RNA Structure
Genetic Code
&
Translation

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Type of RNA

1. **Ribosomal RNA (rRNA)**
    - **16S (small ribosomal subunit)**
    - **23S (large ribosomal subunit)**
    - **5S (large ribosomal subunit)**
2. **Transfer RNA (tRNA)**
3. **Messenger RNA (mRNA)**

Type of RNA

1. **Small Nuclear RNA (snRNA)**
2. **Micro RNA (miRNA)**
3. **Small Interfering RNA (siRNA)**
4. **Double Stranded RNA (dsRNA)**

RNA Silencing (Interferenc) family

Micro RNA = **miRNA** = Endogenous

Small Interfering RNA = **siRNA** = Exogenous

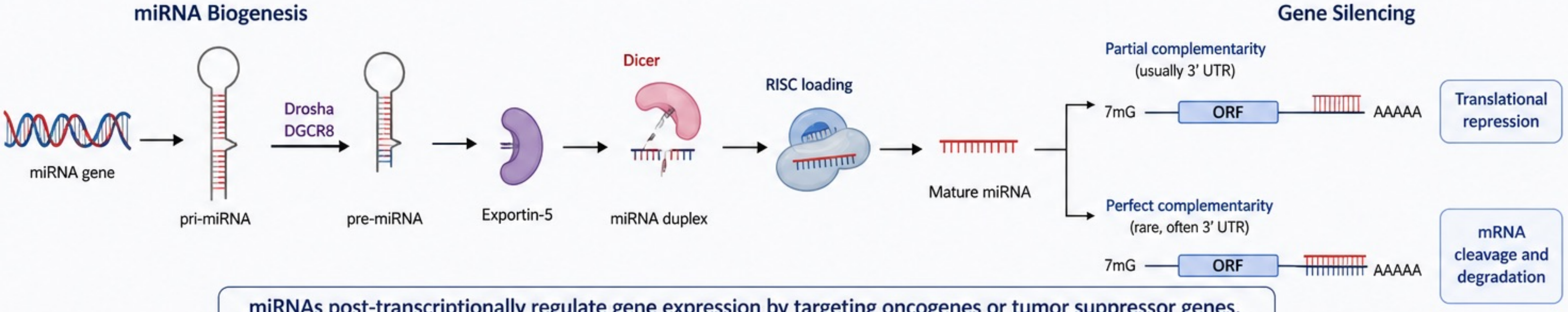
RNA Silencing (Interference) family

- **20 – 25 Nucleotide**

- **Non Coding Sequence**
  - No Protein synthesis

- **Negative Regulation of The Gene**
  - Break m-RNA
  - Repress the translation of m-RNA

Role of miRNA in Cancer


miRNA Biogenesis

miRNA gene → pri-miRNA → Drosha DGCR8 → pre-miRNA → Exportin-5 → Dicer → miRNA duplex → RISC loading → Mature miRNA

Gene Silencing

Partial complementarity (usually 3' UTR)

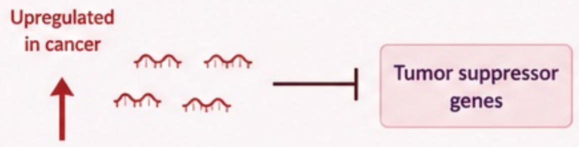
7mG — ORF — AAAAA → Translational repression

Perfect complementarity (rare, often 3' UTR)

7mG — ORF — AAAAA → mRNA cleavage and degradation

miRNAs post-transcriptionally regulate gene expression by targeting oncogenes or tumor suppressor genes, thereby acting as OncomiRs or Tumor Suppressor miRNAs

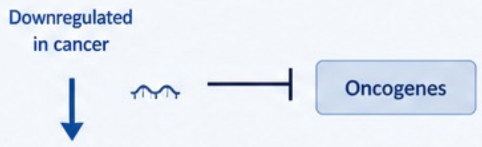
OncomiRs (miRNAs acting as oncogenes)


Upregulated in cancer

Tumor suppressor genes

- Promote cell proliferation
- Inhibit apoptosis
- Enhance invasion
- Induce metastasis
- Promote angiogenesis

Tumor Suppressor miRNAs


Downregulated in cancer

Oncogenes

- Inhibit cell proliferation
- Promote apoptosis
- Reduce invasion
- Suppress metastasis
- Inhibit angiogenesis

Pathogenesis of Atherosclerosis

- Over Activity of Proteinase **Enzyme Gene**
- Activation of Proteinase Enzyme
- Increase Arterial Endothelium Damage
- Atherosclerosis

Role of mi-RNA in Disease

- mi-RNA712 - Endogenes
- mi-RNA712 >>>Bind With TIMP3 gene
- Tissue Inhibitor of Metallo-proteinases 3 (TIMP3)
- Decrease —— TIMP3 synthesis
- Increase Proteinase Enzyme
- Increase Endothelium Damage
- Arterial Damage
- Atherosclerosis

What does increase risk of atherosclerosis ?

A. Increase mi-RNA712 & Increase TIMP3 gene expression
B. Decrease mi-RNA712 & Decrease TIMP3 gene expression
C. Increase mi-RNA712 & Decrease TIMP3 gene expression
D. Decrease mi-RNA712 & Increase TIMP3 gene expression

What does increase risk of atherosclerosis ?

A. Increase mi-RNA712 & Increase TIMP3 gene expression
B. Decrease mi-RNA712 & Decrease TIMP3 gene expression
C. Increase mi-RNA712 & Decrease TIMP3 gene expression
D. Decrease mi-RNA712 & Increase TIMP3 gene expression

What can be early marker for detection of probability of atherosclerosis ?

A. Mutation / Increase mi-RNA712
B. Non-Mutated Increase mi-RNA712
C. Mutated / Decrease mi-RNA712
D. Non-Mutation / Decrease mi-RNA712

What can be early marker for detection of probability of atherosclerosis ?

A. Mutation mi-RNA712 Gene and Increase mi-RNA712

B. Non-Mutated mi-RNA712 Gene and Increase mi-RNA712

C. Mutated mi-RNA712 Gene / Decrease mi-RNA712

D. Non-Mutation mi-RNA712 Gene / Decrease mi-RNA712

What can be done to decrease risk of atherosclerosis ?

A. Anti-mi-RNA712
B. mi-RNA712
C. Anti-TIMP3 RNA
D. TIMP3 RNA

What can be done to decrease risk of atherosclerosis ?

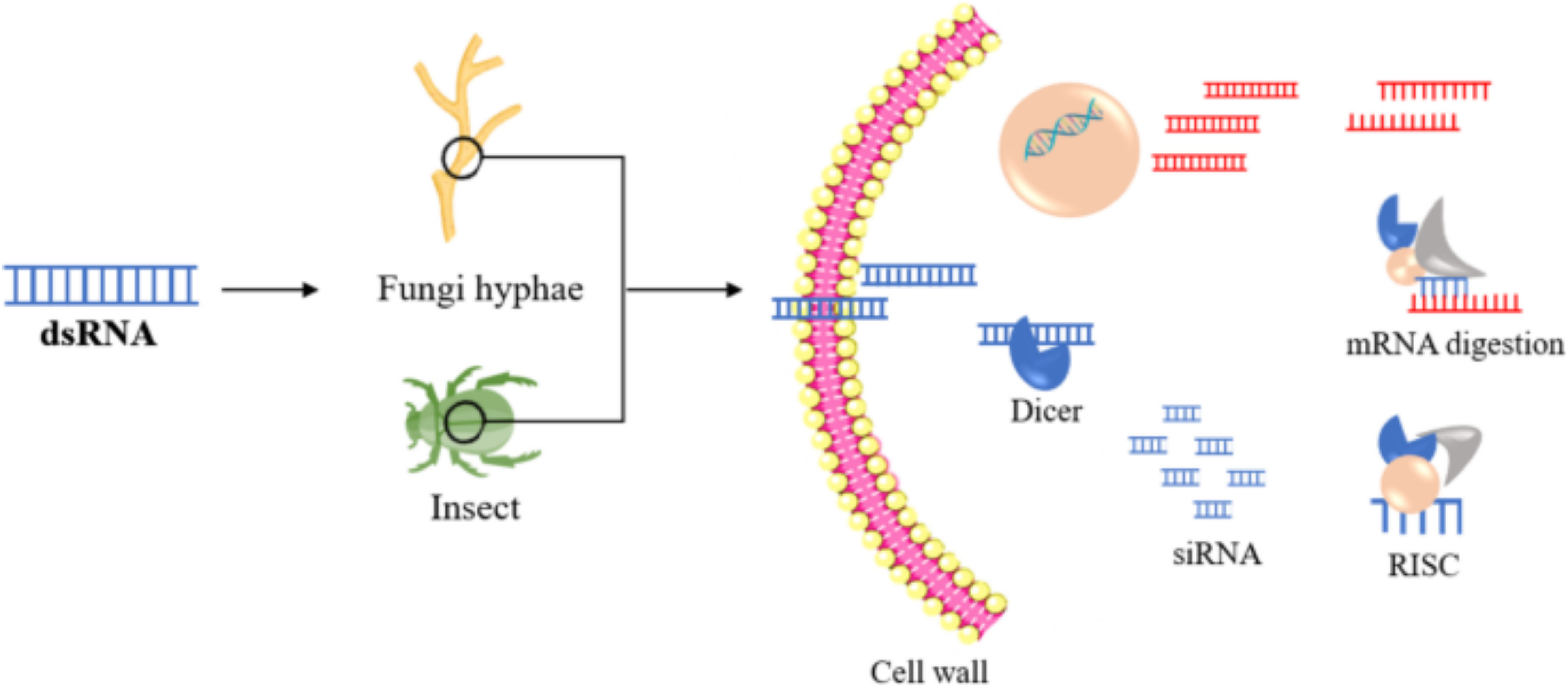
A. Anti-mi-RNA712
B. mi-RNA712
C. Anti-TIMP3 RNA
D. TIMP3 RNA

