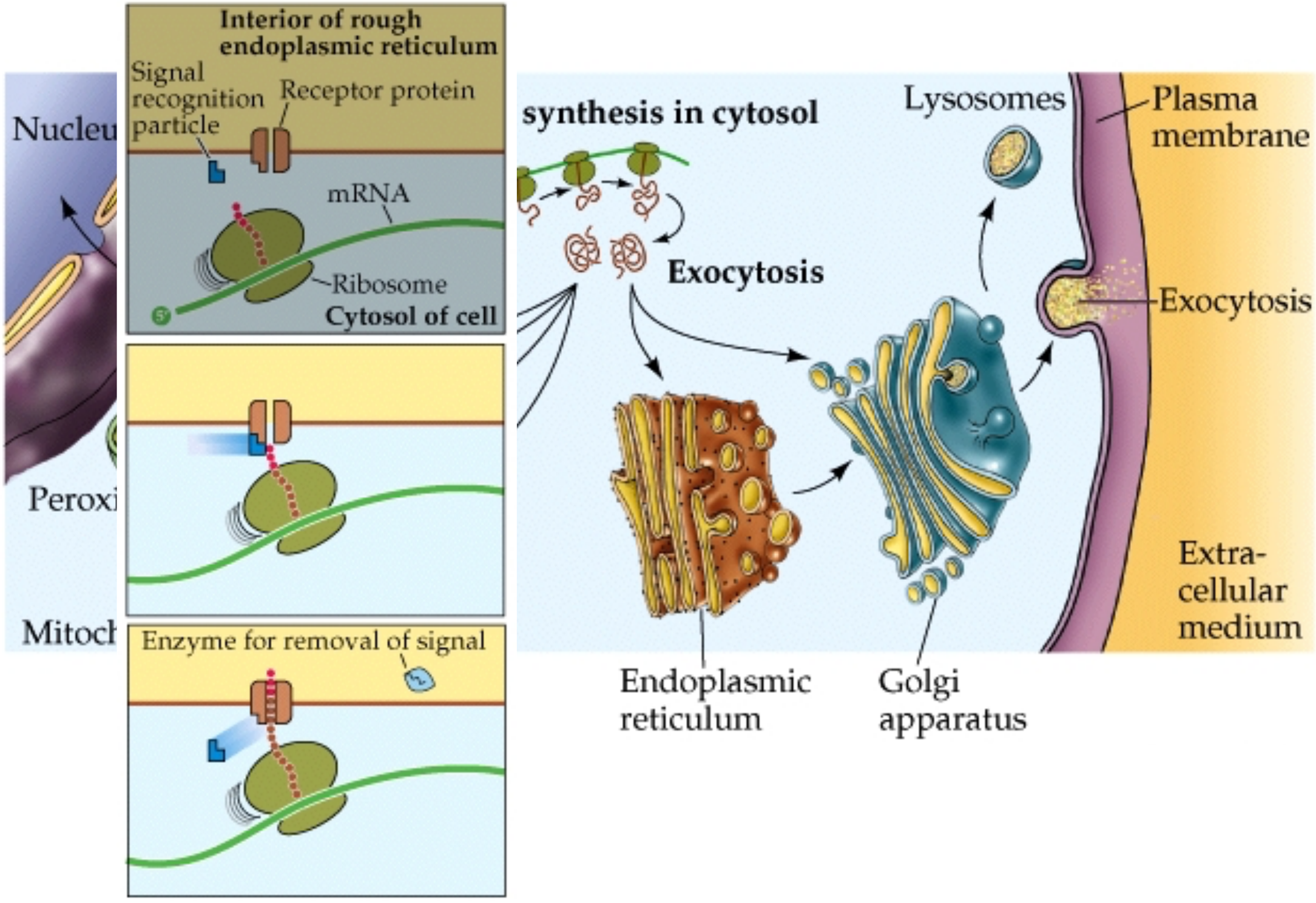
Golgi apparatus
Extra-cellular medium


Nucleu
Peroxi
Mitoch
Interior of rough endoplasmic reticulum
Signal recognition particle
Receptor protein
mRNA
Ribosome
Cytosol of cell
Enzyme for removal of signal
synthesis in cytosol
Exocytosis
Lysosomes
Plasma membrane
Exocytosis
Extra-cellular medium
Endoplasmic reticulum
Golgi apparatus

Nucleu

Peroxi

Mitoch

Interior of rough endoplasmic reticulum

Signal recognition particle

Receptor protein

mRNA

Ribosome

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synthesis in cytosol

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Lysosomes

Plasma membrane

Exocytosis

Extra-cellular medium

Endoplasmic reticulum

Golgi apparatus

Nucleu

Peroxi

Mitoch

Interior of rough endoplasmic reticulum

Signal recognition particle

Receptor protein

mRNA

Ribosome

5'

Cytosol of cell

Enzyme for removal of signal

synthesis in cytosol

Excised signal

3'

Completed protein

Ribosome released

3'