Positron Emission Tomography Scan

Use

of

FDG = Fluro-Deoxy-Glucose



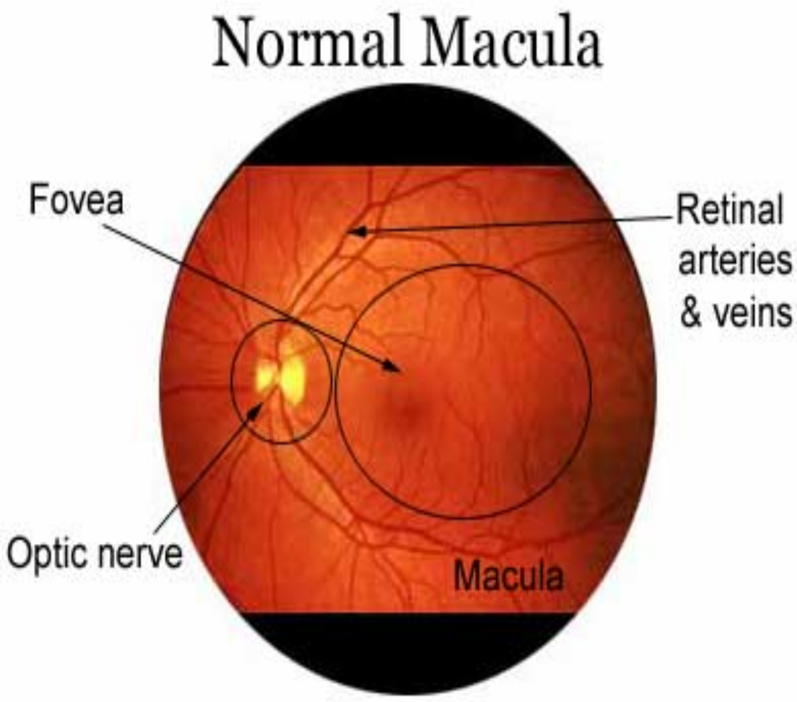
Dicer = Endogenous Enzyme – Ribonuclease

RISC = RNA Induce Silencer Complex

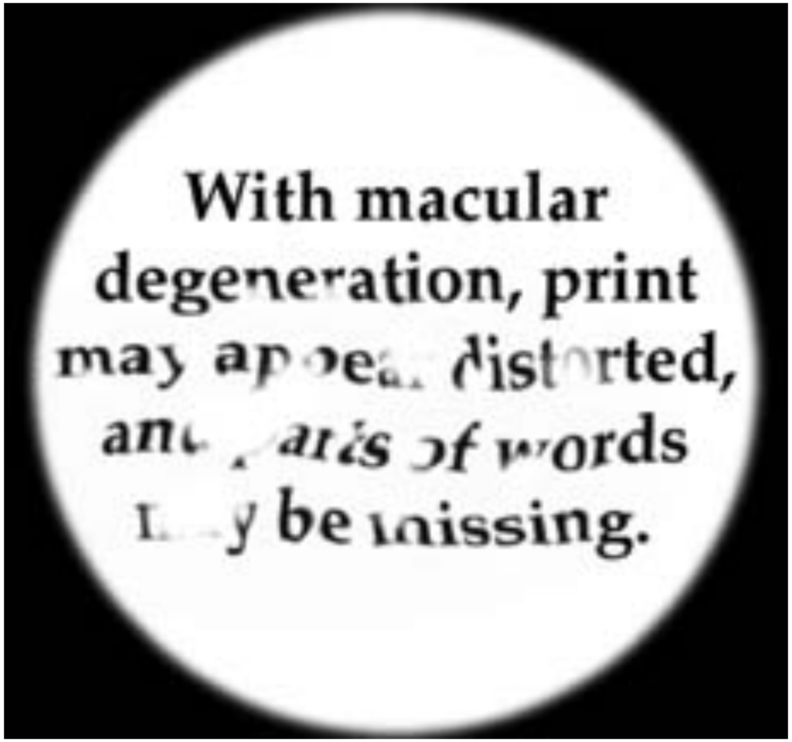
Age related Macular Degeration (AMD)

↓

Blindness



- Visual blurring



Very High --- Vascular Endothelial Growth Factor **(VEGF)**
VEGF --- **Increase blood vessel growth.**
Excess blood vessels behind the retina - **Blurring of Vision**

siRNA —dsRNA (as drug)- **injected into the eye**
specifically **targets the mRNA of VEGF**.

Destroy hundreds of **mRNA**,
So **Suppression VEGF Synthesis**

Youtube Link

- Gene Silencing by microRNAs (youtube.com)

- Explained! 2024 Nobel Prize in Physiology or Medicine. What is microRNA mediated gene regulation? (youtube.com)

snRNA vs snRNP

- Small Nuclear RNA
- U1,U2,U3,U4,U5,U6
- Small Nuclear Ribonucleoproteins

Medulloblastoma

- Brain Cancer
- Mutation >>> U1 snRNA

r-RNA (Ribosomal RNA)

Association with several proteins

Type :

- In Prokaryots = 23S, 16S, and 5S
- In Eukaryots = 28S, 18S, 5.8S, and 5S

“S” = Svedberg unit

Related to the molecular weight and shape.

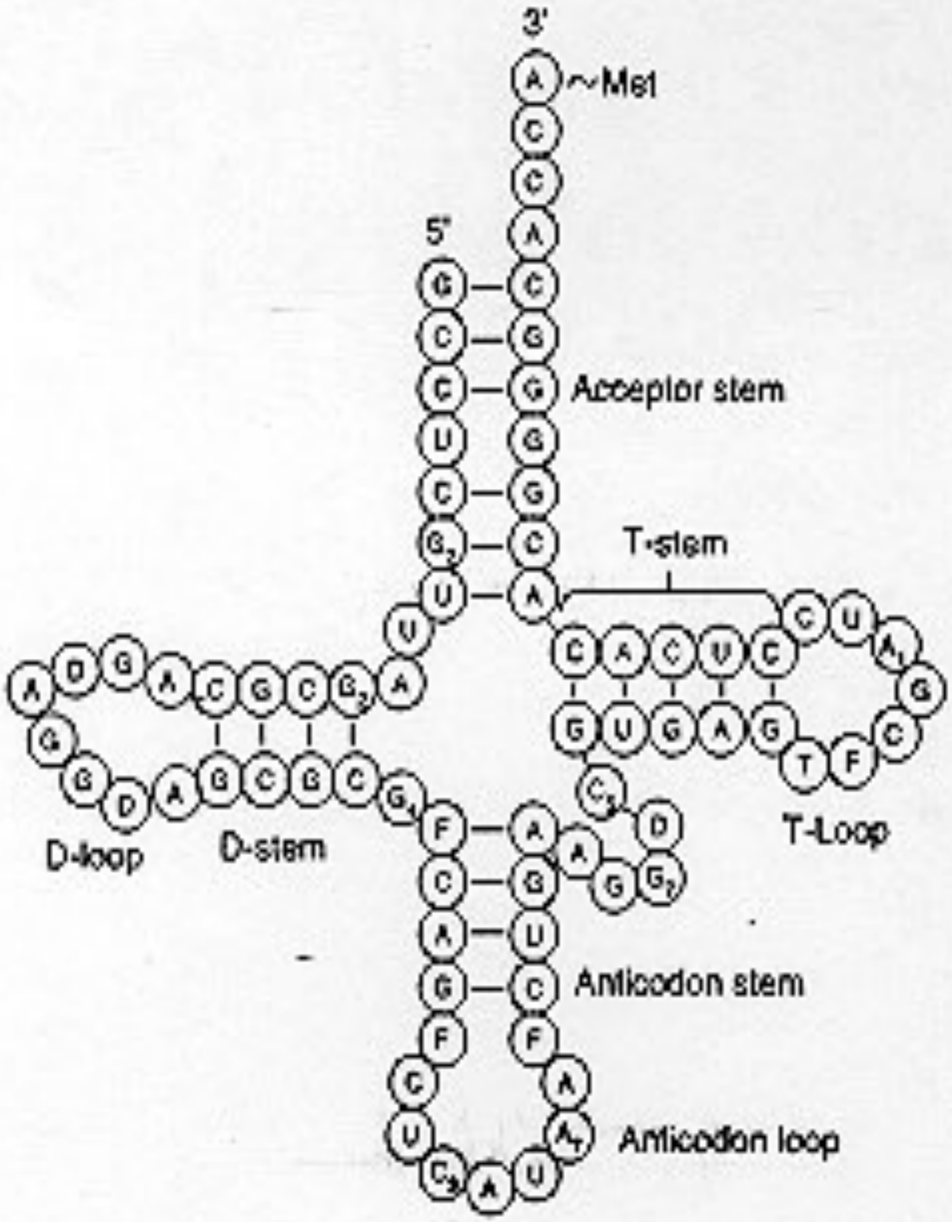
Function :

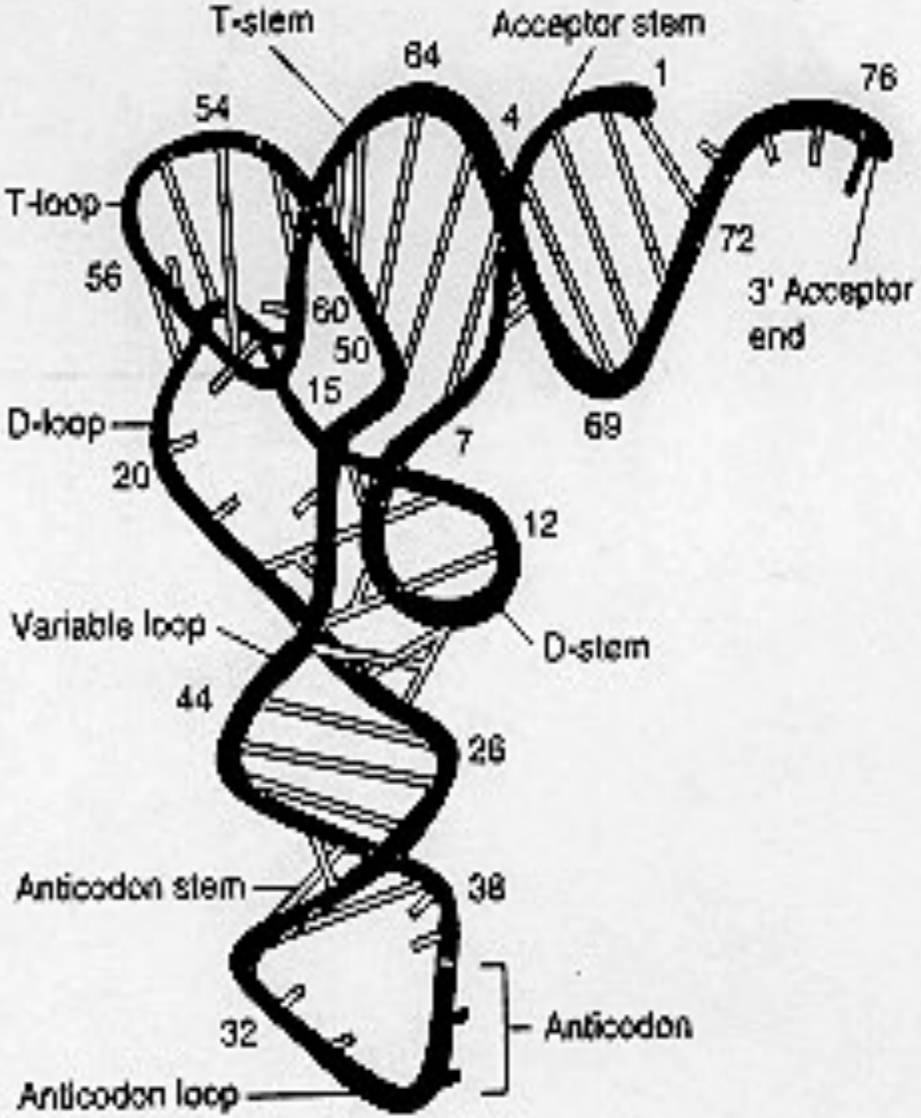
Sites for protein synthesis.

Catalysts in protein synthesis.