Lysosomes

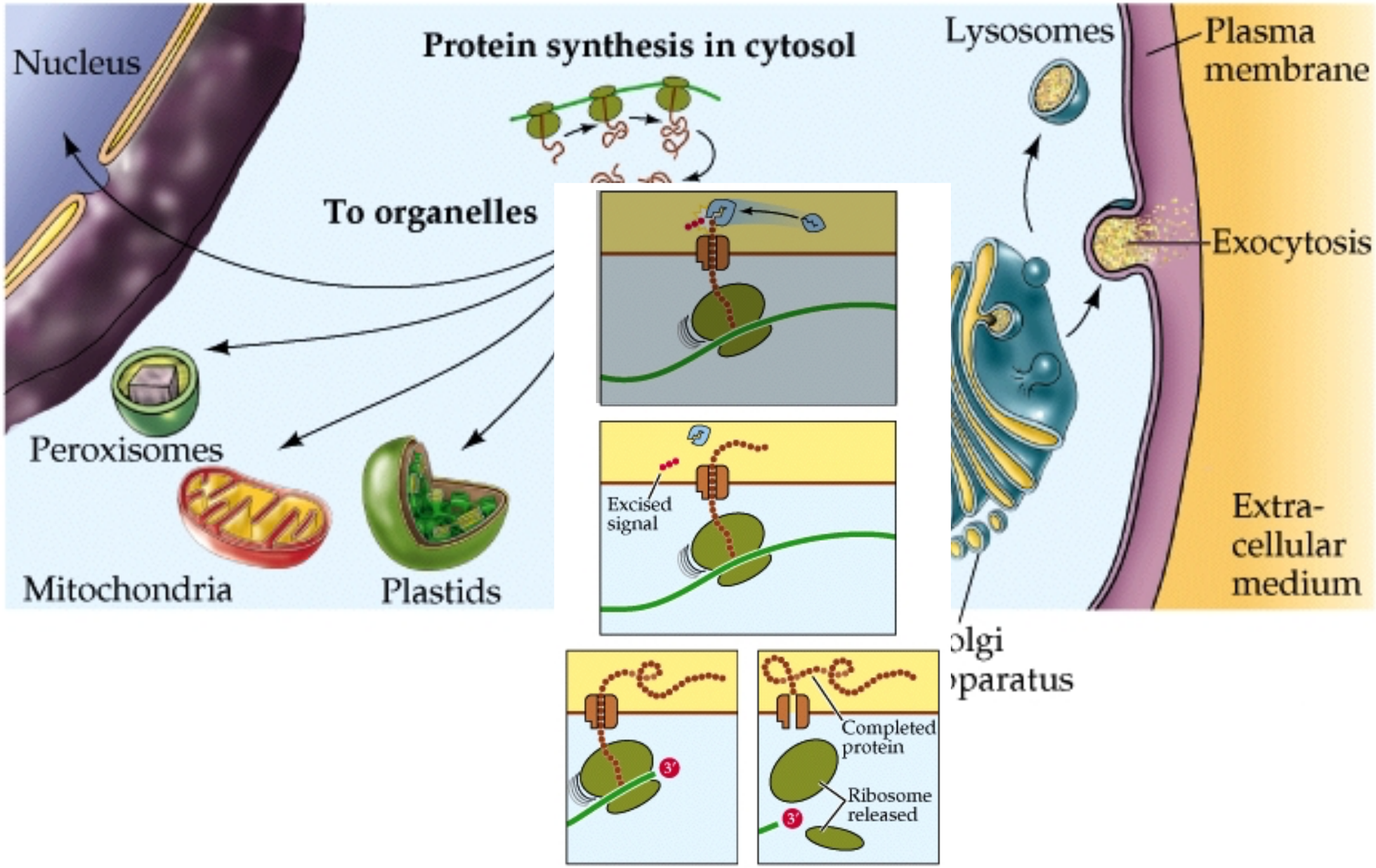
Plasma membrane

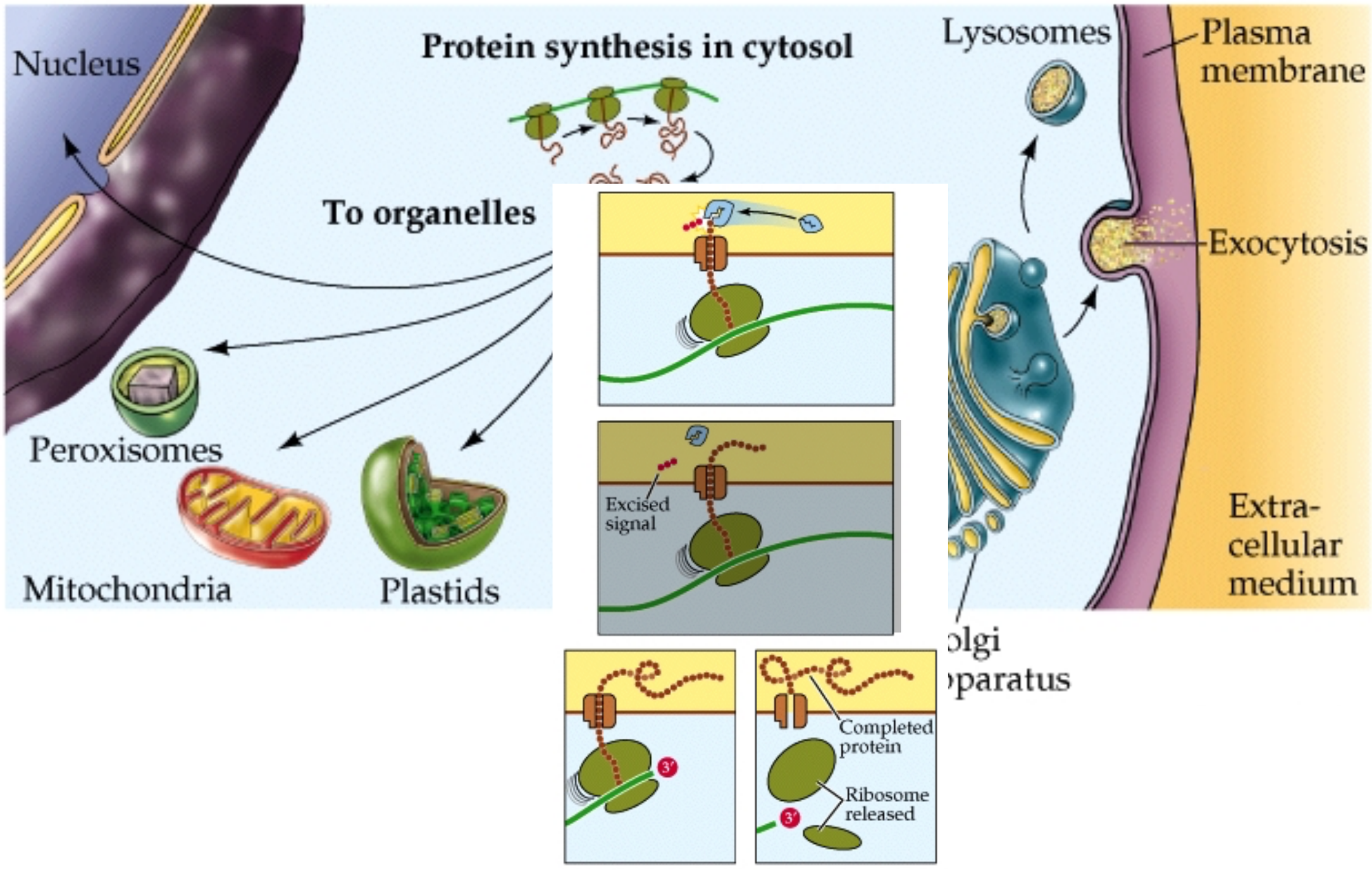
Exocytosis

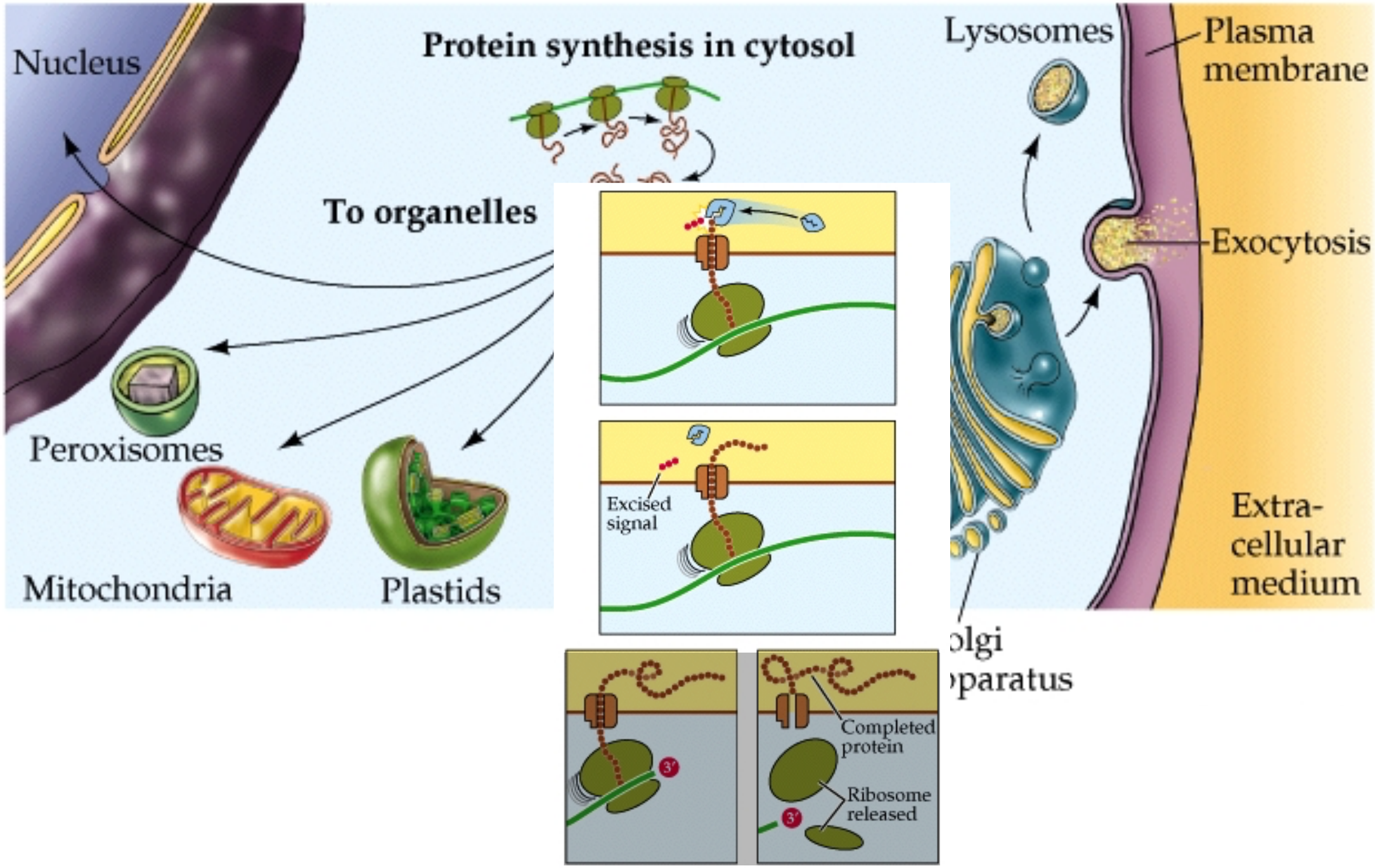
Extra-cellular medium

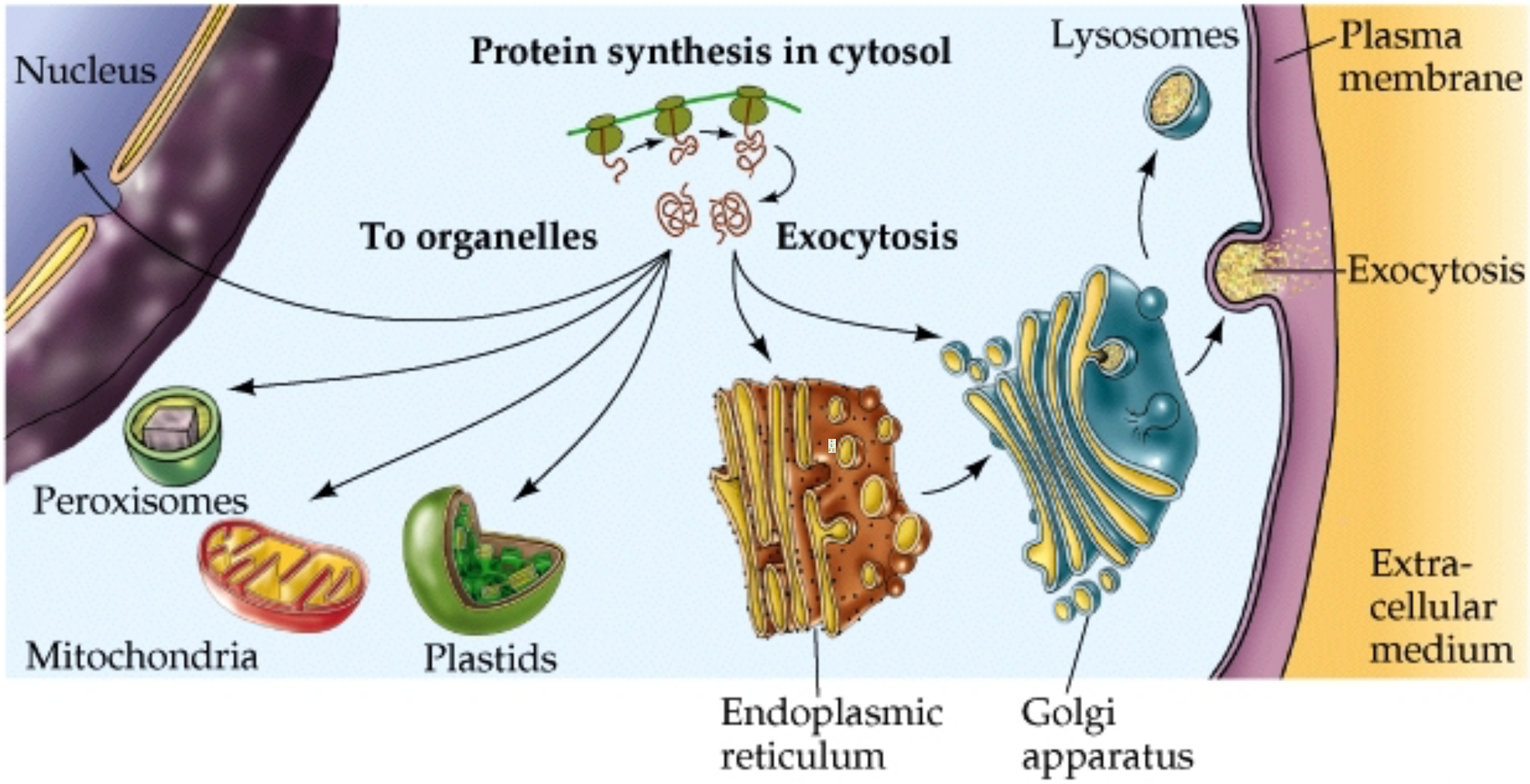
olgi

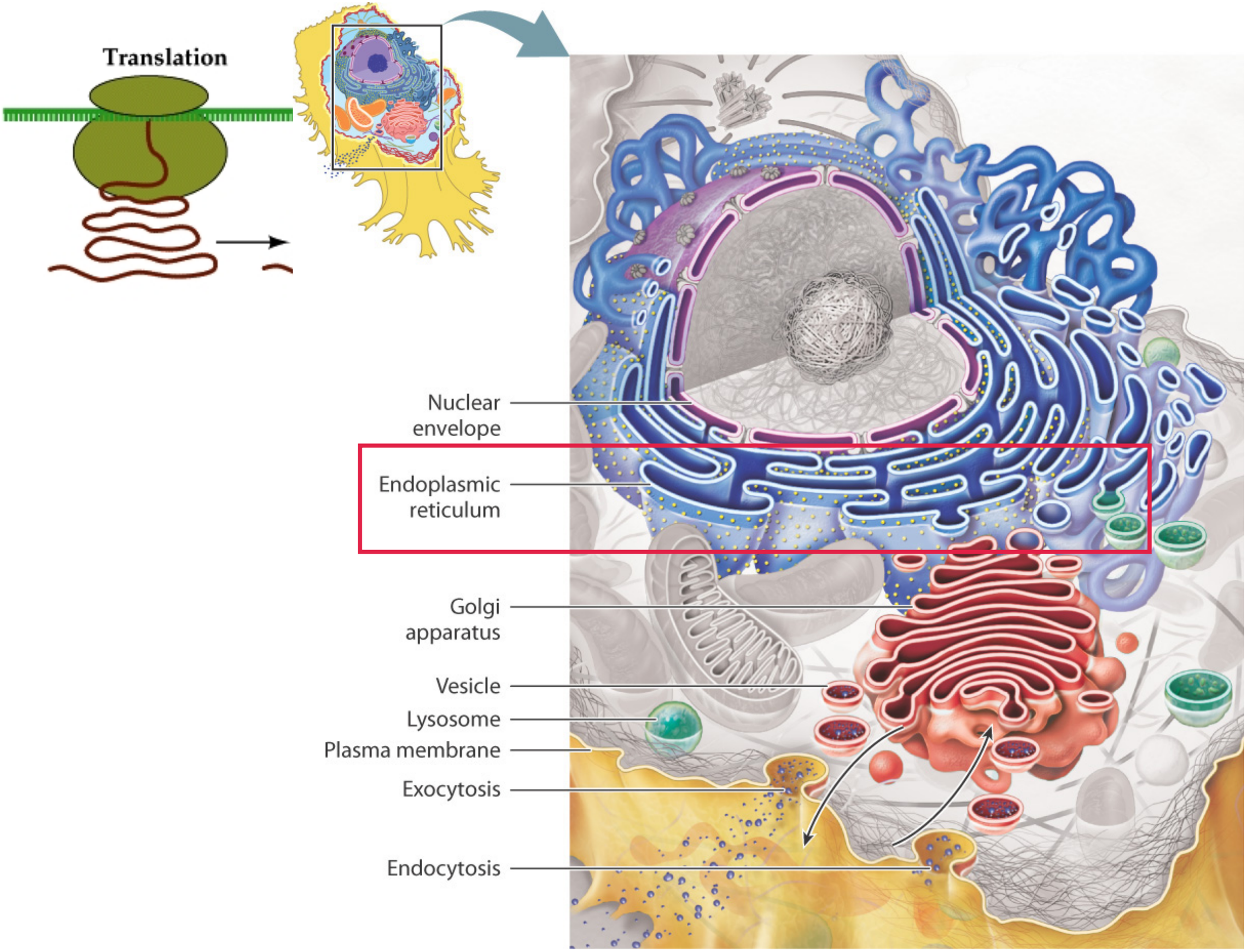
paratus

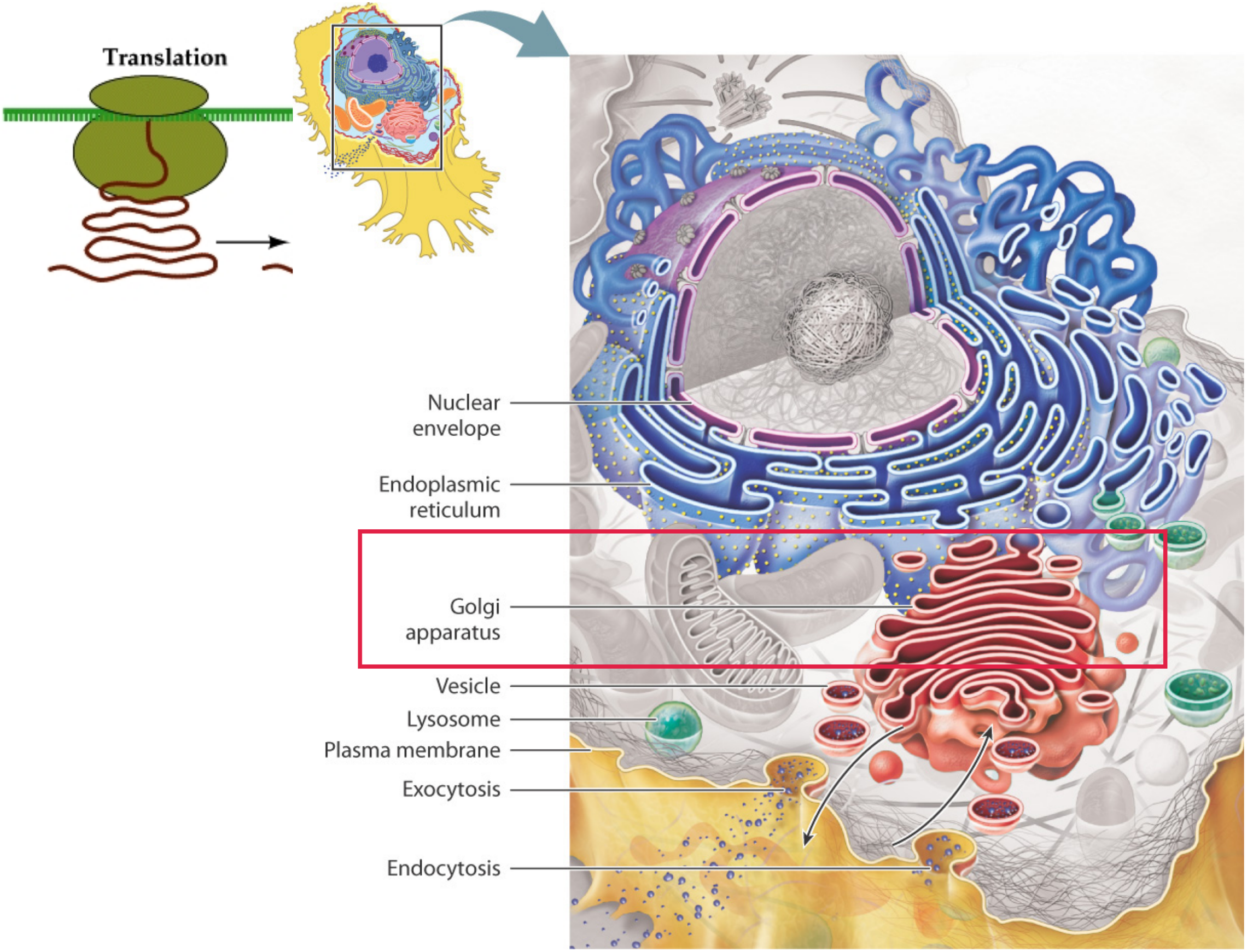

Protein synthesis in cytosol
Nucleus
To organelles
Peroxisomes
Mitochondria
Plastids
Excised signal
3′
Completed protein
Ribosome released
3′
Lysosomes
Plasma membrane
Exocytosis
Extra-cellular medium
olgi
paratus

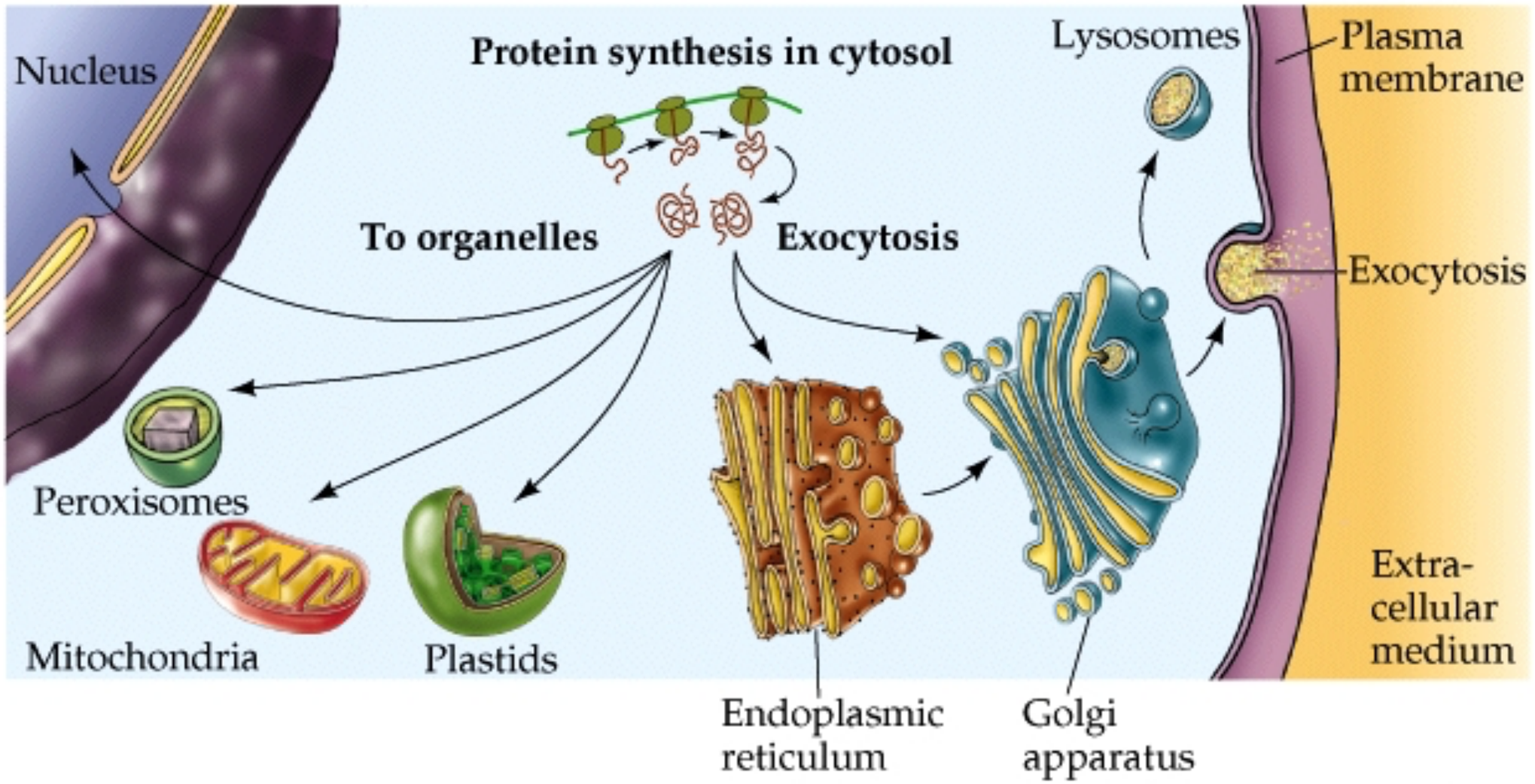

Nucleus
Protein synthesis in cytosol
To organelles
Peroxisomes
Mitochondria
Plastids
Lysosomes
Plasma membrane
Exocytosis
Extra-cellular medium
olgi
paratus
Excised signal
3′
Completed protein
Ribosome released
3′

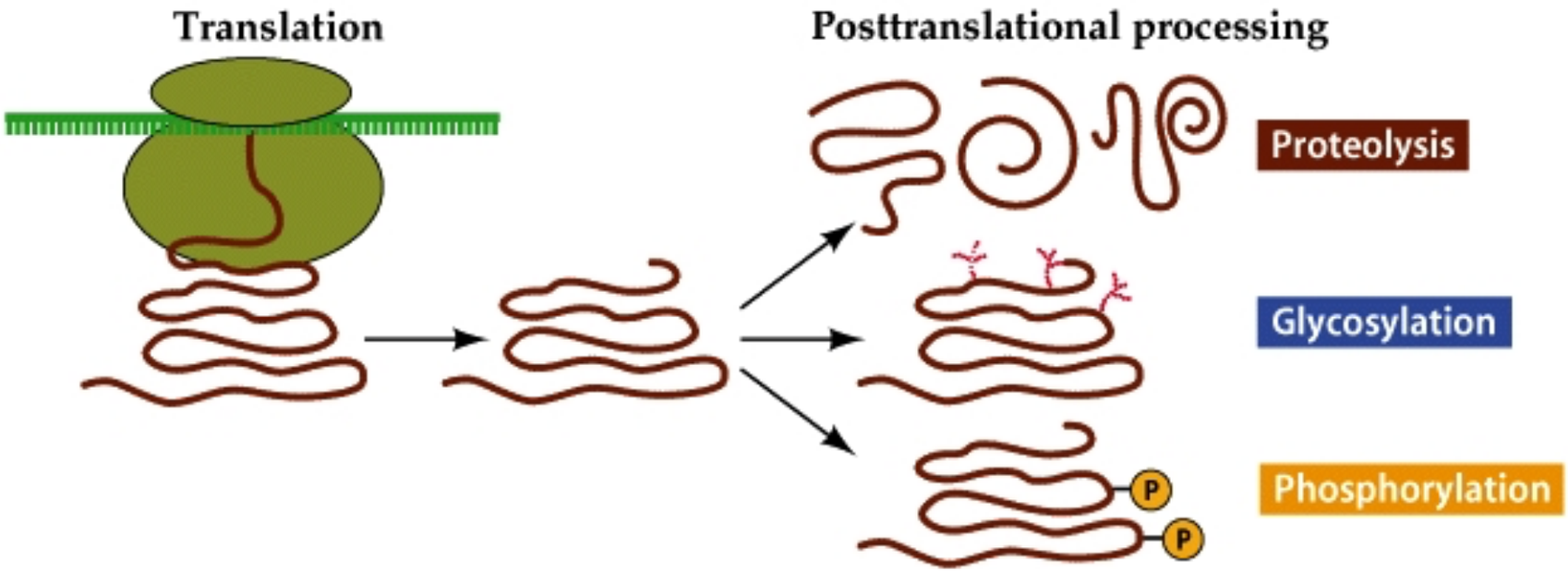

Protein synthesis in cytosol
Nucleus
To organelles
Peroxisomes
Mitochondria
Plastids
Excised signal
3′
Completed protein
Ribosome released
Lysosomes
Plasma membrane
Exocytosis
Extra-cellular medium
olgi
paratus