E.g. **“Ribozyme”.**

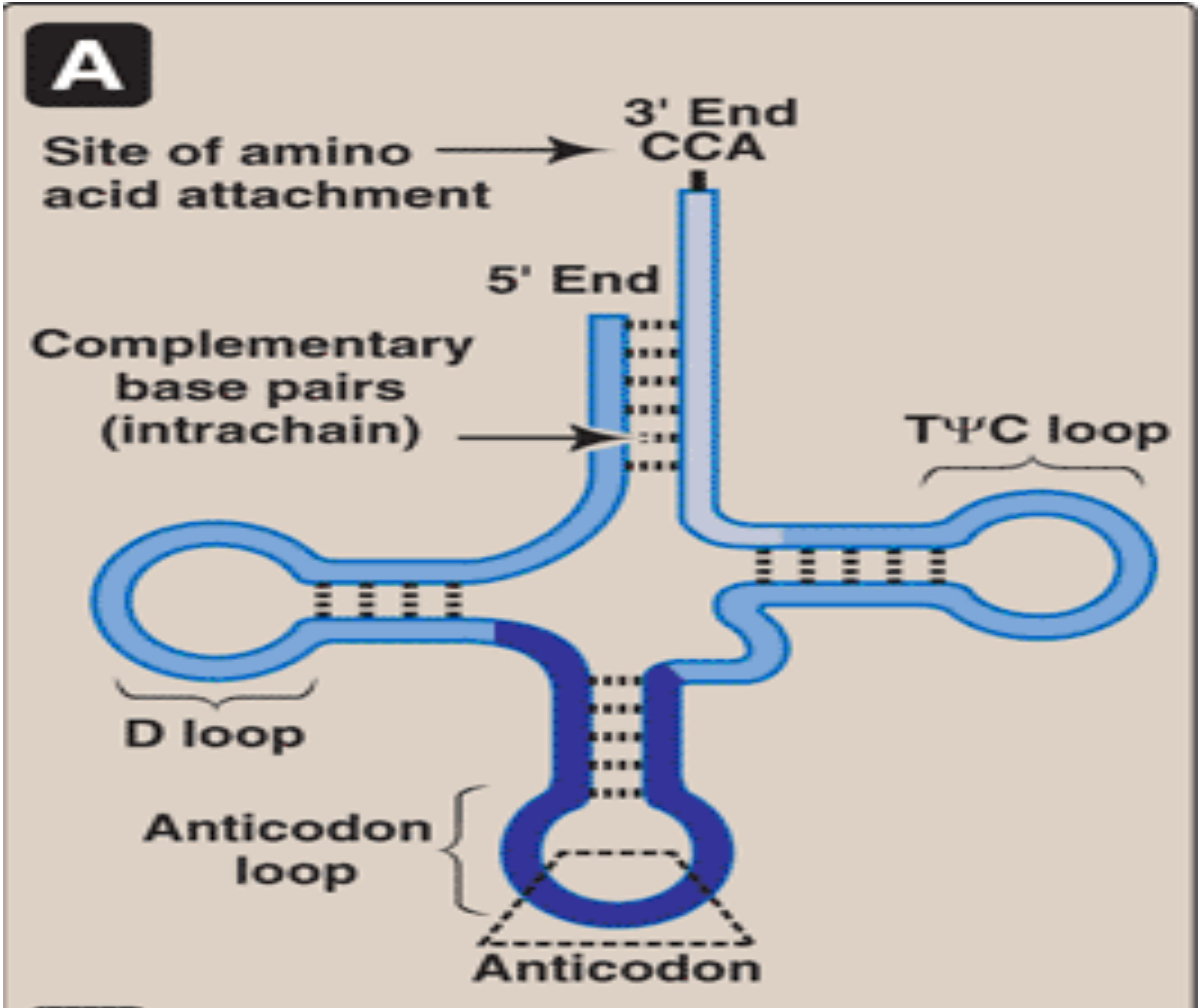
Secondary structure





Tertiary structure

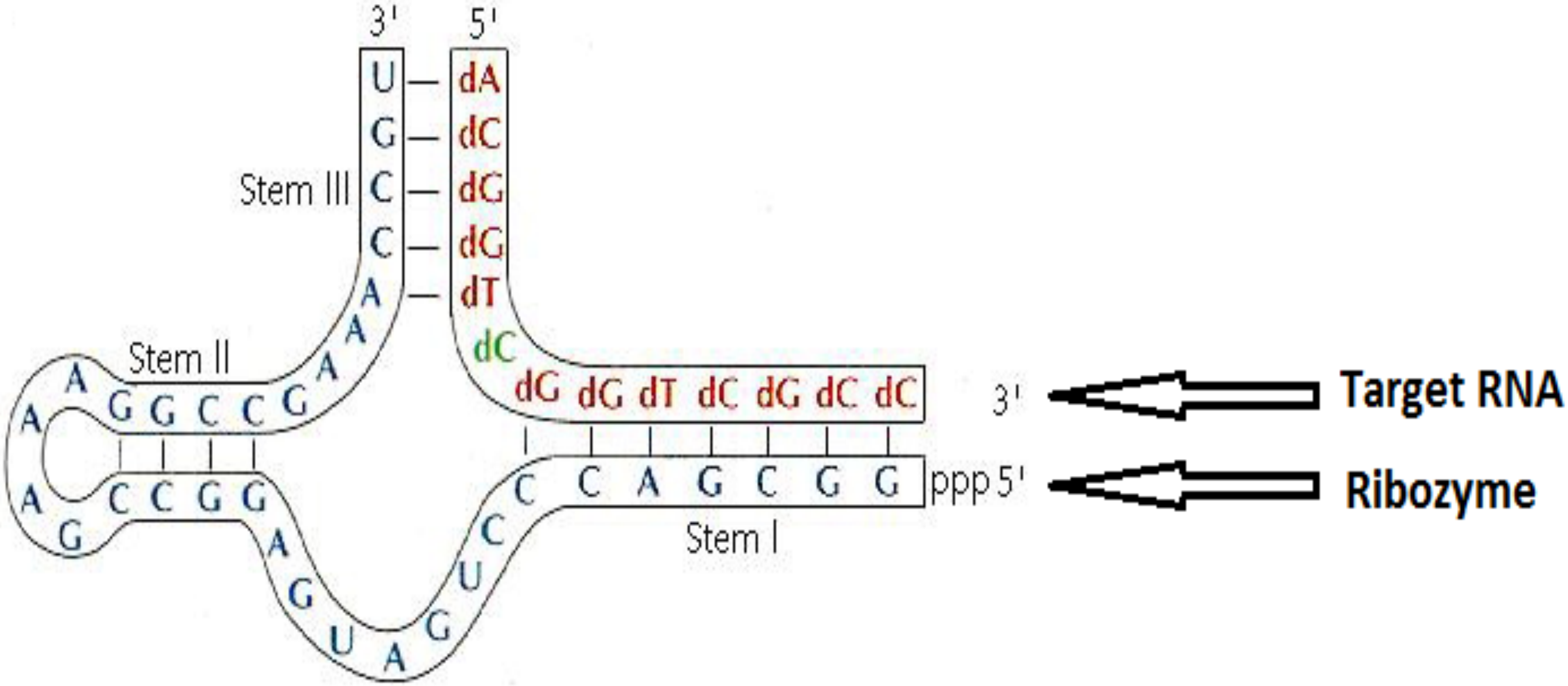
t-RNA

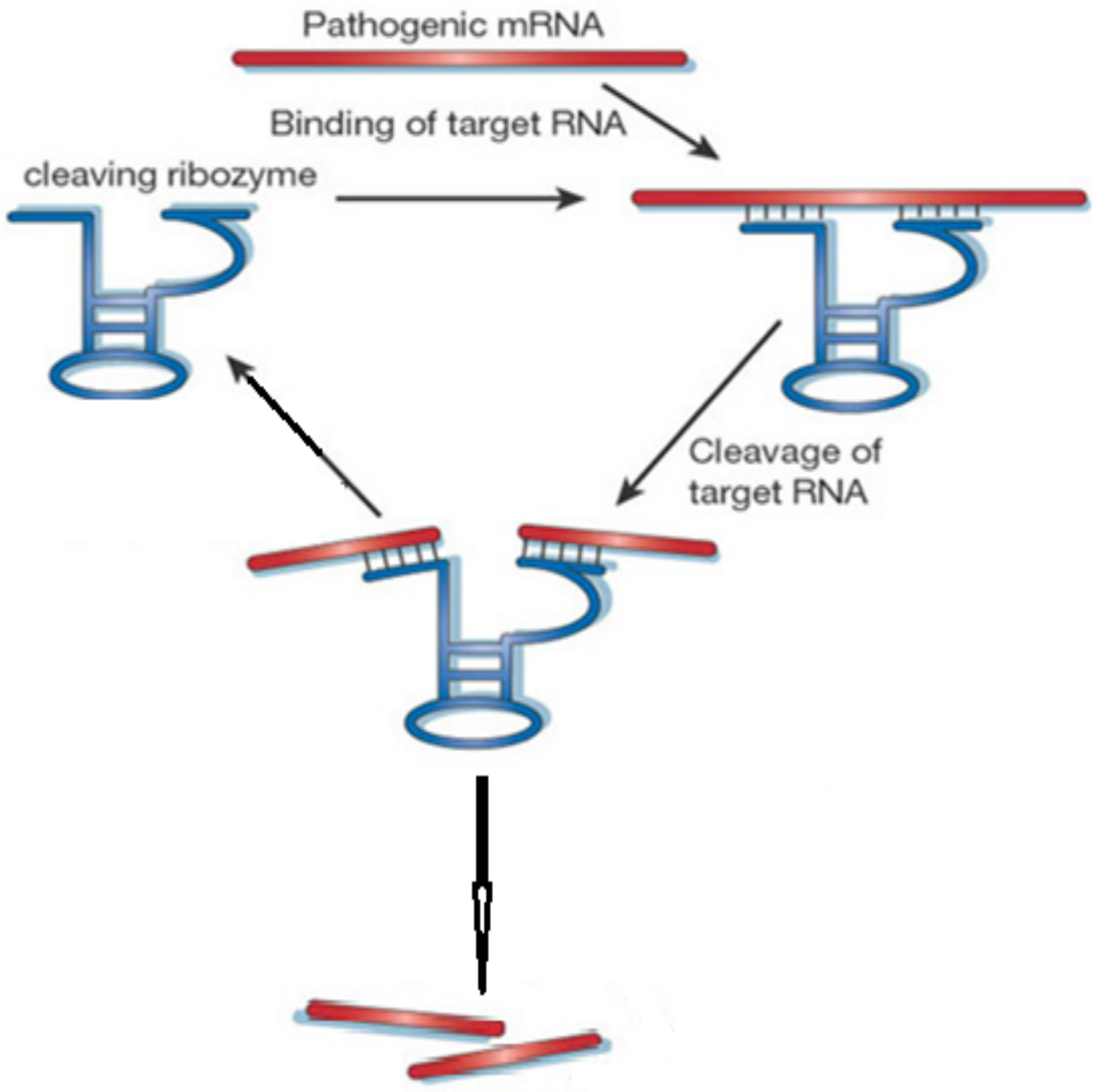

A
3' End
CCA
Site of amino acid attachment
5' End
Complementary base pairs (intrachain)
TΨC loop
D loop
Anticodon loop
Anticodon

t- RNA (transfer RNA)

- Smallest (73 – 93 ns)
- Easily soluble = s-RNA
- Specific tRNA for All 20 amino acids.
- Clover leaf like structure.
- Unusual bases (for example, dihydrouracil,)
- Intrachain base-pairing = Looks secondary & tertiary structure.
- Serves as an “adaptor” molecule

- **Dihydrouracil arm** = Recognition Enzyme to add amino acid
- **Pseudouridine arm** = Binding t-RNA to ribosome
- **Anticodon arm** = Recognize triplet codon on m-RNA
- **Accepter arm** **=** carries amino acid


3'
5'
U G C C A A A G
dA dC dG dG dT
Stem III
dC
dG dG dT dC dG dC dC
3'
Target RNA
Stem II
A A A A G
G G C C
C C G G
A G U A G U C C
C A G C G G
ppp 5'
Ribozyme
Stem I