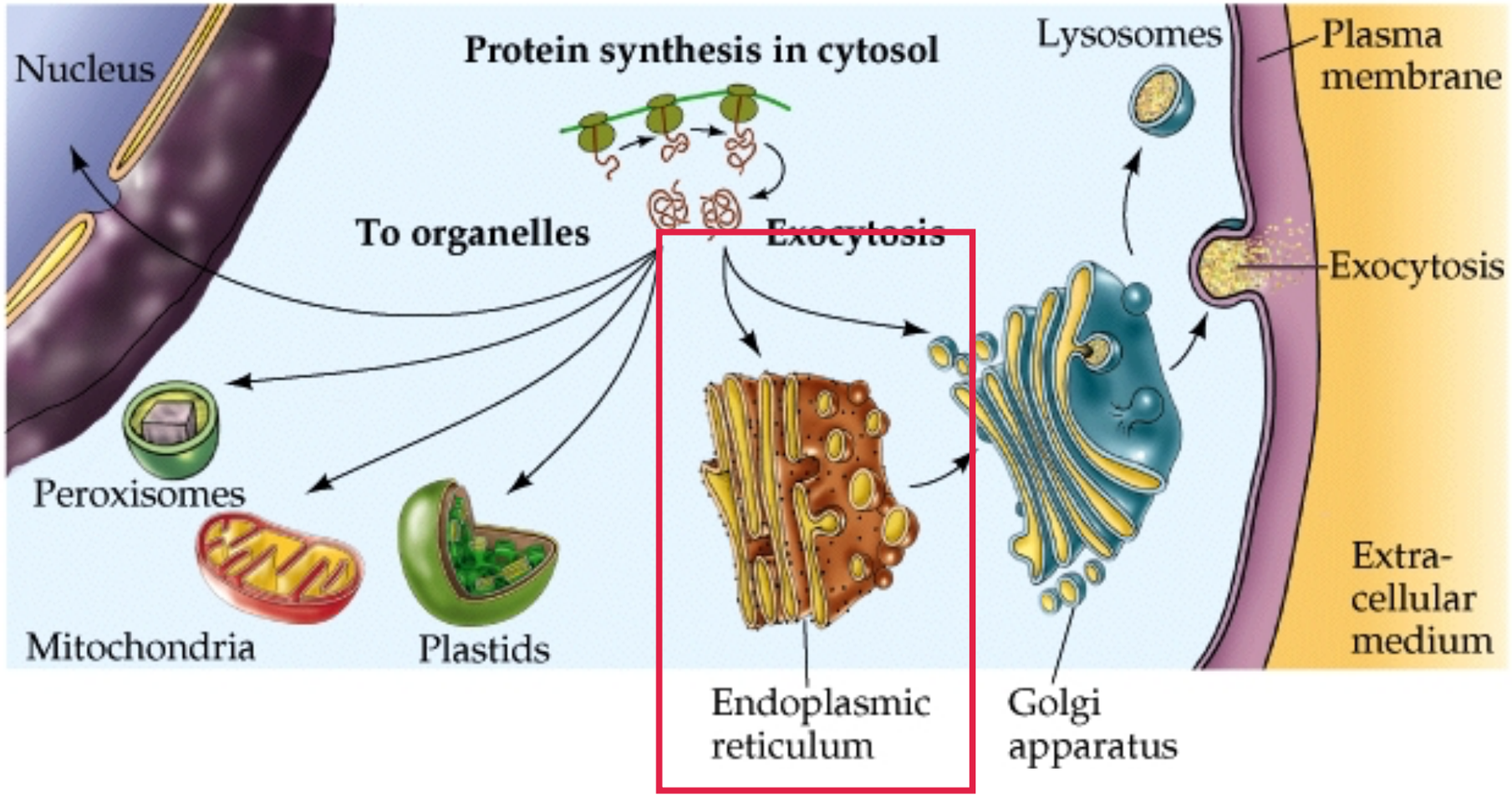

Nucleus
Protein synthesis in cytosol
Lysosomes
Plasma membrane
To organelles
Exocytosis
Exocytosis
Peroxisomes
Mitochondria
Plastids
Endoplasmic reticulum
Golgi apparatus
Extra-cellular medium


Translation
Nuclear envelope
Endoplasmic reticulum
Golgi apparatus
Vesicle
Lysosome
Plasma membrane
Exocytosis
Endocytosis


Translation
Nuclear envelope
Endoplasmic reticulum
Golgi apparatus
Vesicle
Lysosome
Plasma membrane
Exocytosis
Endocytosis


Nucleus
Protein synthesis in cytosol
Lysosomes
Plasma membrane
To organelles
Exocytosis
Exocytosis
Peroxisomes
Mitochondria
Plastids
Endoplasmic reticulum
Golgi apparatus
Extra-cellular medium


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


Nucleus
Protein synthesis in cytosol
Lysosomes
Plasma membrane
To organelles
Exocytosis
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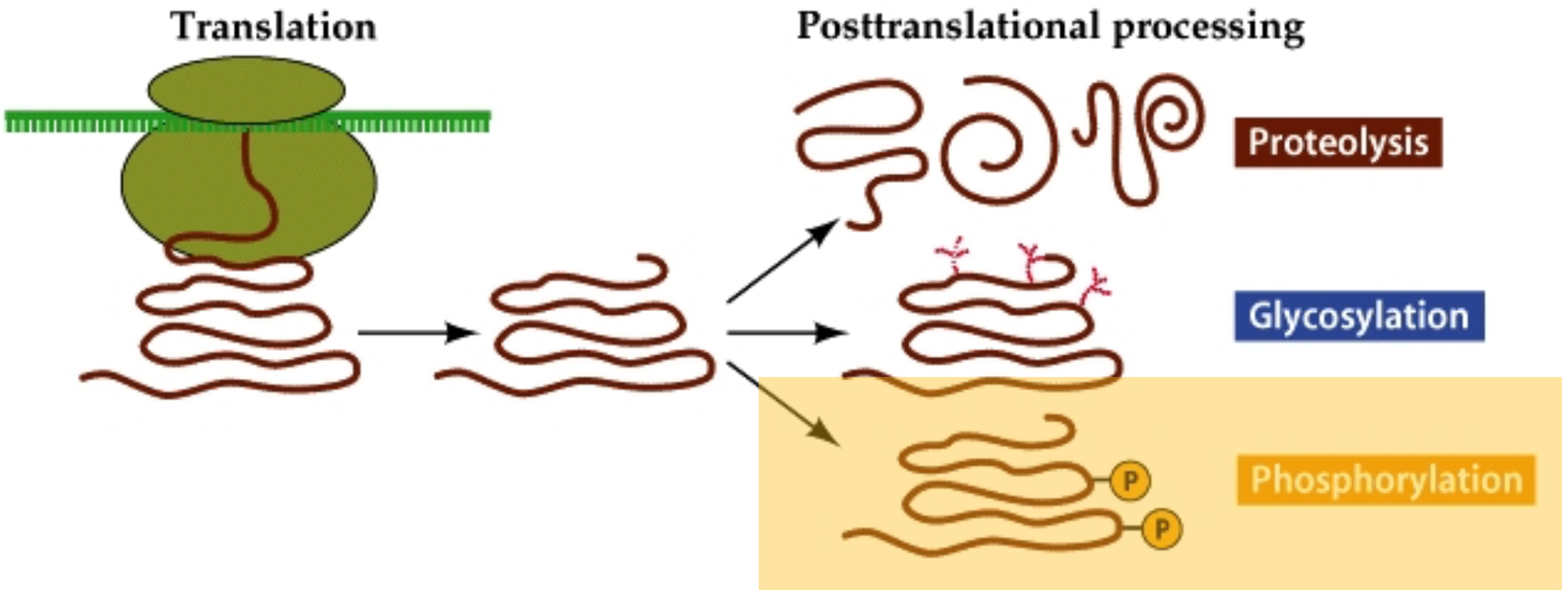
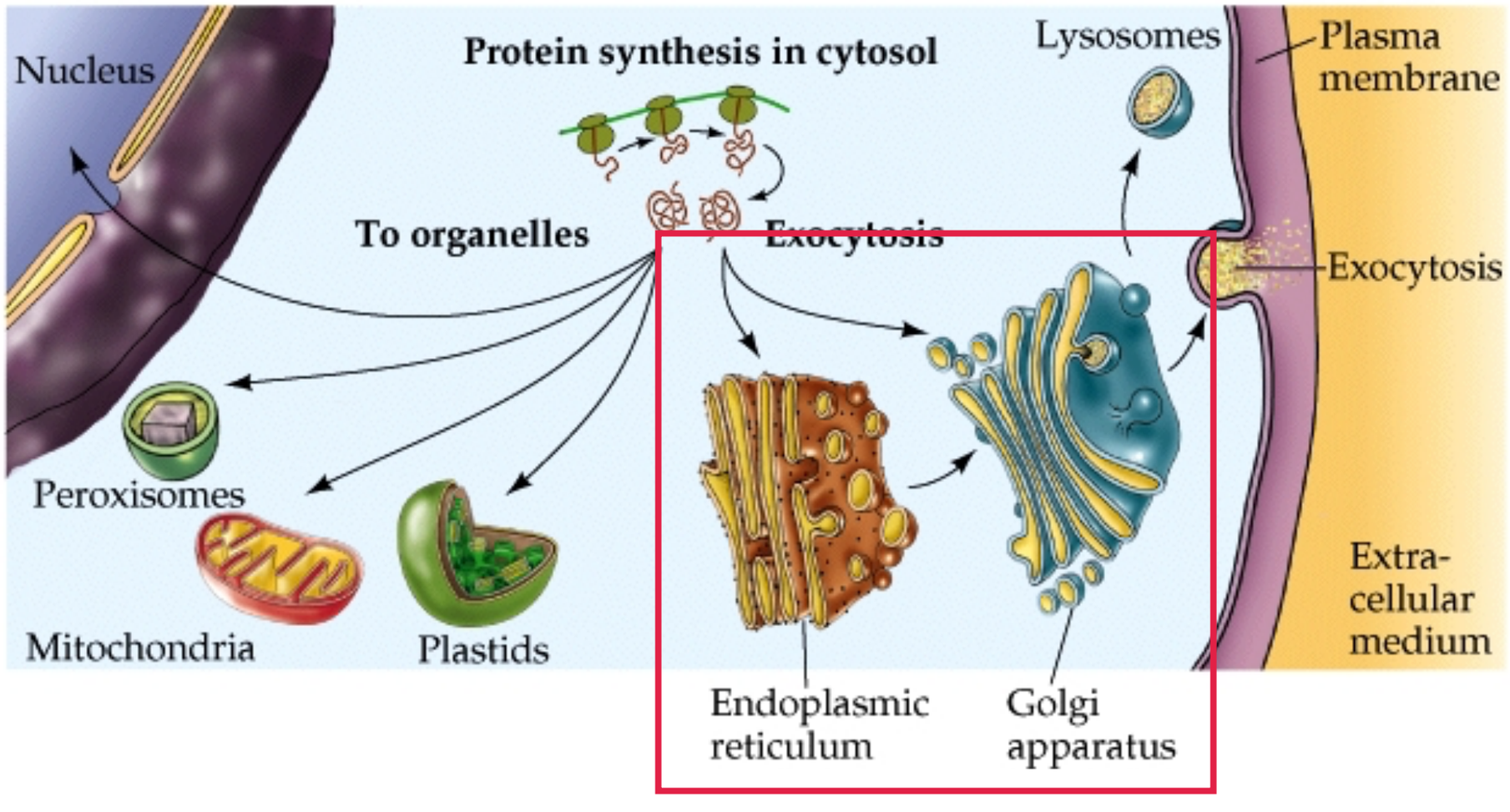
Mitochondria
Plastids
Endoplasmic reticulum
Golgi apparatus
Extra-cellular medium


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


Nucleus
Protein synthesis in cytosol
Lysosomes
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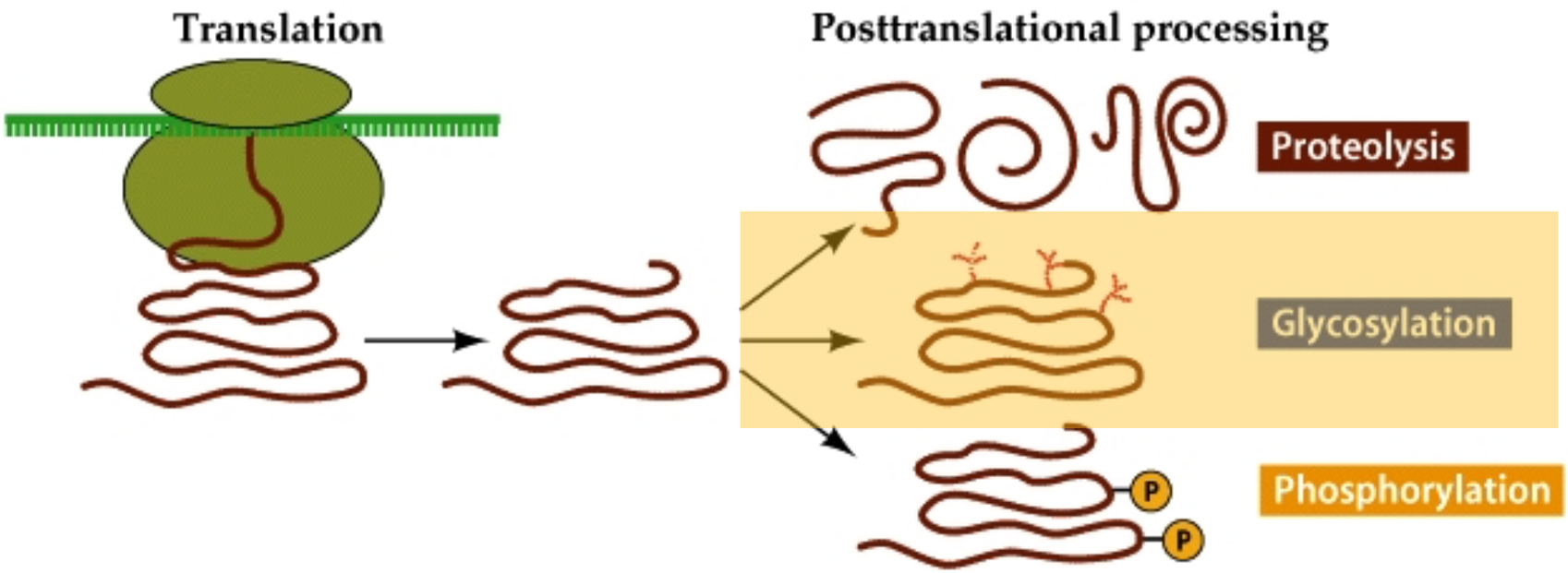
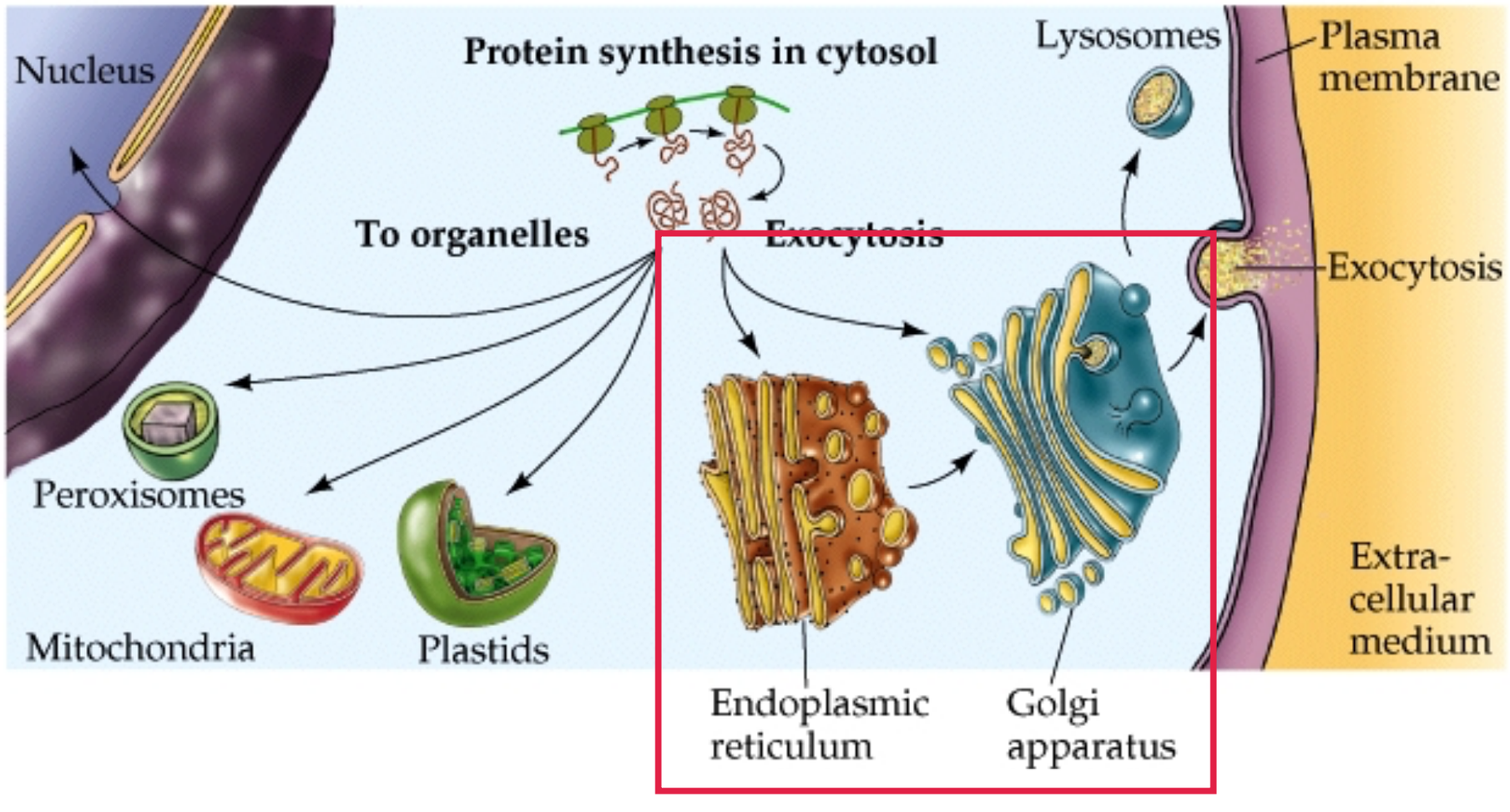
Golgi apparatus
Extra-cellular medium