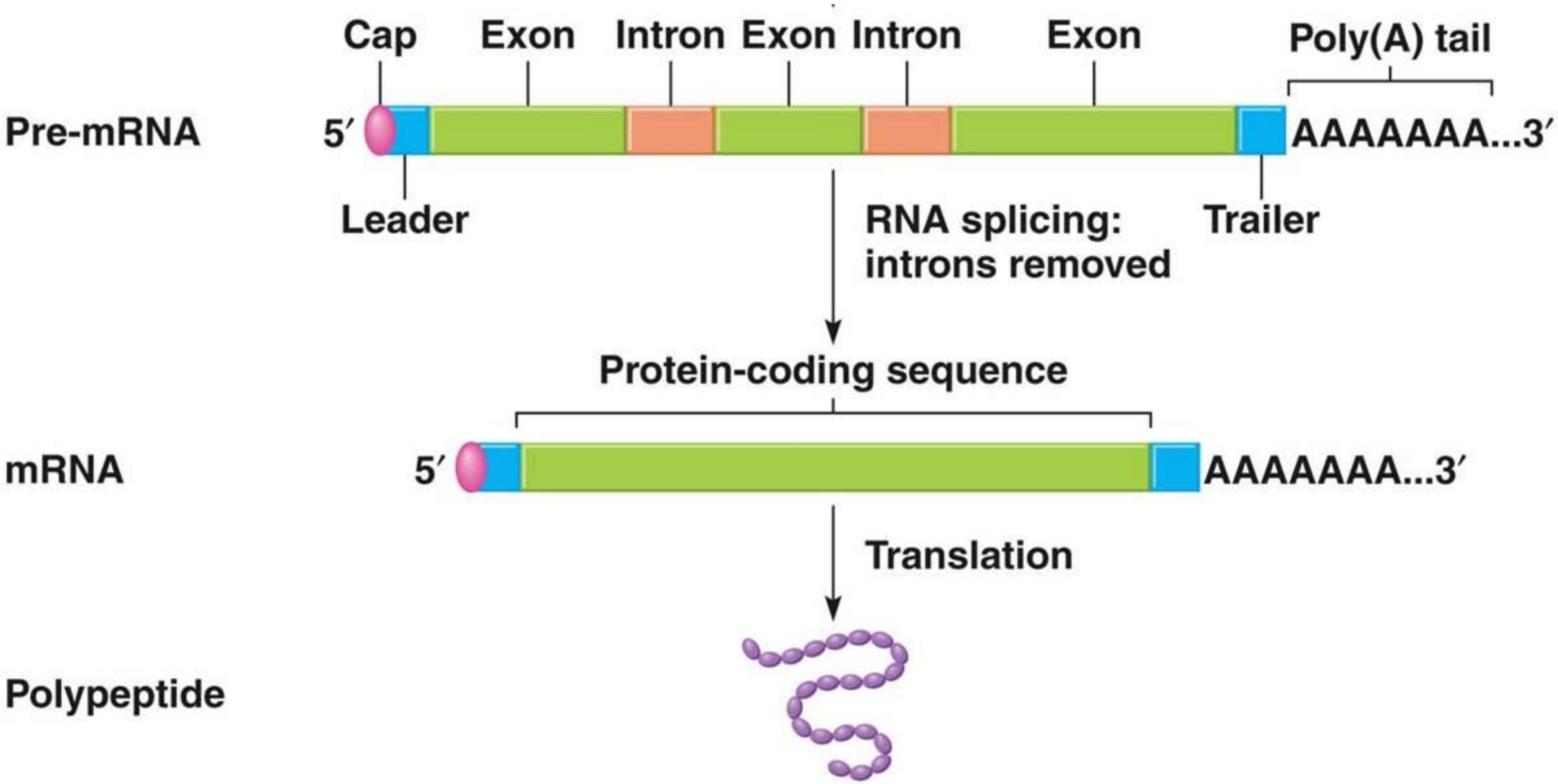
Pathogenic mRNA

Binding of target RNA

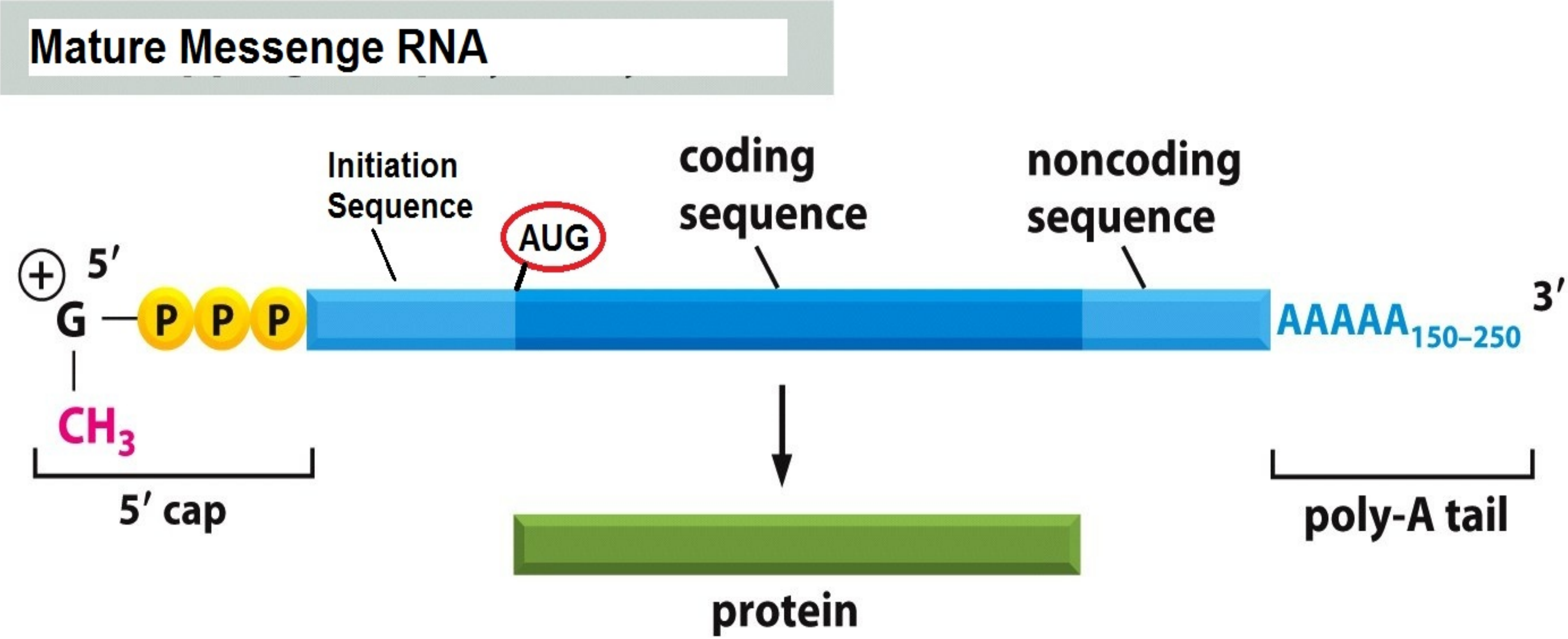
cleaving ribozyme

Cleavage of target RNA

hn-RNA (Pre-mRNA) & m-RNA



m-RNA

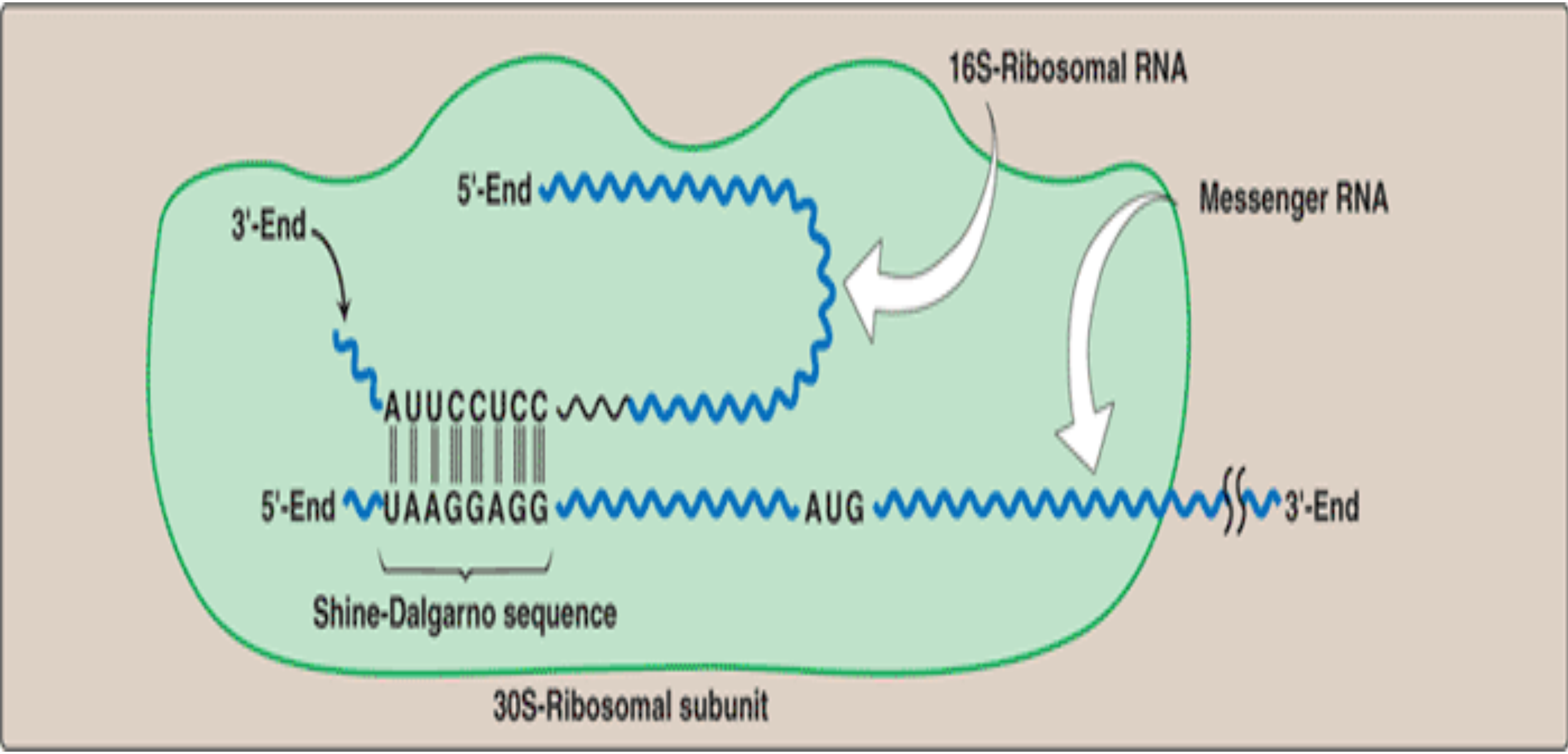


Mature Messenge RNA

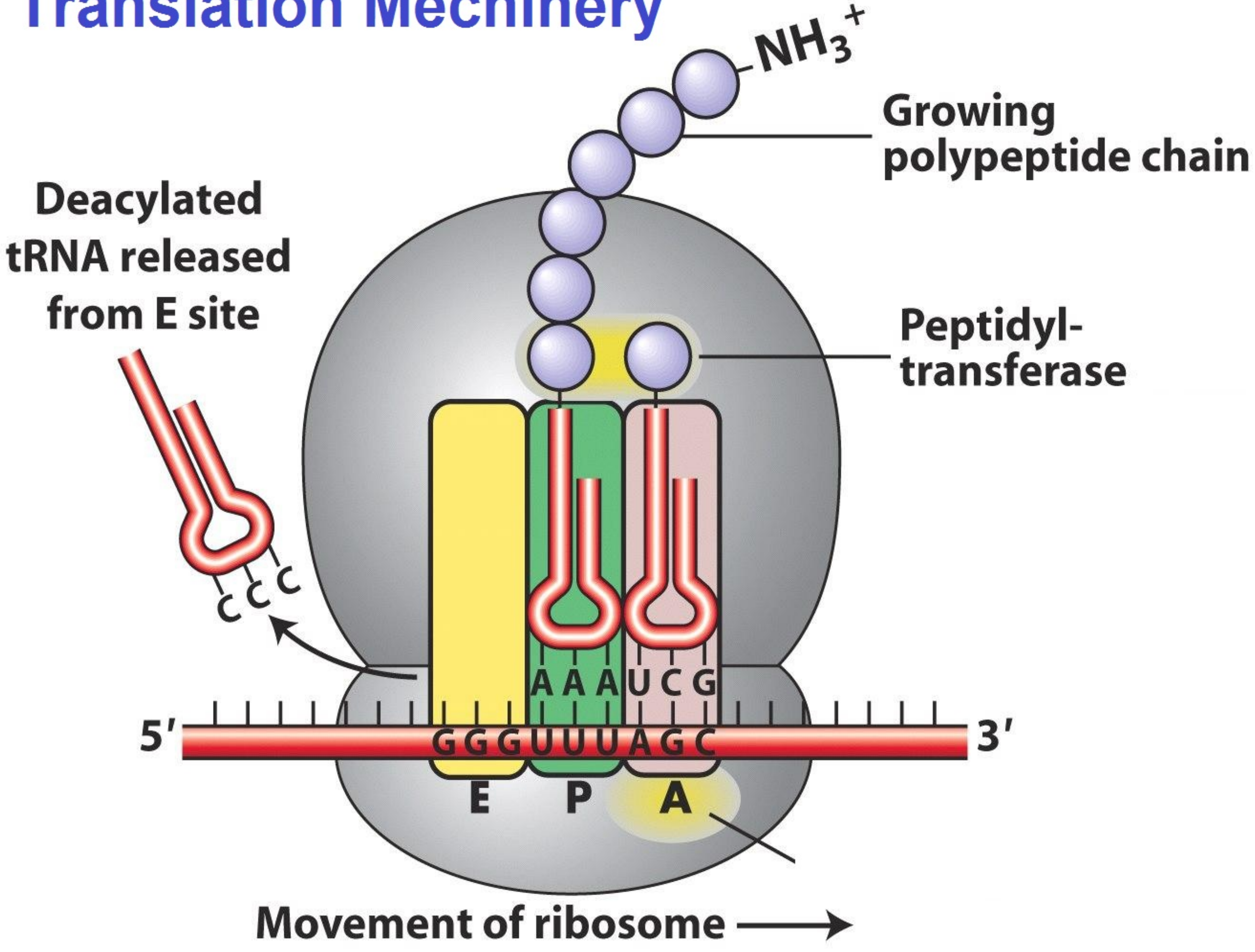
Figure 7-16a Essential Cell Biology 3/e (© Garland Science 2010)

Shine – Dalgarno Sequence

“Facilitate Initiation of Translation”