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P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Golgi apparatus
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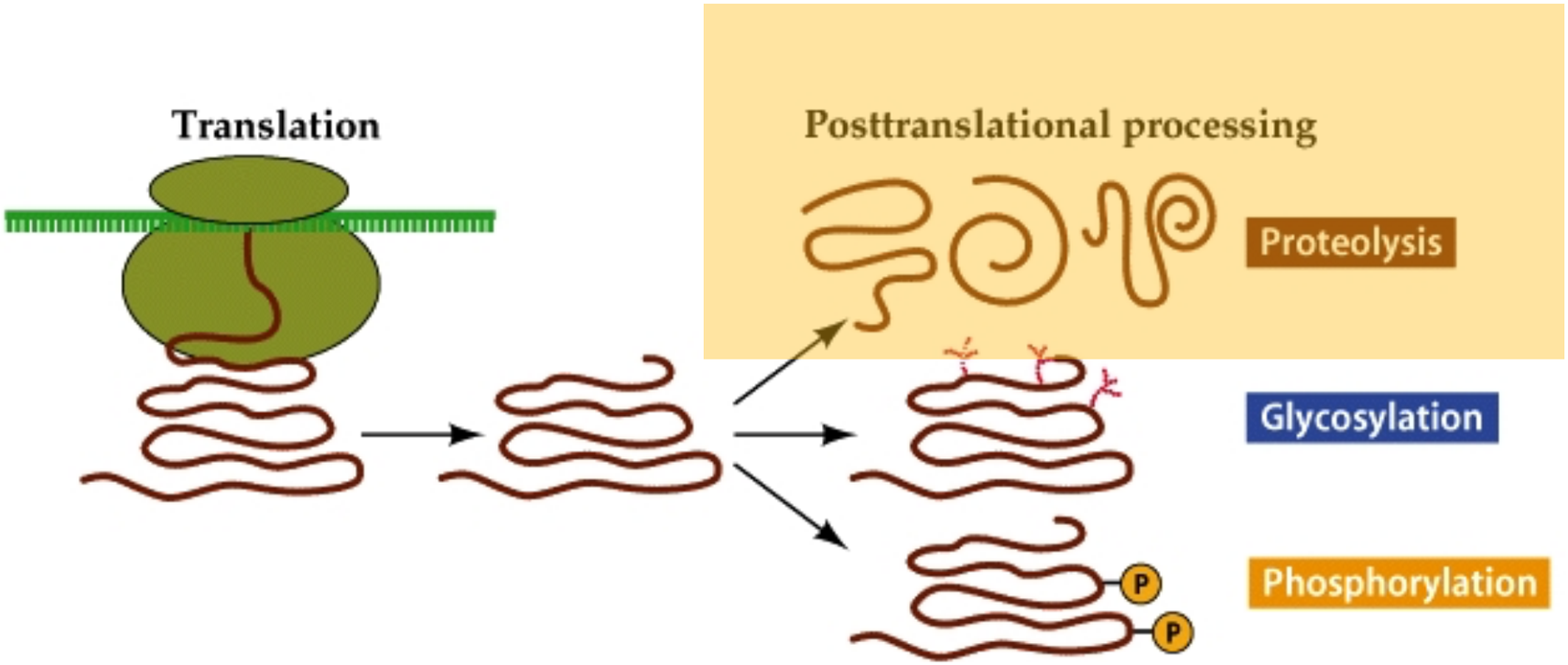
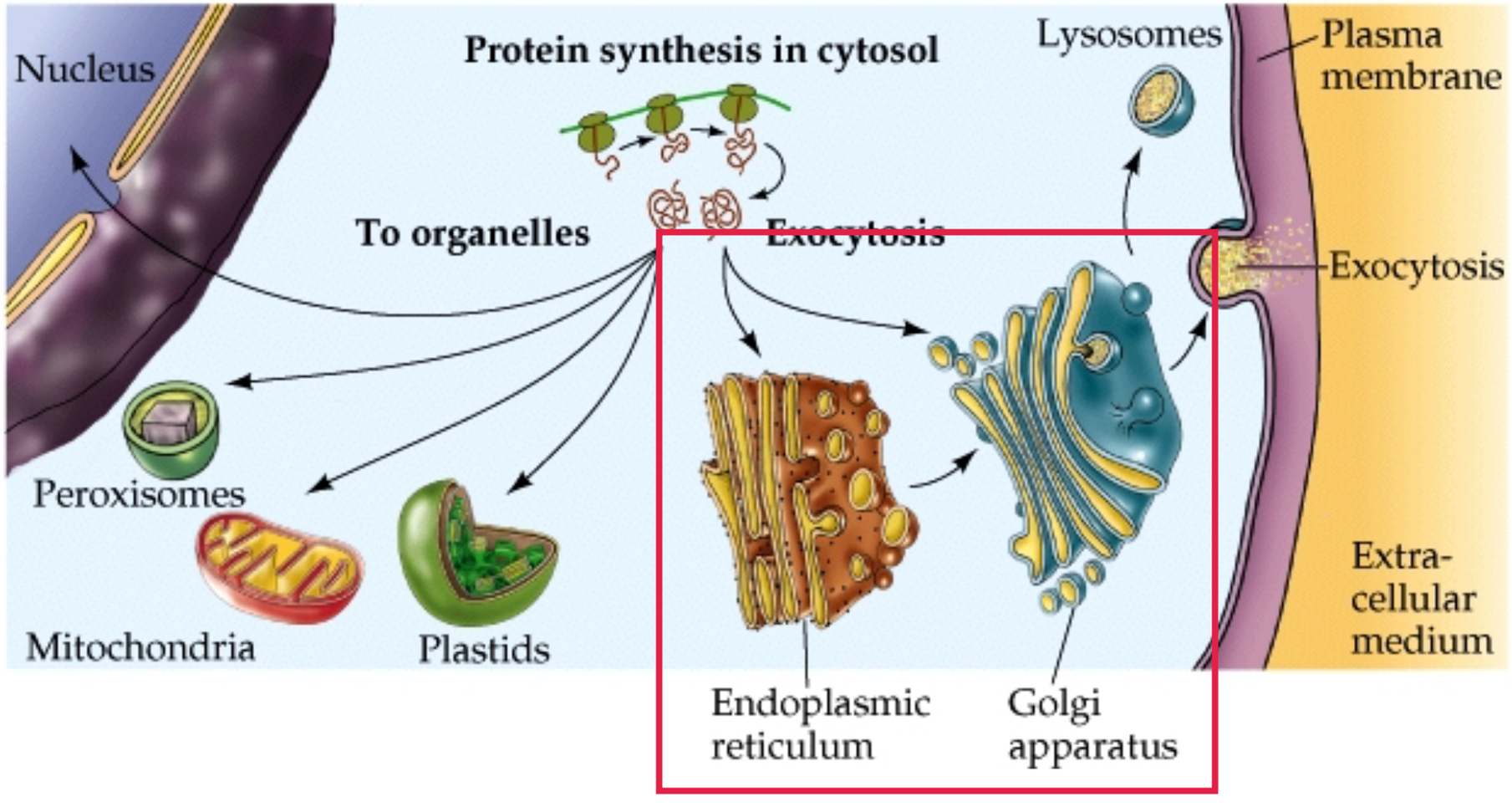

Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


Nucleus
Protein synthesis in cytosol
Lysosomes
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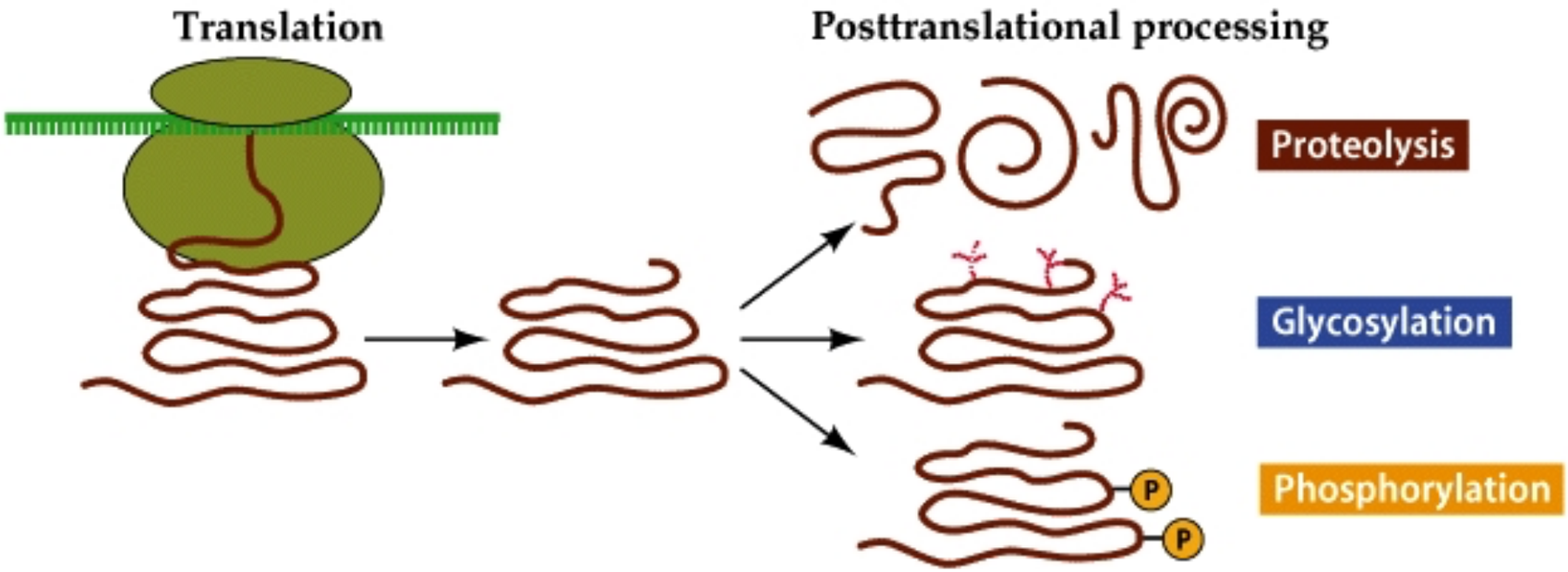
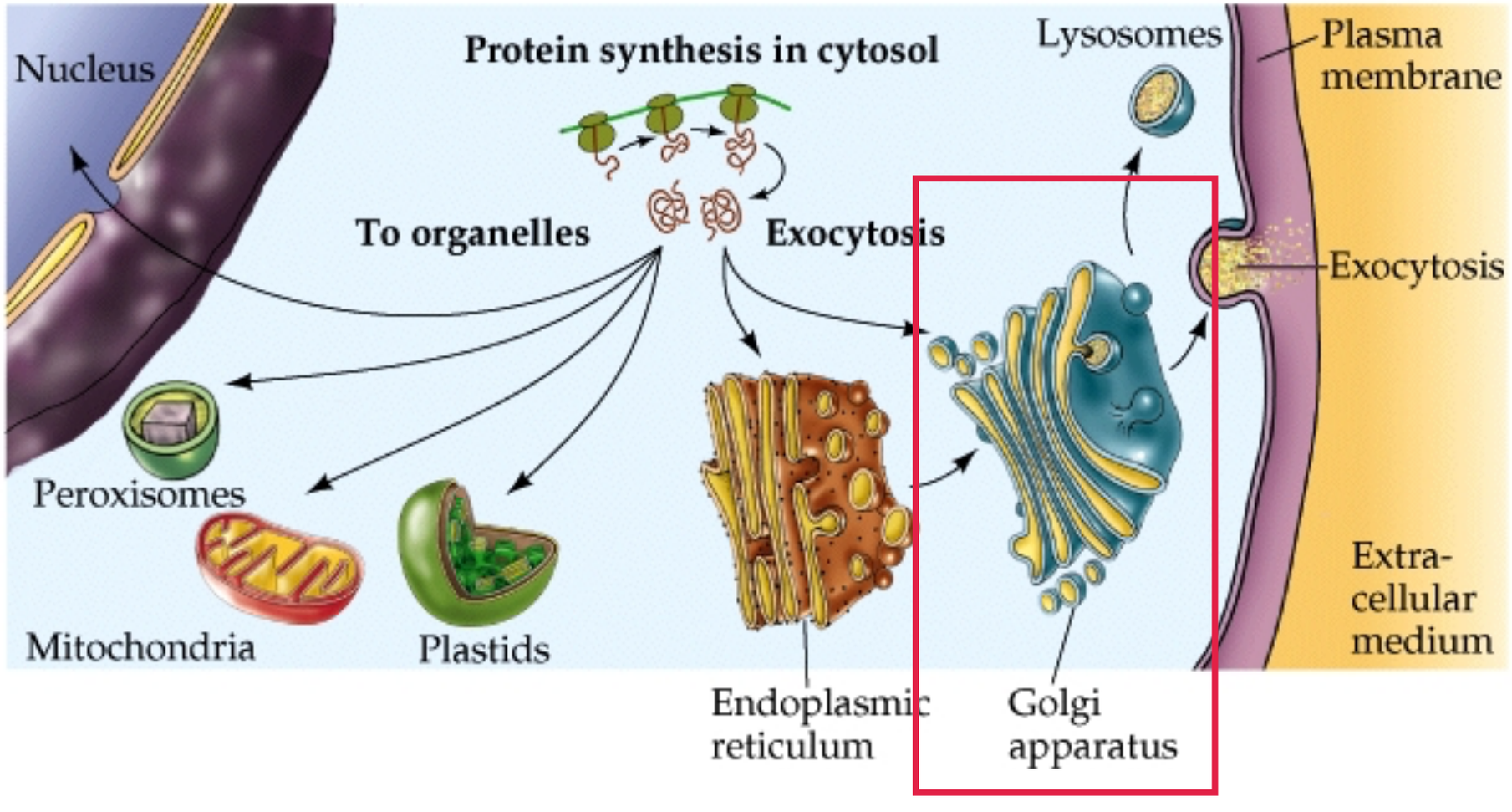
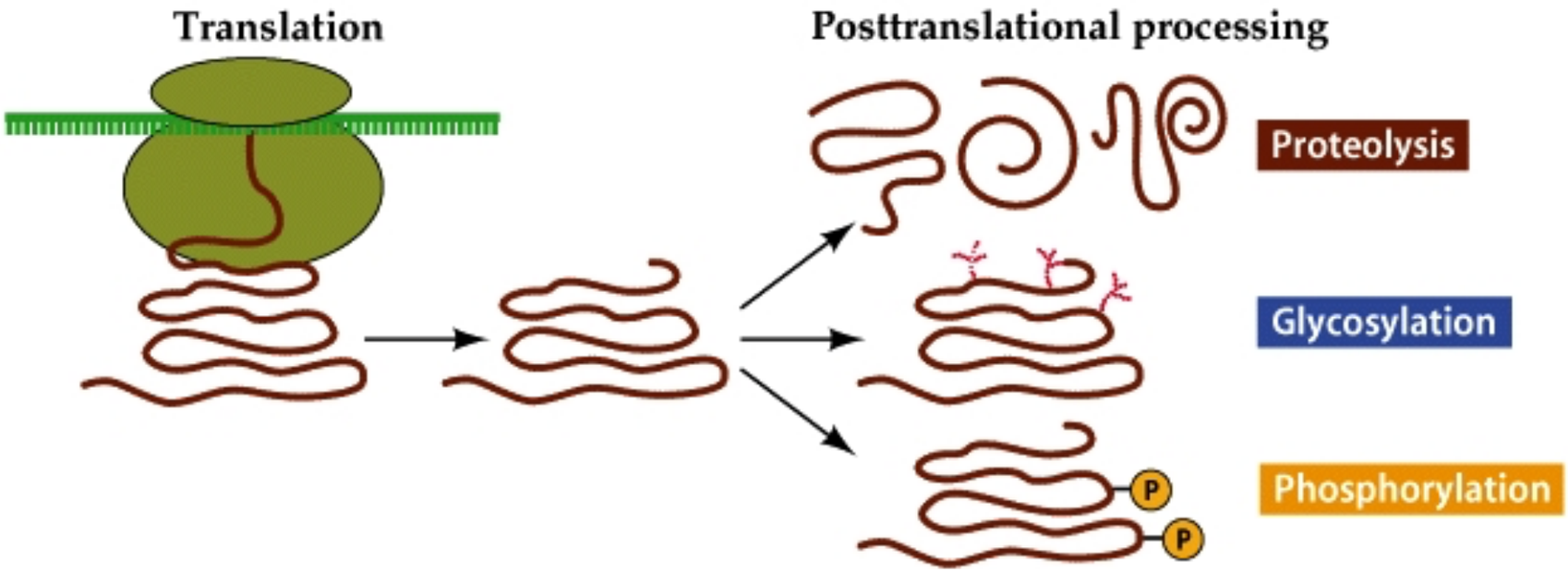
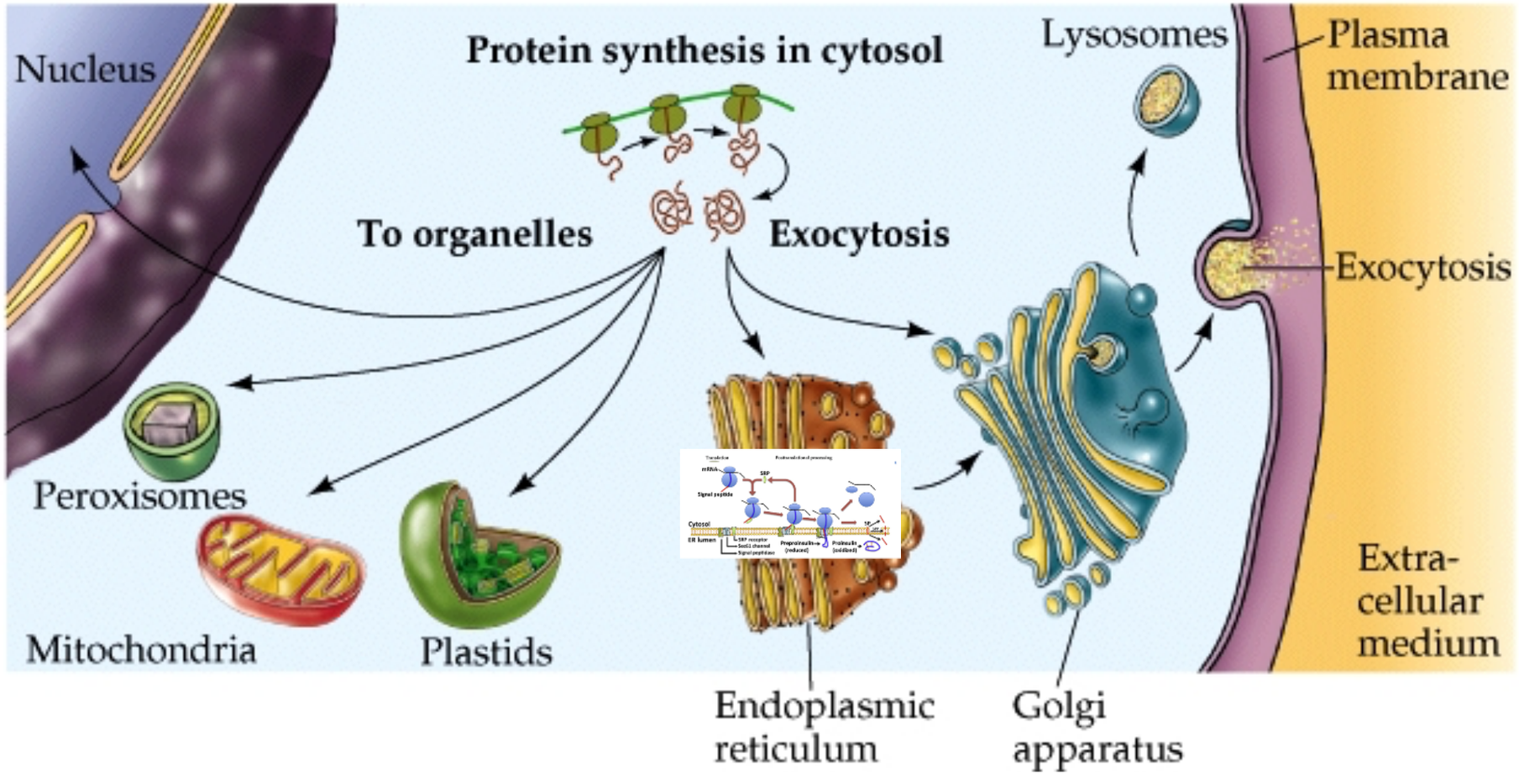
Mitochondria
Plastids
Endoplasmic reticulum
Golgi apparatus
Extra-cellular medium