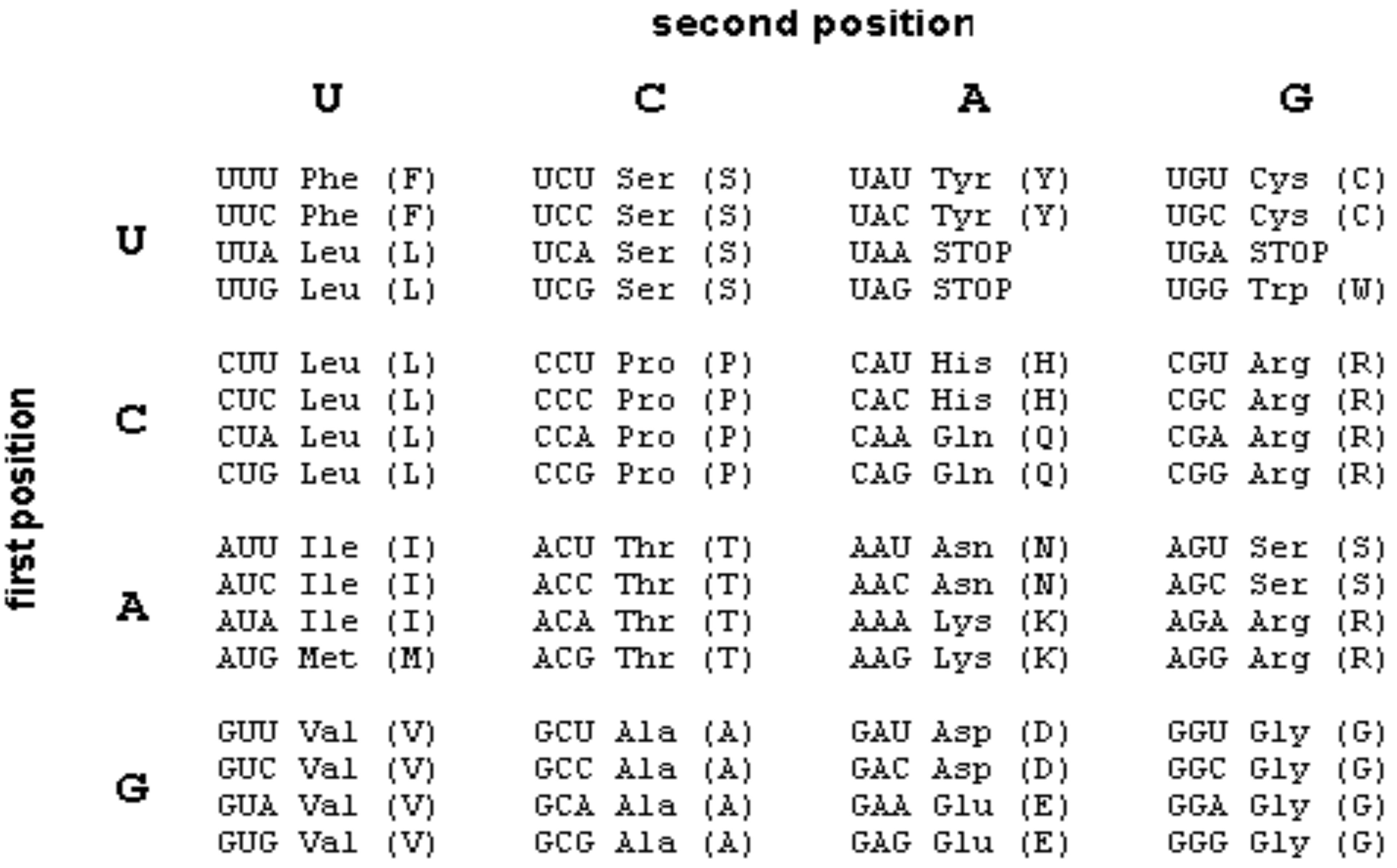
Translation Mechinery



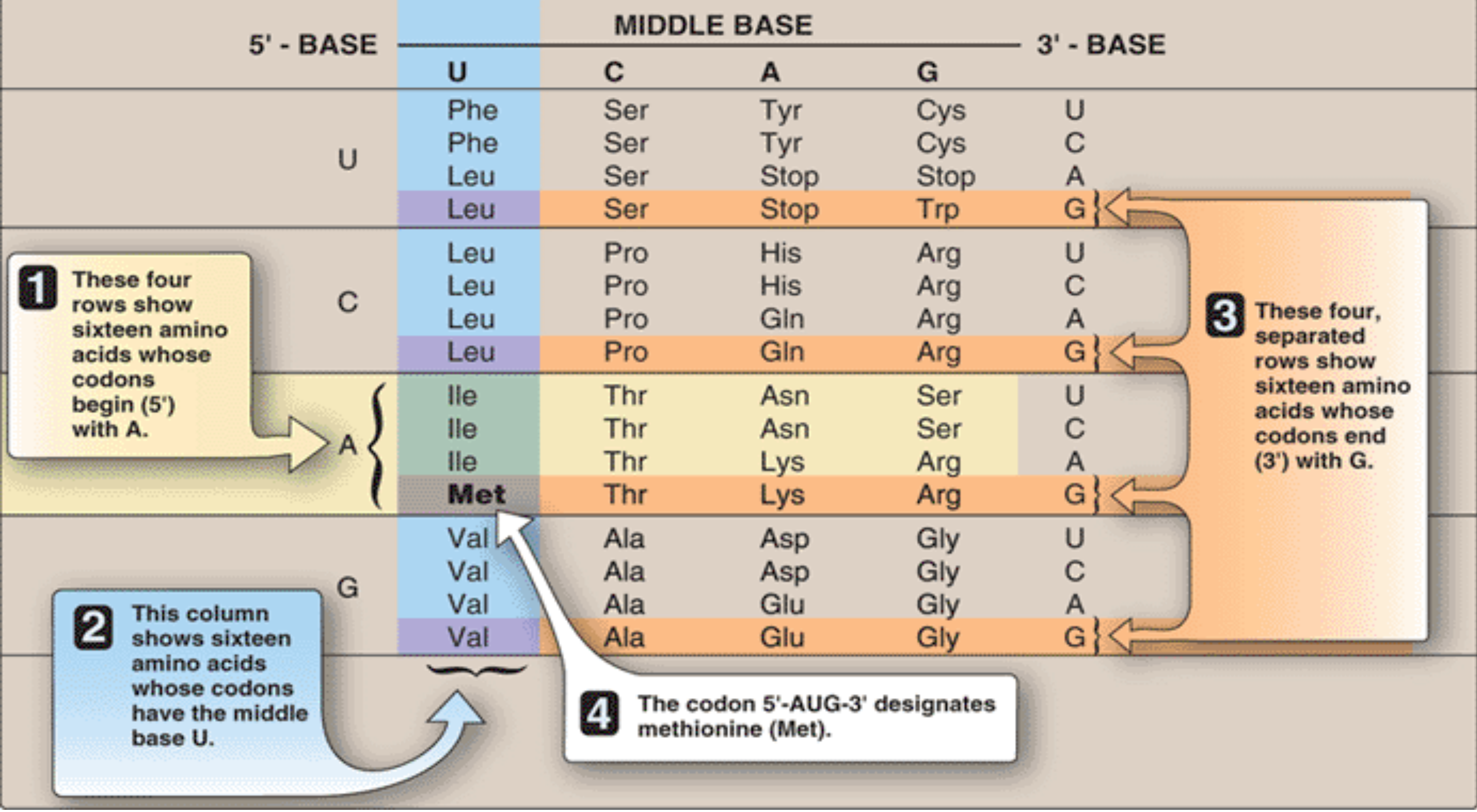
Genetic Code

- Nucleotides read in triplet “codons”
  - 5’ -→ 3’
- Each codon translates to an amino acid
- 64 possible codons
  - 3 positions and 4 possiblities (AGCU) makes 4^3 or 64 possibilities
  - Degeneracy or redundancy of code
    - Only 20 amino acids
    - Implications for mutations

Genetic Code



	second position			
first position	U	C	A	G
U	UUU Phe (F) UUC Phe (F) UUA Leu (L) UUG Leu (L)	UCU Ser (S) UCC Ser (S) UCA Ser (S) UCG Ser (S)	UAU Tyr (Y) UAC Tyr (Y) UAA STOP UAG STOP	UGU Cys (C) UGC Cys (C) UGA STOP UGG Trp (W)
C	CUU Leu (L) CUC Leu (L) CUA Leu (L) CUG Leu (L)	CCU Pro (P) CCC Pro (P) CCA Pro (P) CCG Pro (P)	CAU His (H) CAC His (H) CAA Gln (Q) CAG Gln (Q)	CGU Arg (R) CGC Arg (R) CGA Arg (R) CGG Arg (R)
A	AUU Ile (I) AUC Ile (I) AUA Ile (I) AUG Met (M)	ACU Thr (T) ACC Thr (T) ACA Thr (T) ACG Thr (T)	AAU Asn (N) AAC Asn (N) AAA Lys (K) AAG Lys (K)	AGU Ser (S) AGC Ser (S) AGA Arg (R) AGG Arg (R)
G	GUU Val (V) GUC Val (V) GUA Val (V) GUG Val (V)	GCU Ala (A) GCC Ala (A) GCA Ala (A) GCG Ala (A)	GAU Asp (D) GAC Asp (D) GAA Glu (E) GAG Glu (E)	GGU Gly (G) GGC Gly (G) GGA Gly (G) GGG Gly (G)



5' - BASE	MIDDLE BASE U	C	A	G	3' - BASE
U	Phe	Ser	Tyr	Cys	U
	Phe	Ser	Tyr	Cys	C
	Leu	Ser	Stop	Stop	A
	Leu	Ser	Stop	Trp	G
C	Leu	Pro	His	Arg	U
	Leu	Pro	His	Arg	C
	Leu	Pro	Gln	Arg	A
	Leu	Pro	Gln	Arg	G
A	Ile	Thr	Asn	Ser	U
	Ile	Thr	Asn	Ser	C
	Ile	Thr	Lys	Arg	A
	Met	Thr	Lys	Arg	G
G	Val	Ala	Asp	Gly	U
	Val	Ala	Asp	Gly	C
	Val	Ala	Glu	Gly	A
	Val	Ala	Glu	Gly	G

1 These four rows show sixteen amino acids whose codons begin (5') with A.

2 This column shows sixteen amino acids whose codons have the middle base U.

3 These four, separated rows show sixteen amino acids whose codons end (3') with G.

4 The codon 5'-AUG-3' designates methionine (Met).

Use of the genetic code table to translate the codon AUG

Genetic Code

1. **Triplet Codons** :
   Each codon is a consecutive sequence of three bases
2. **Non-overlapping** :
   Codes are always read one after another.
3. **Non-punctuated** :
   Codes are always continues.
4. **Specificity (unambiguous)** :
   One codon always codes for specific amino acid
5. **Universal** :
   Codons represent same amino acid in all species.
   Except in Mitochondria

6. **Degenerate** :

Each codon corresponds to a single A.A.

But A.A. may have more than one triplet codon.