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


Nucleus
Protein synthesis in cytosol
Lysosomes
Plasma membrane
To organelles
Exocytosis
Exocytosis
Peroxisomes
Mitochondria
Plastids
Extra-cellular medium
Endoplasmic reticulum
Golgi apparatus


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P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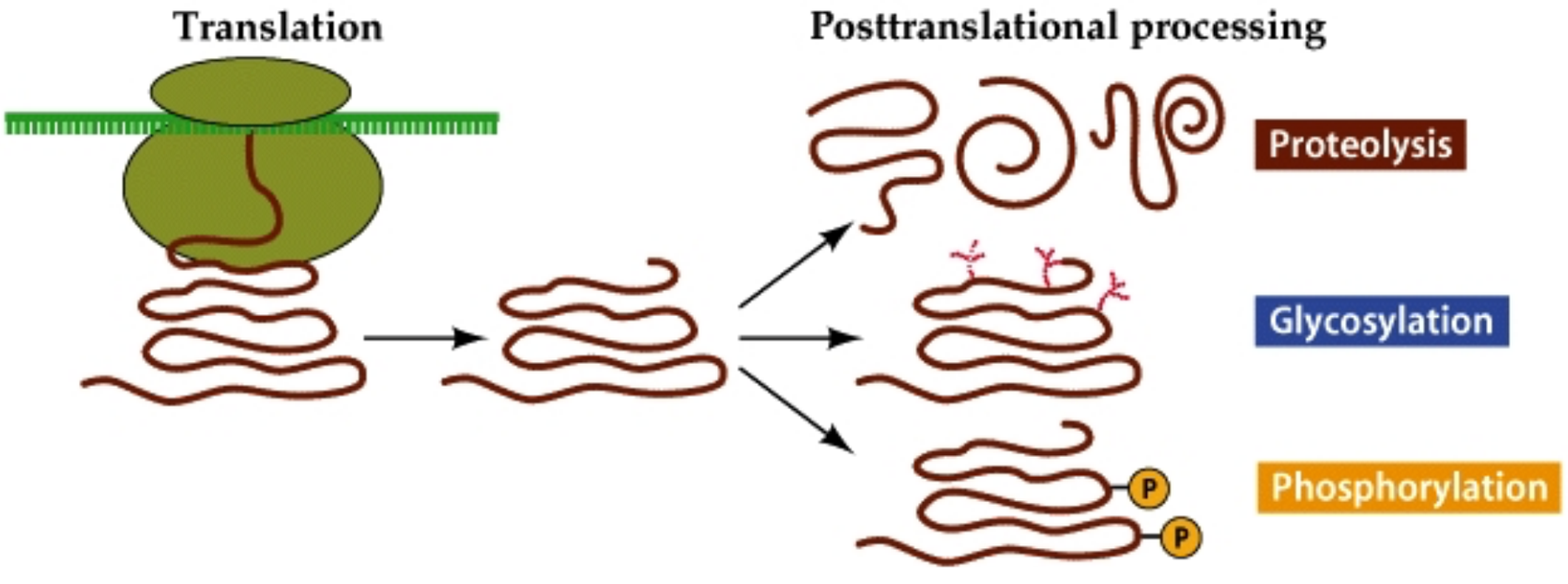
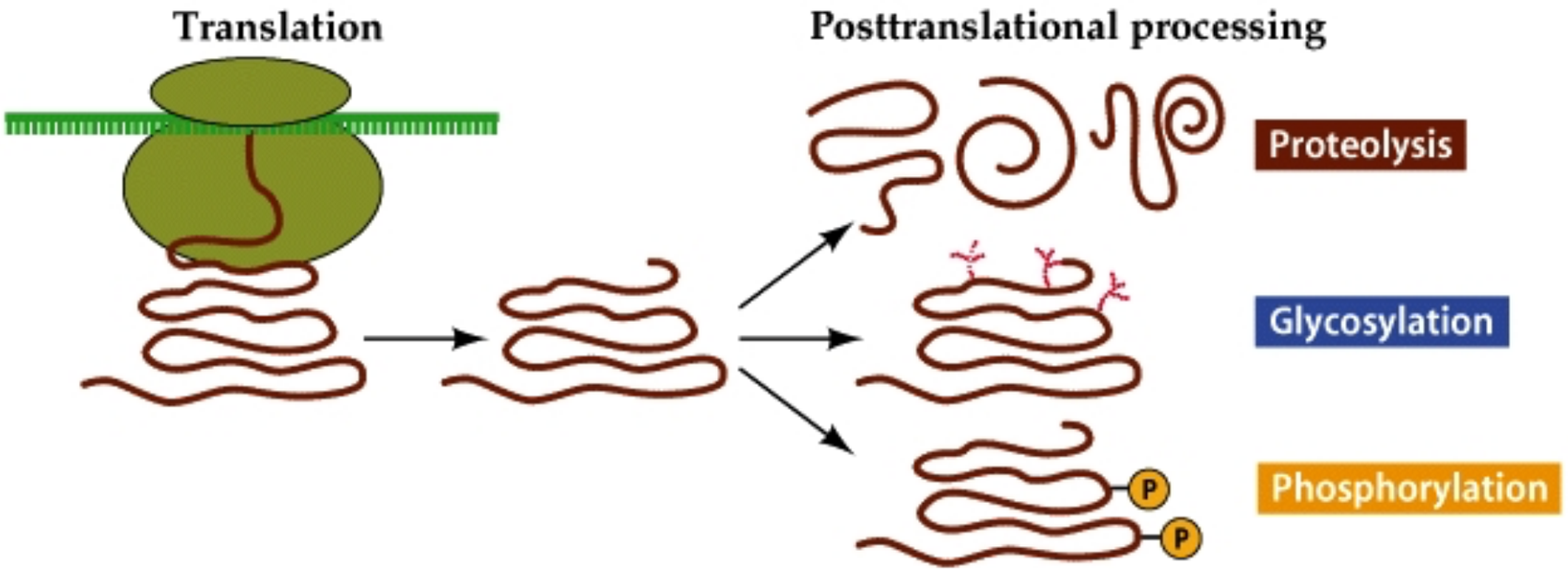
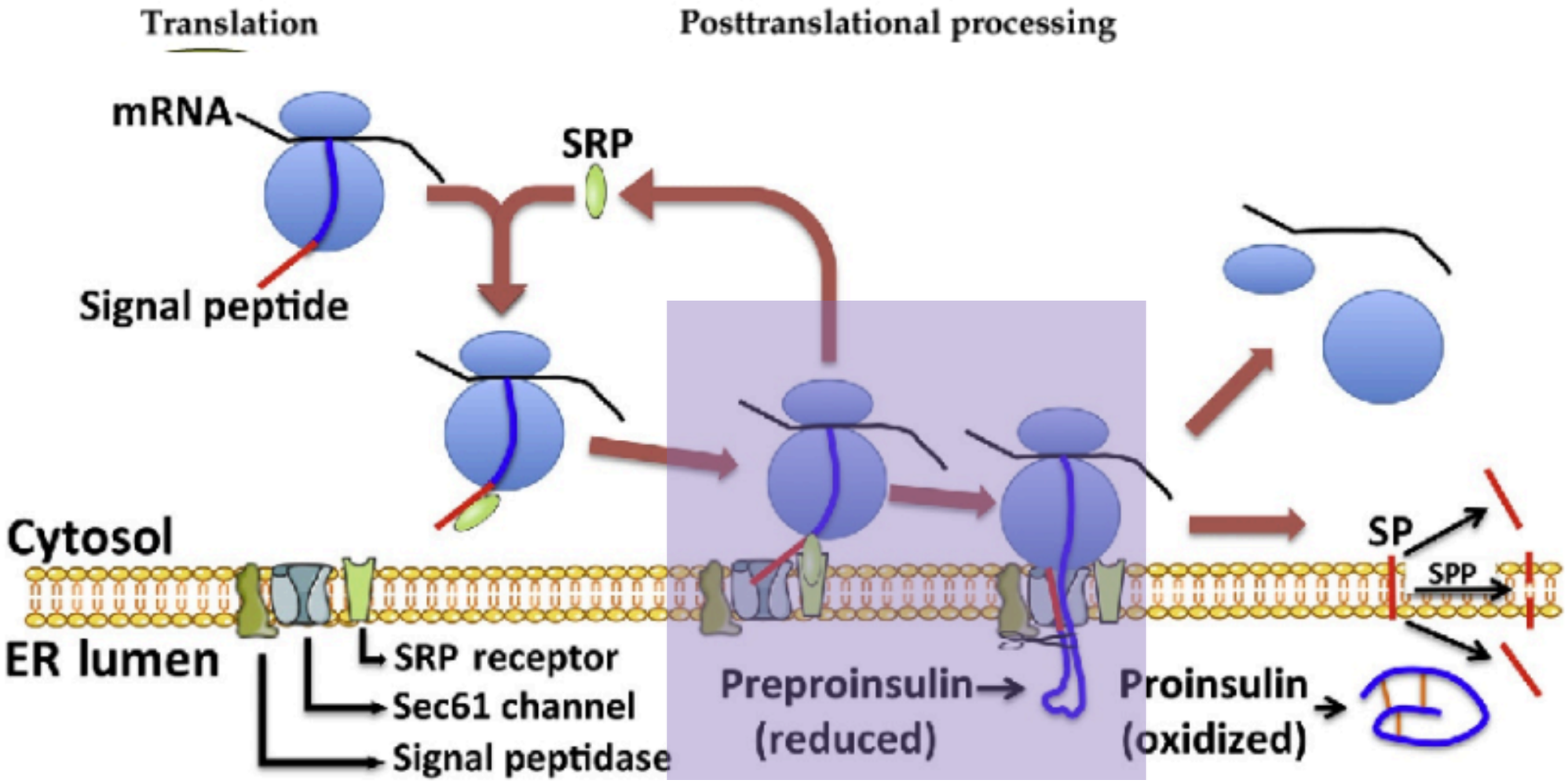
Extra-cellular medium
Endoplasmic reticulum
Golgi apparatus


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P

Translation
Posttranslational processing
mRNA
Signal peptide
SRP
Cytosol
ER lumen
SRP receptor
Sec61 channel
Signal peptidase
Preproinsulin
(reduced)
Proinsulin
(oxidized)
SP
SPP


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


Translation
Posttranslational processing
mRNA
SRP
Signal peptide
Cytosol
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SRP receptor
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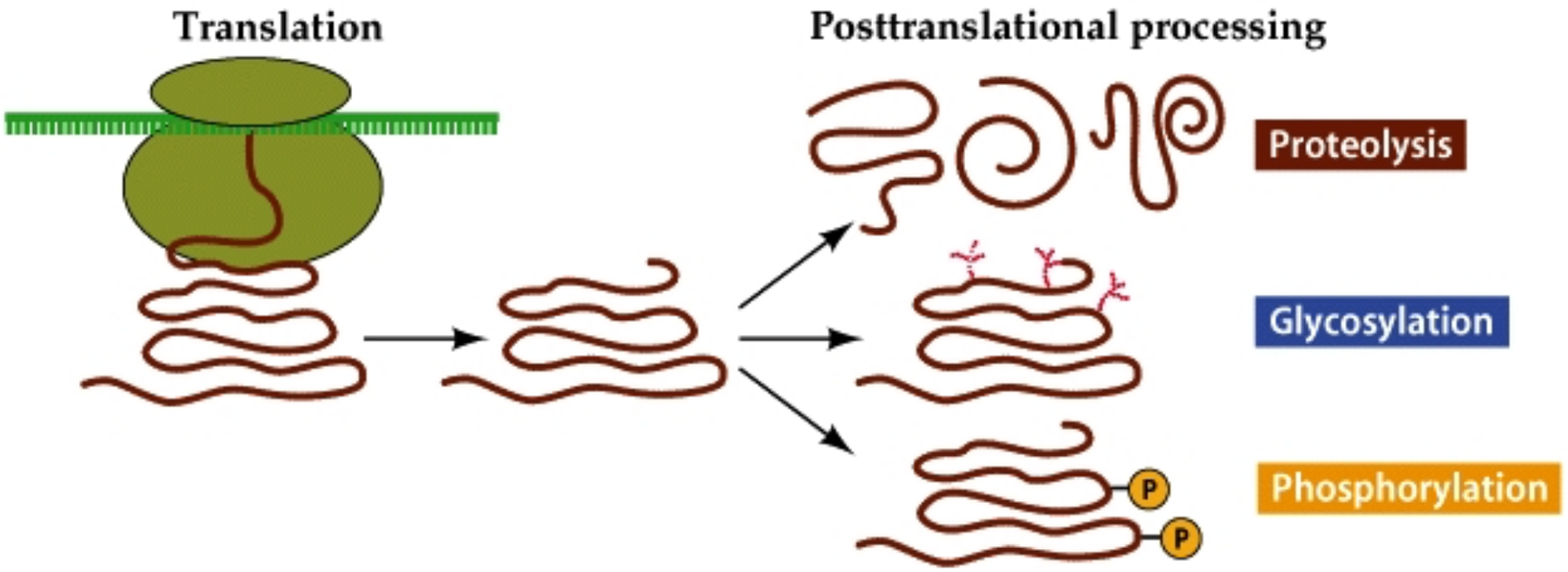
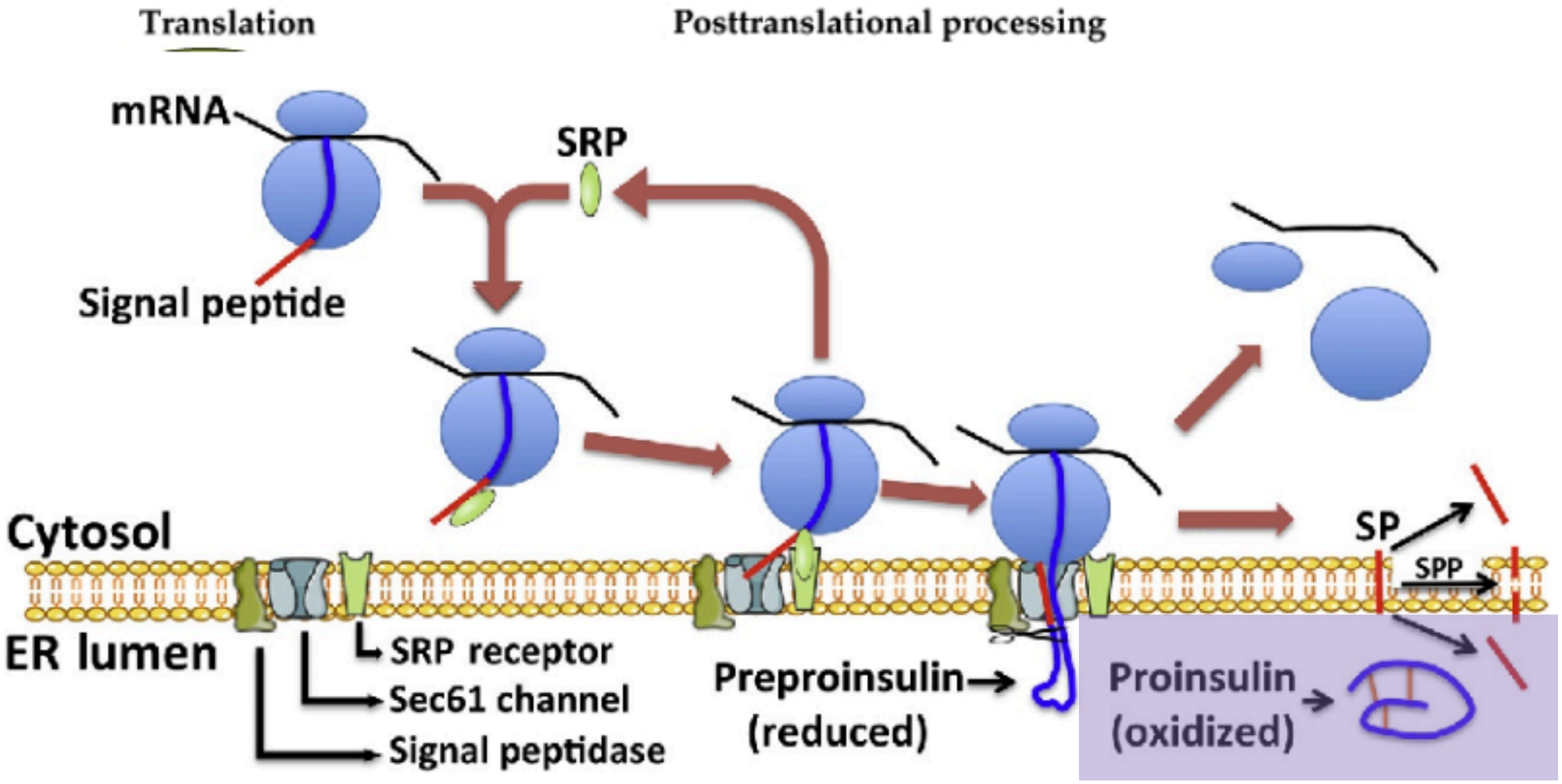
(reduced)
Proinsulin
(oxidized)
SP
SPP


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P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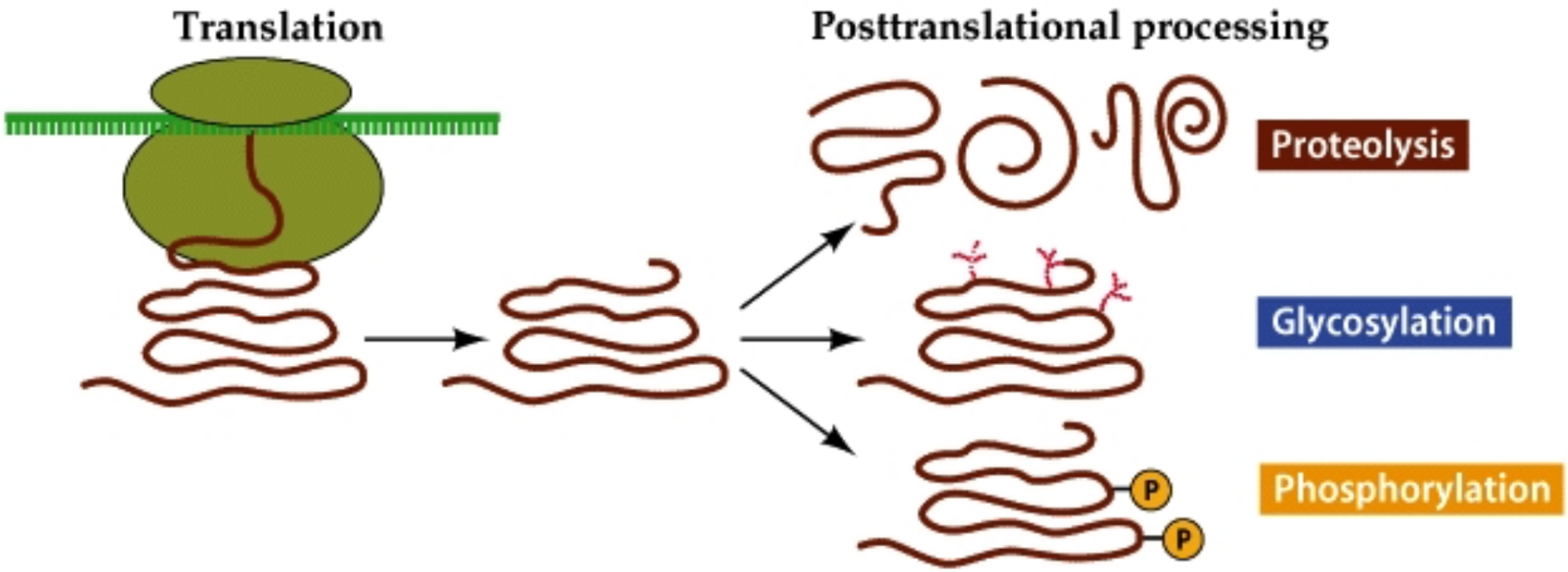
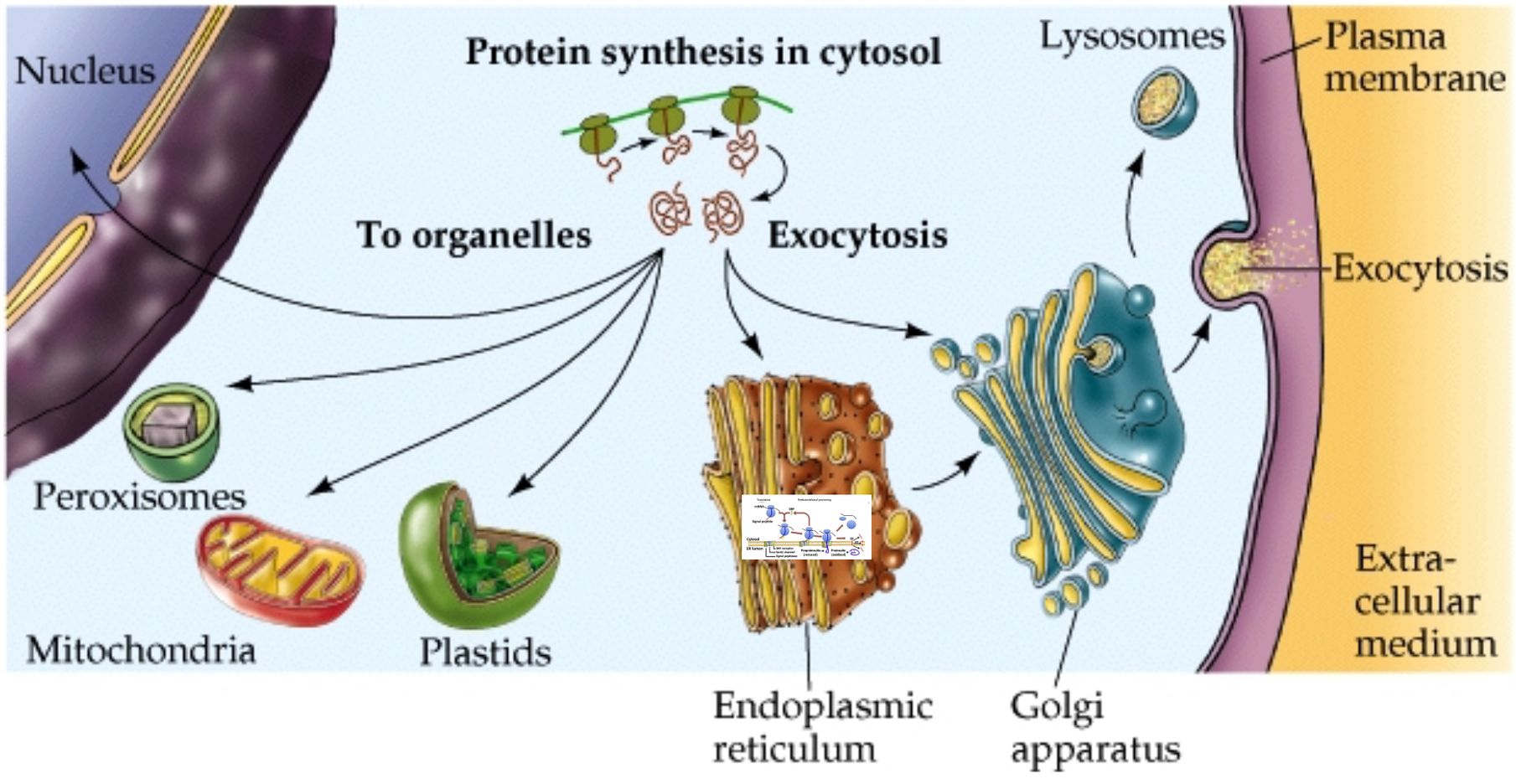
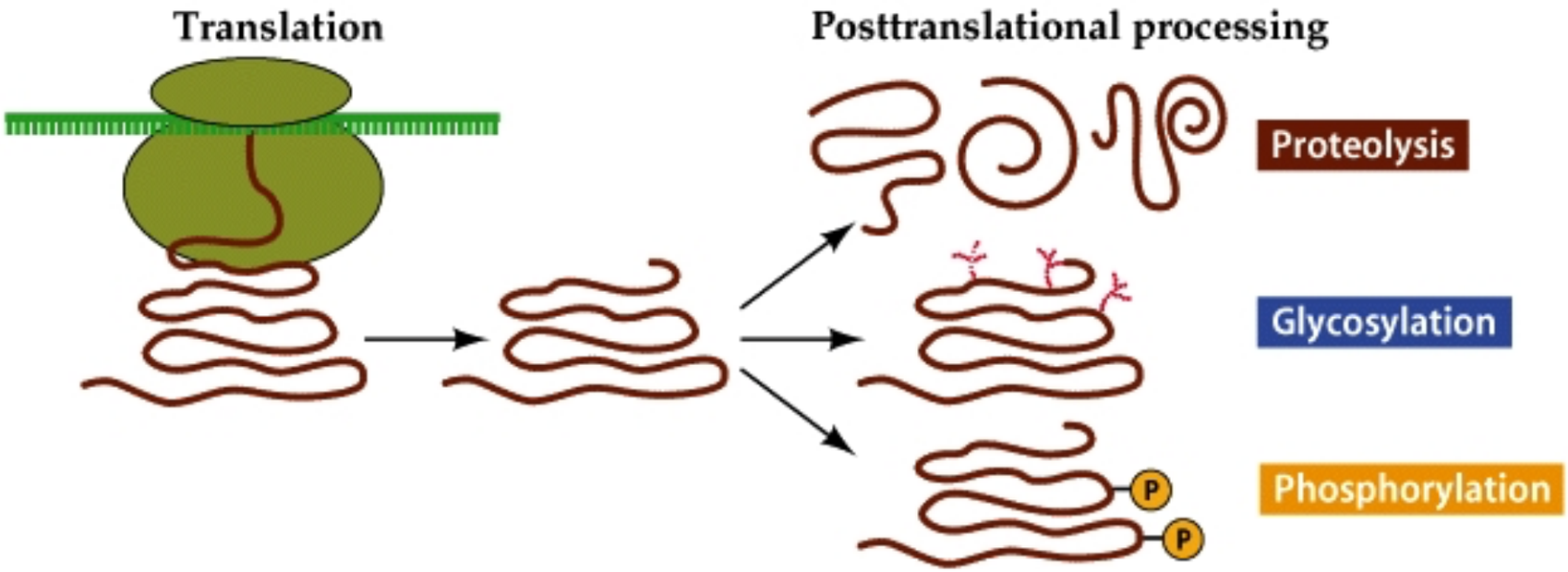
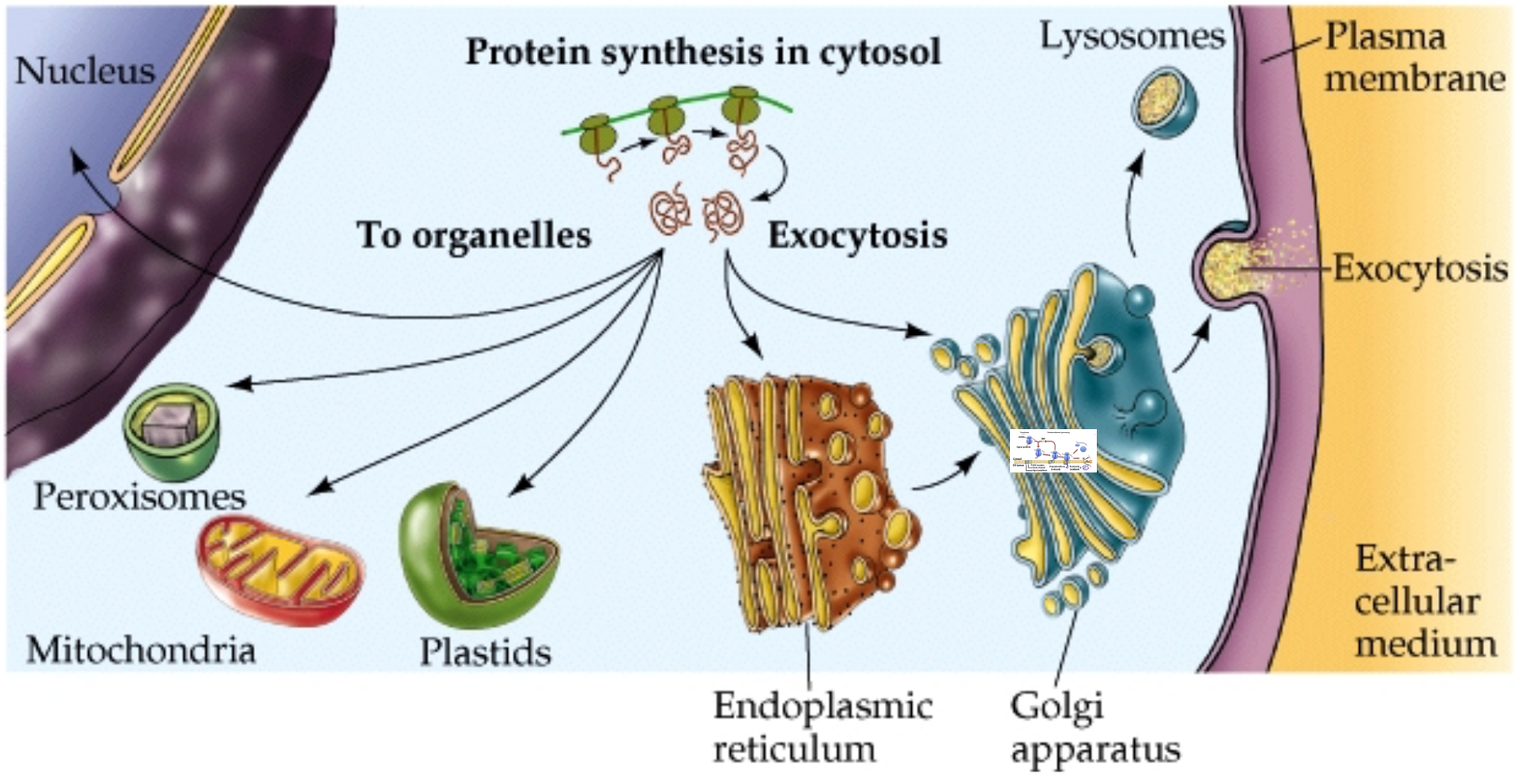

Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


Nucleus
Protein synthesis in cytosol
Lysosomes
Plasma membrane
To organelles
Exocytosis
Exocytosis
Peroxisomes
Mitochondria
Plastids
Extra-cellular medium
Endoplasmic reticulum
Golgi apparatus


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


Nucleus
Protein synthesis in cytosol
Lysosomes
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Exocytosis
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Peroxisomes
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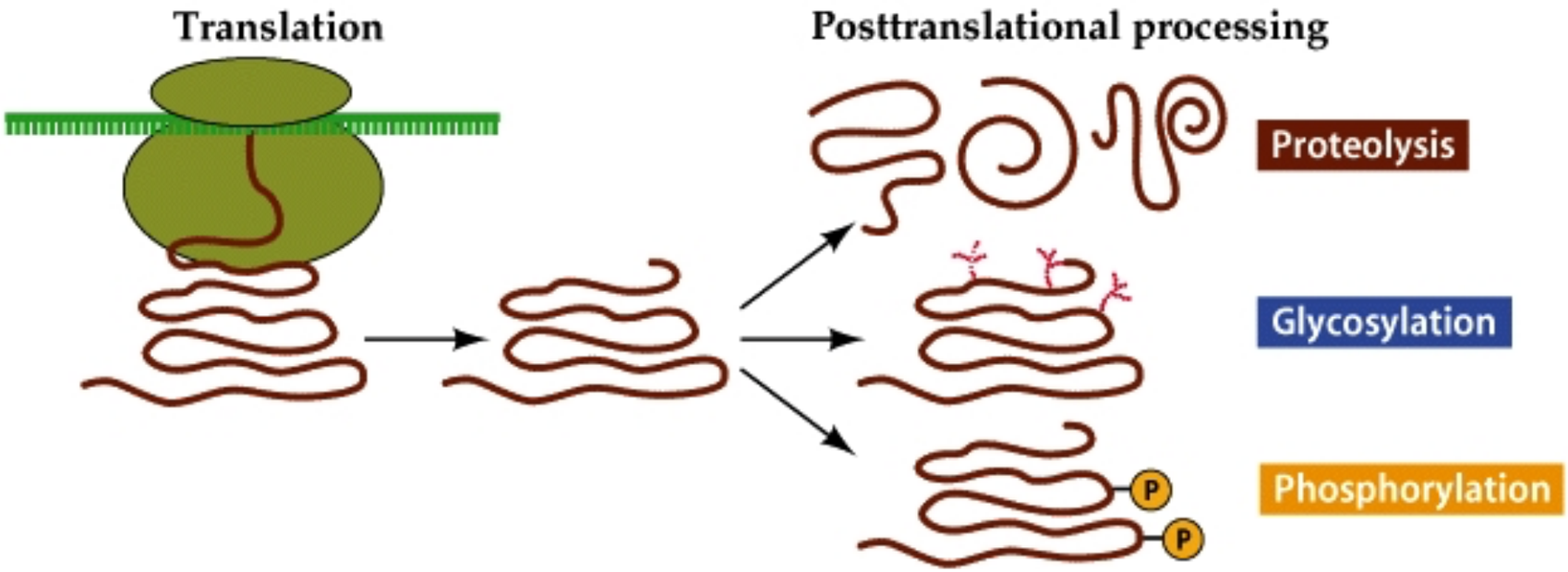
Extra-cellular medium
Endoplasmic reticulum
Golgi apparatus


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P

Nucleus
Protein synthesis in cytosol
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Plastids
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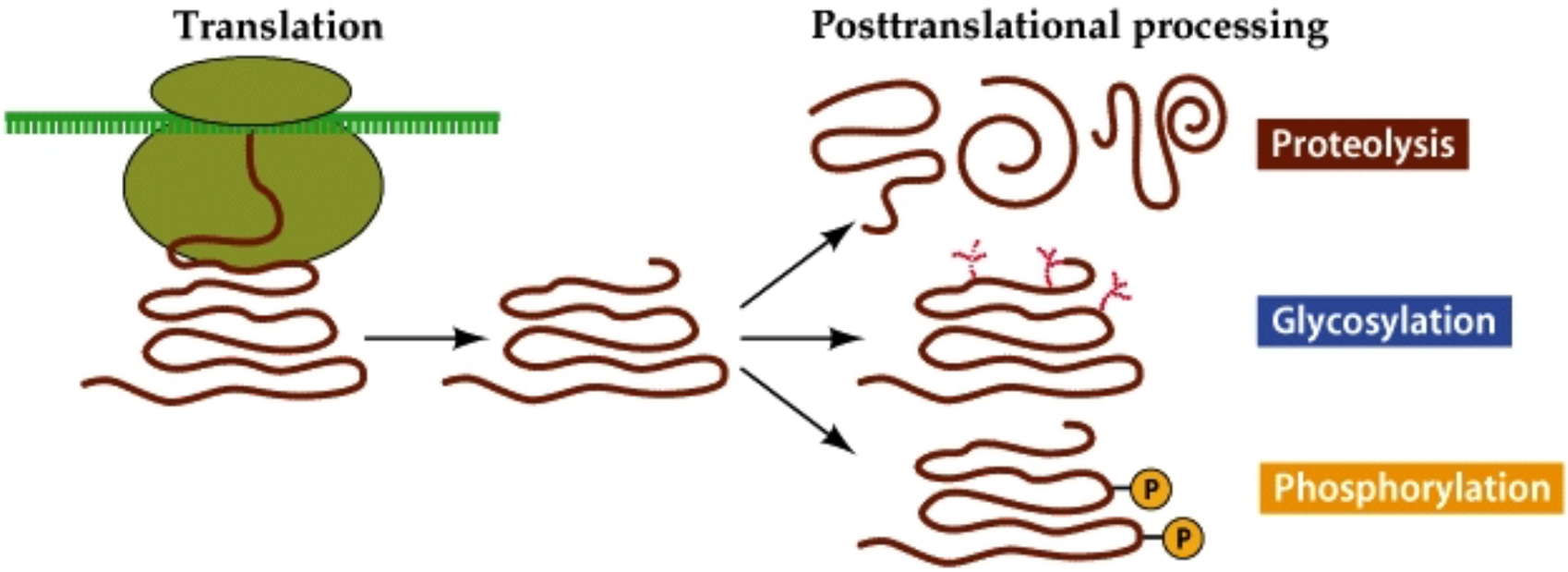
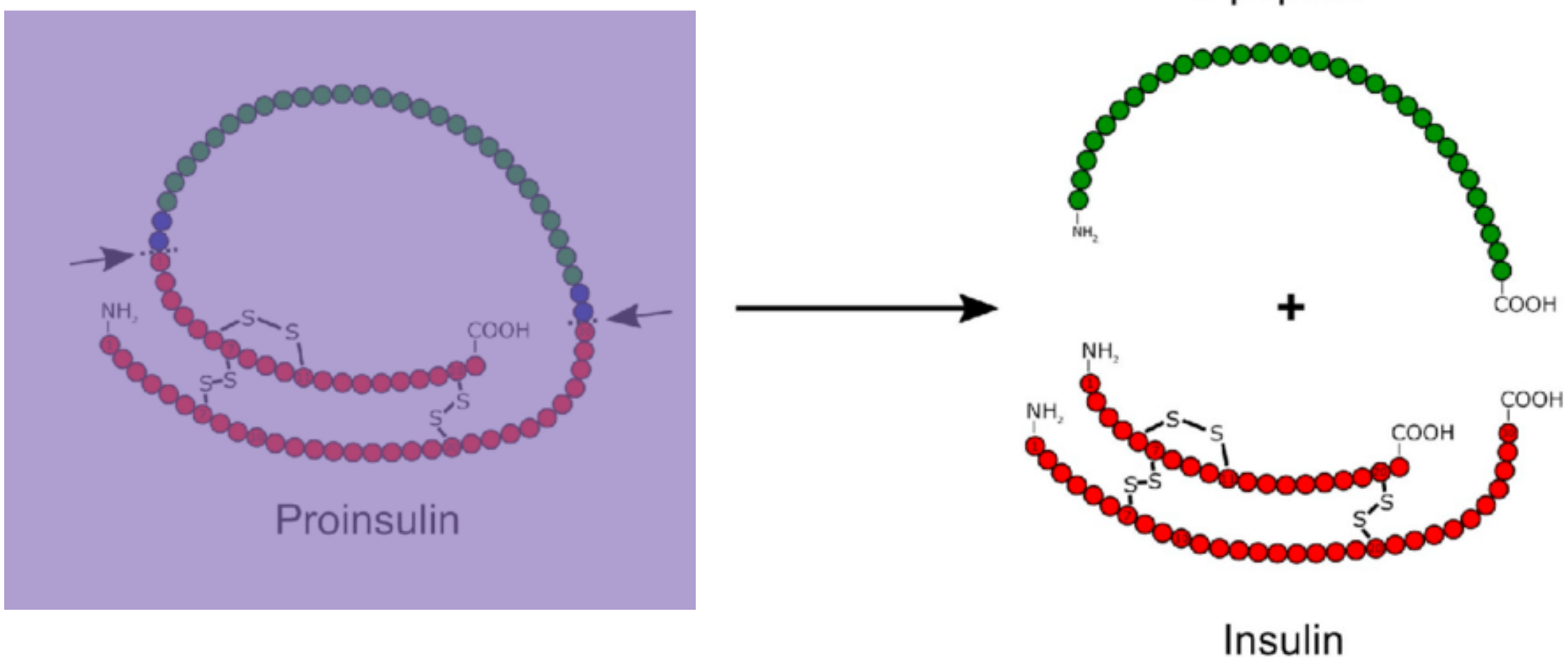
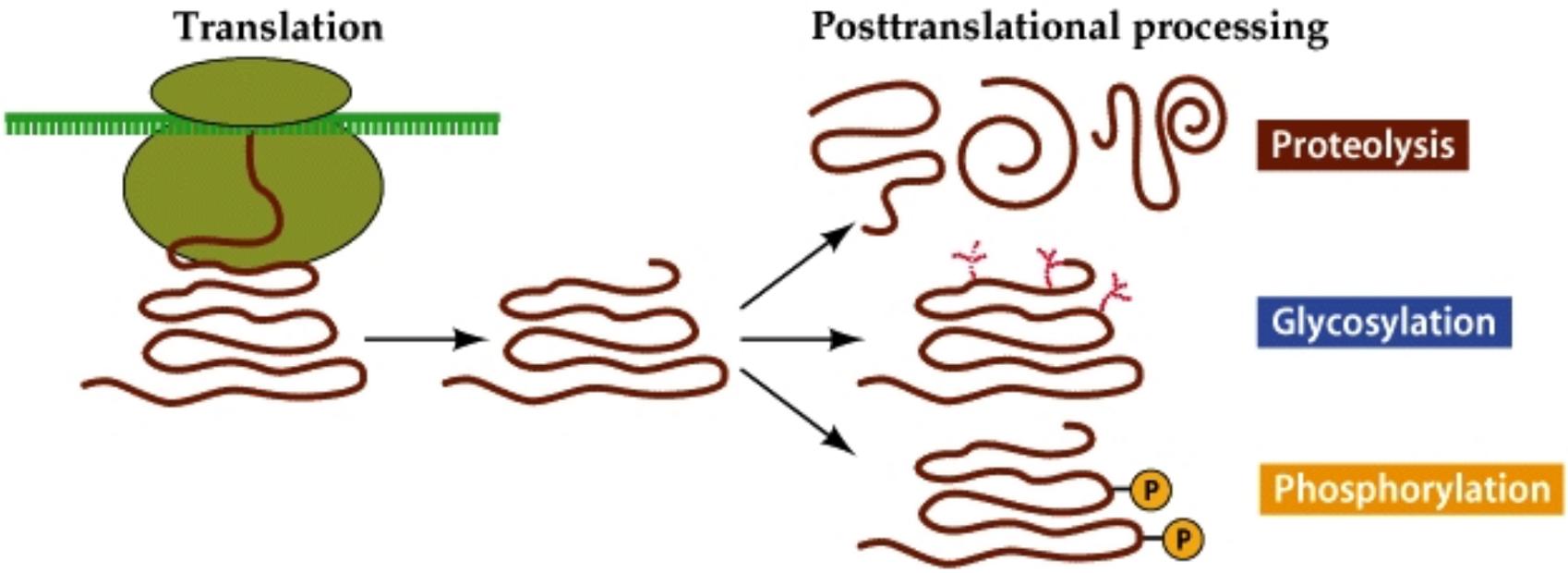
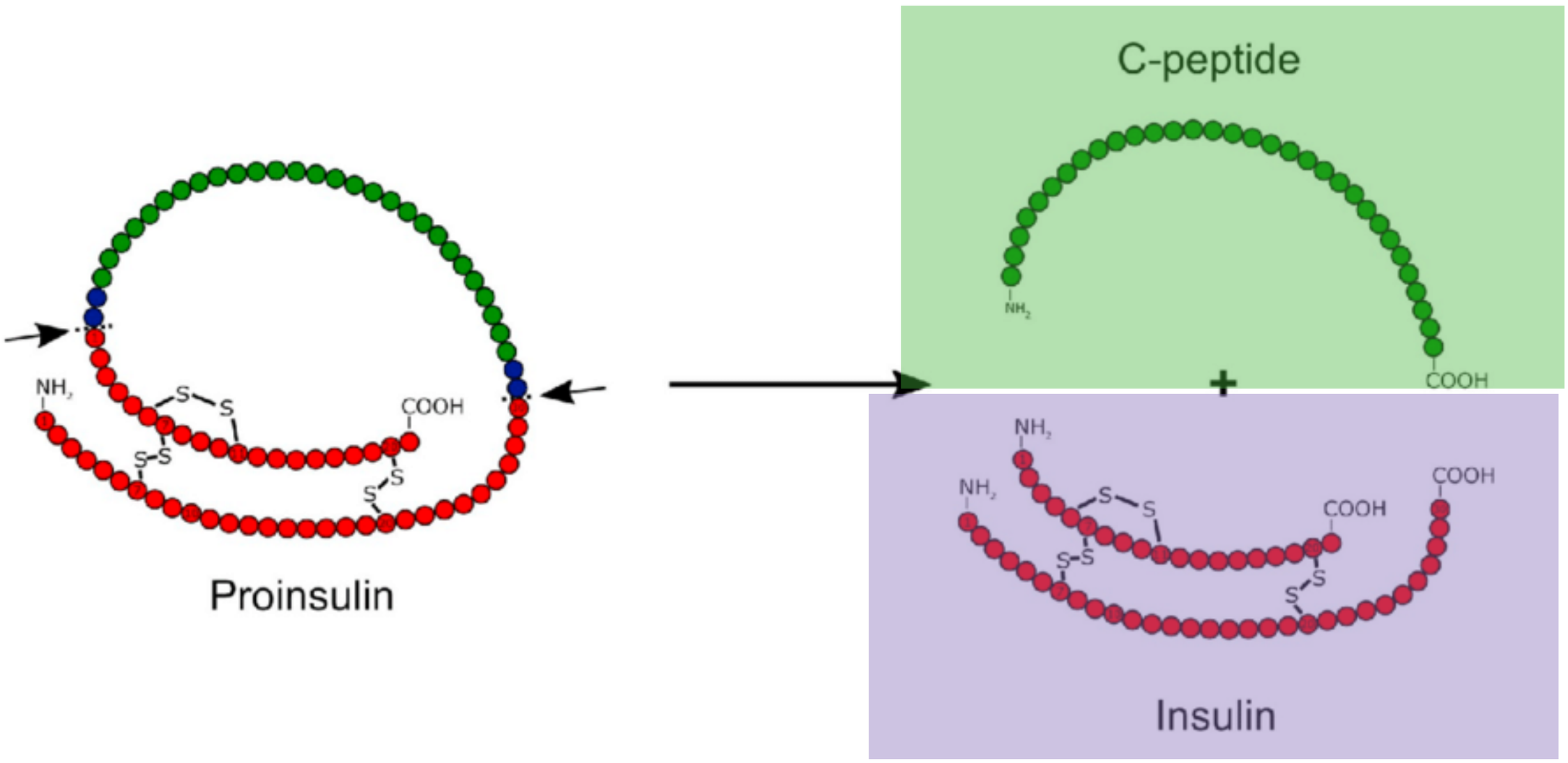
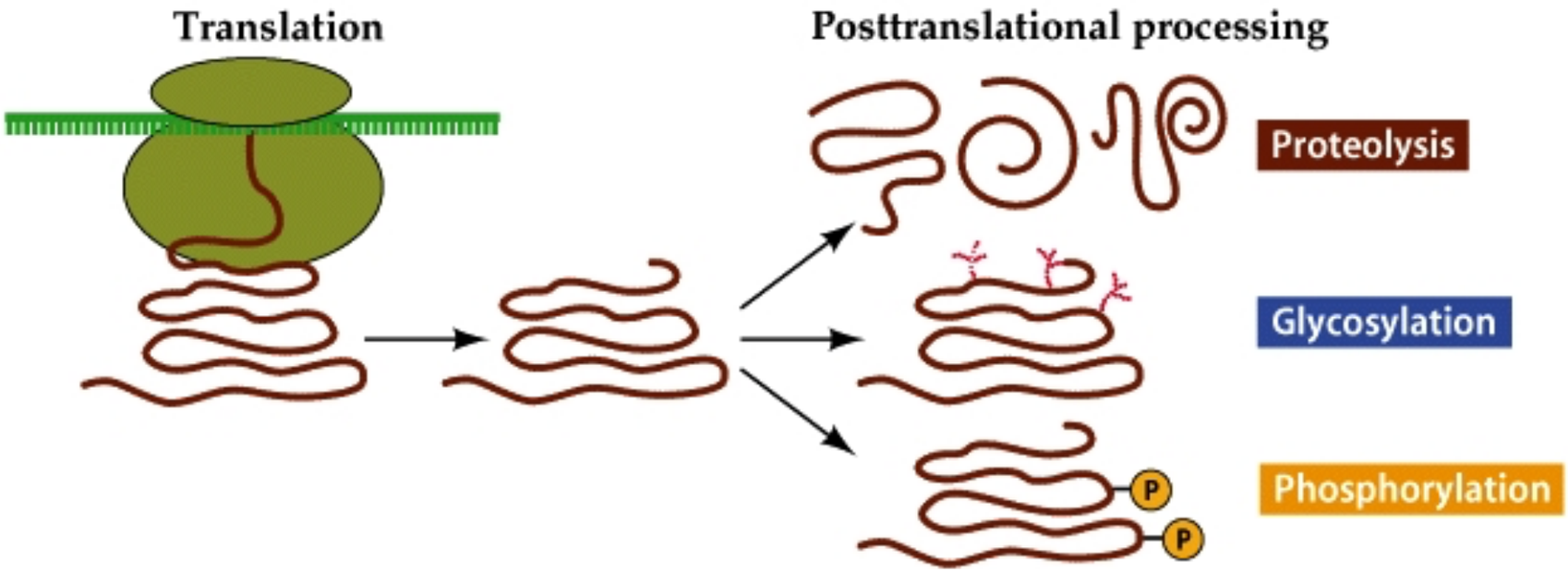
Golgi apparatus


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


C-peptide
NH2
S
S
S
S
S
S
COOH
Proinsulin
NH2
COOH
+
NH2
NH2
S
S
S
S
S
S
COOH
COOH
Insulin


Translation
Posttranslational processing
Proteolysis
Glycosylation
Phosphorylation
P
P


NH2
S
S
S
S
S
S
COOH
Proinsulin
C-peptide
NH2
COOH
+
NH2
NH2
S
S
S
S
S
S
COOH
COOH
Insulin


Translation
Posttranslational processing
Proteolysis
Glycosylation
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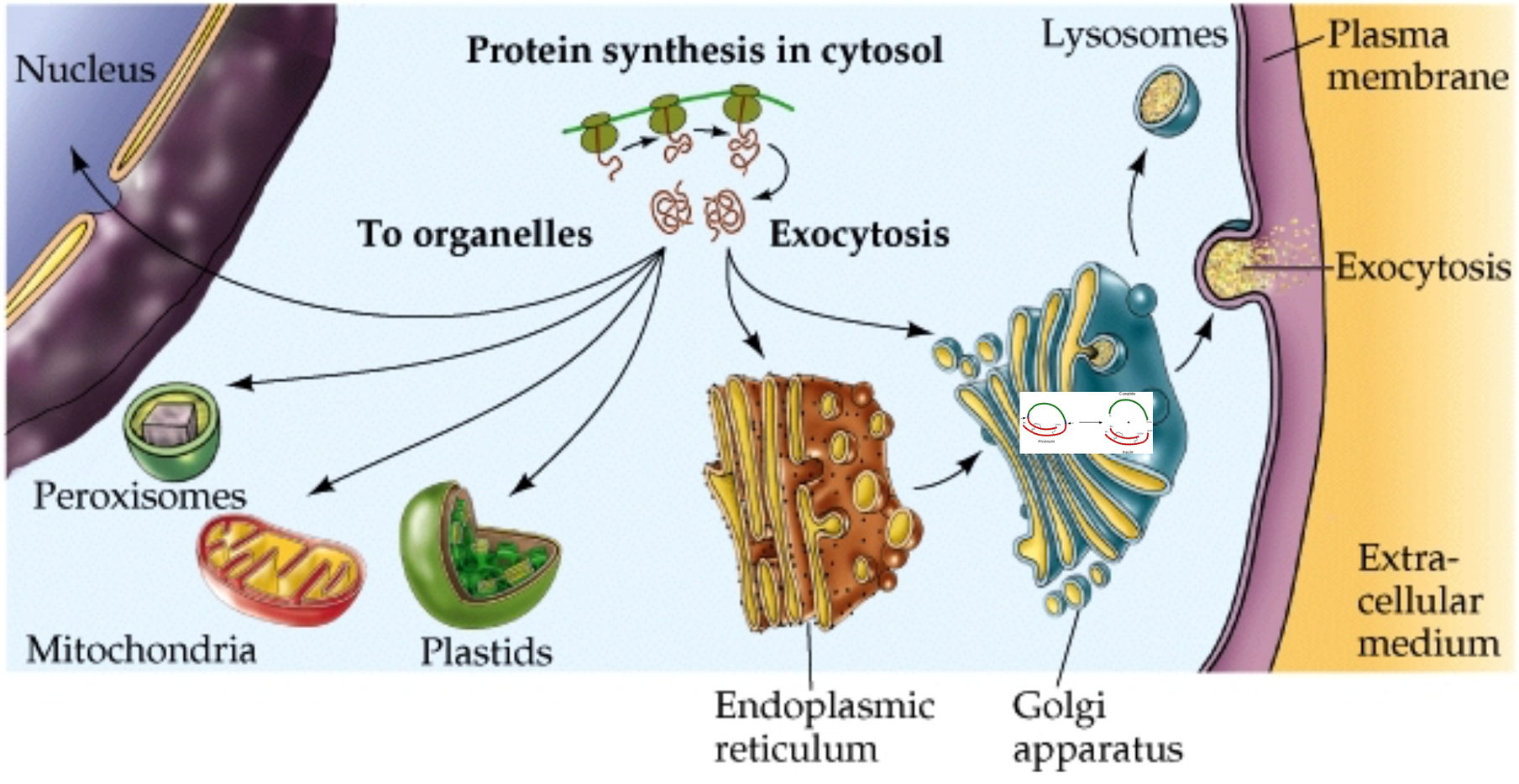
P
P


Nucleus
Protein synthesis in cytosol
Lysosomes
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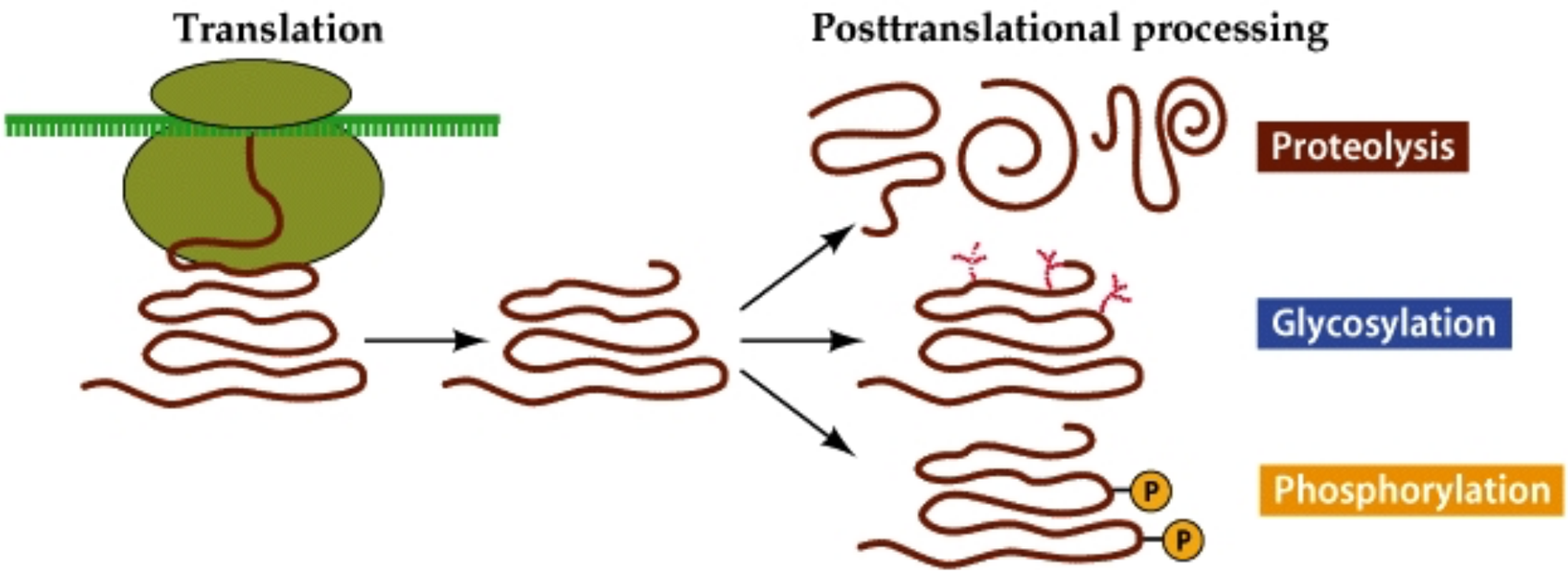
Plastids
Extra-cellular medium
Endoplasmic reticulum
Golgi apparatus


Translation
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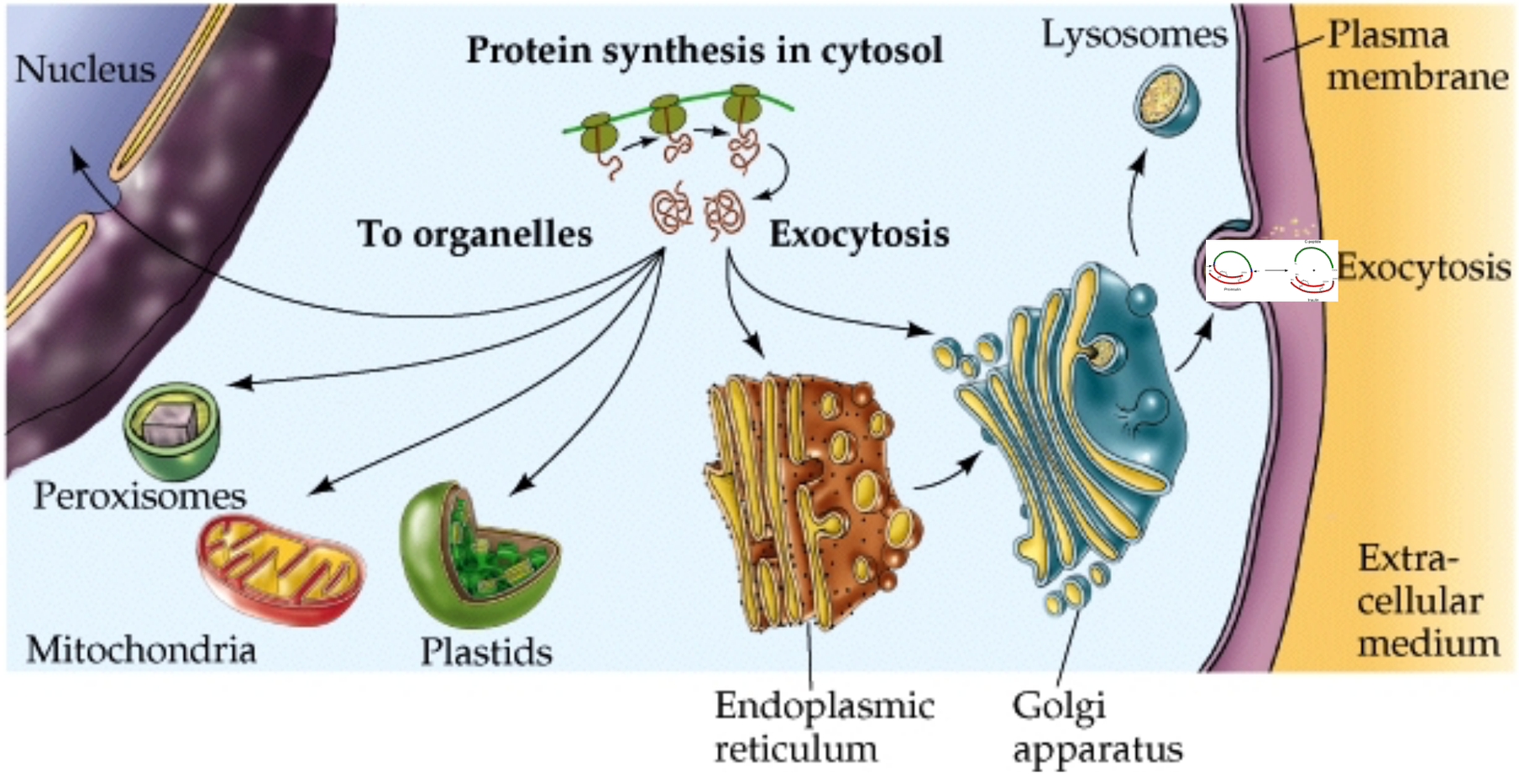
P
P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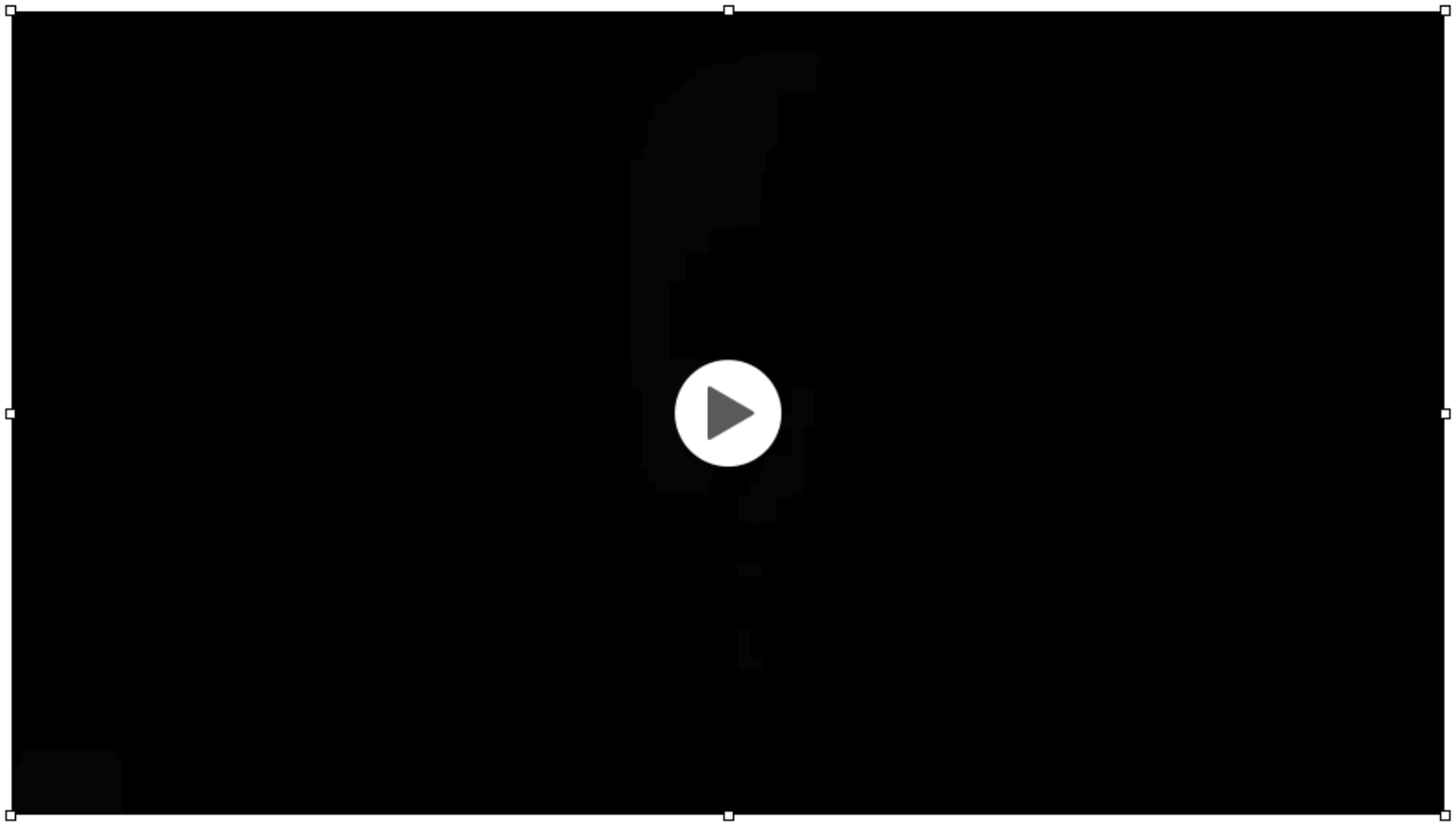
Golgi apparatus
Extra-cellular medium



WHERE and **HOW** do you regulate the whole process?????