7. **Initiator codon** :

AUG is start codon

8. **Termination codons**

Nuclear DNA = UAA,UGA, UAG,

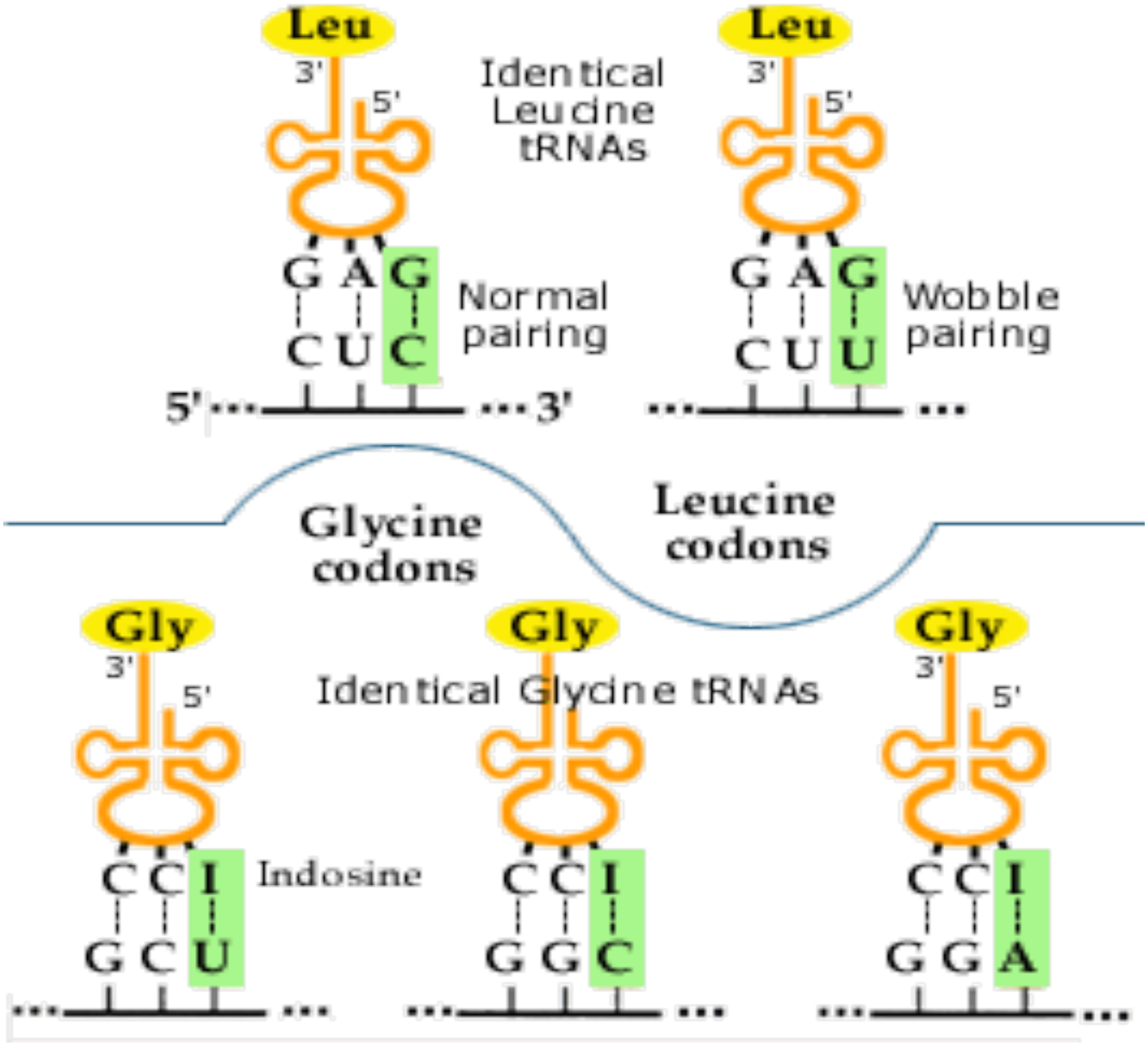
Mitochondrial DNA = AGG,AGA,

9. **Wobbling Phenomenon** :

The reduced stringency between the third base of the codon and the complementary nucleotide in the anticodon is called wobble.

It reduce effect of mutation.

Wobbling Phenomenon



Mutation

Mutation

Vs

Damage

Vs

Polymorphism

Vs

Substitution

Evolution

>>>Before 10,000 Year Ago

……………Hunting was source of Food

>>>Than Human invented

……………………..Agriculture

>>>Until Human unable to digest milk,

……………………..**mutated lactose enzyme gene**

Very High Number of Lactose Intolerance

Than We evolved…..

Same you can think what capacity do you like you generated for 1000 stream down sons or daughters

Find Prevalence of Tuberculosis in Last 100 years

Vs

Find Prevalence of HIV in Last 100 years

Philosophy of Genetical Evolution

Life exists entirely
in the margin of error
between damage and perfect repair.

Evaluation occurs simply,
If Population survive with the tolerable mistake

Philosophy of Genetical Evolution

Matching Perfectly With Life

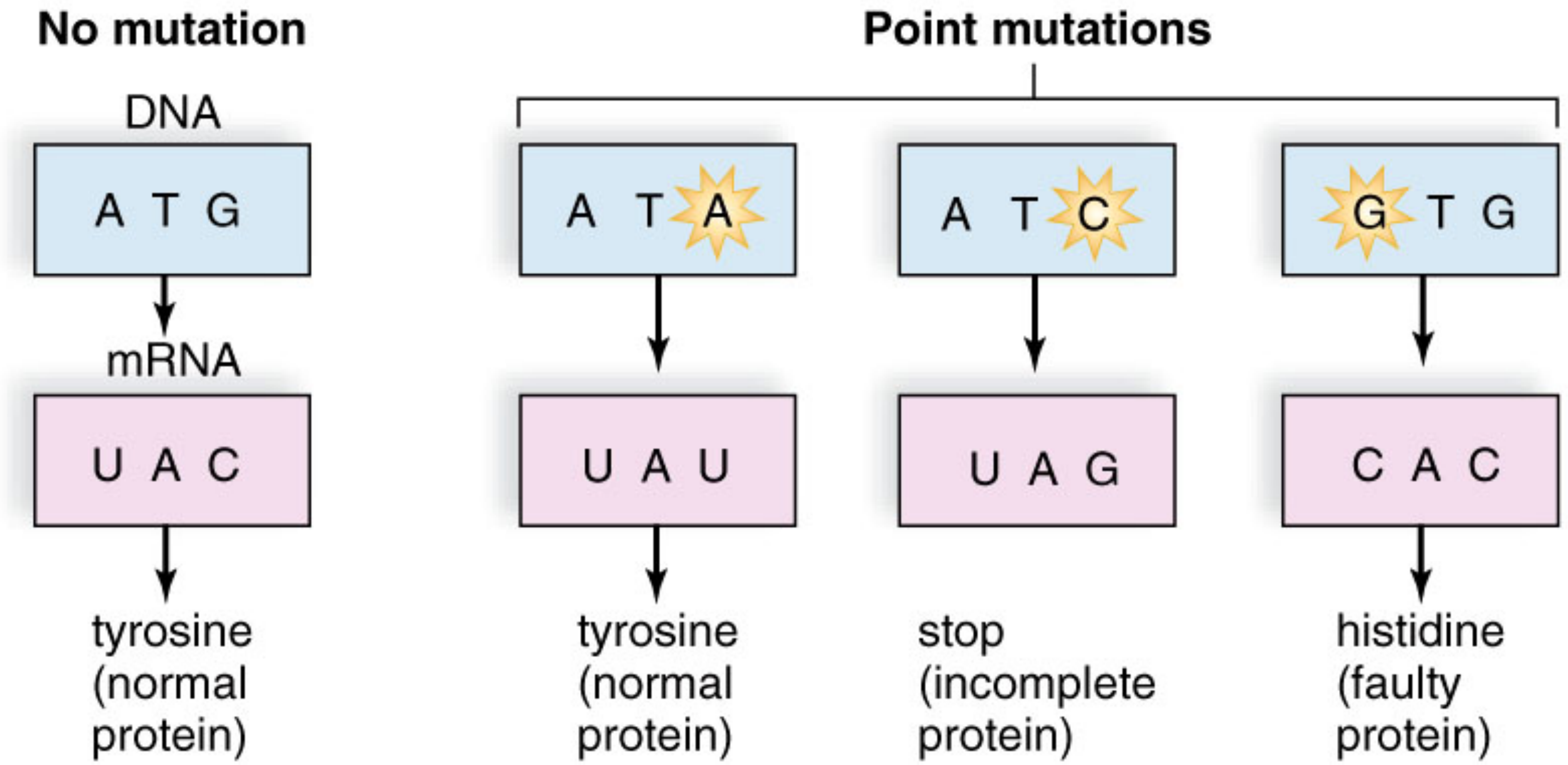
Life exists entirely
in the margin of error
between damage (Multiple GF/BF) and
perfect repair (Breakup and Find New).

Evaluation occurs simply,
If Population survive with the tolerable mistake
(marriage)

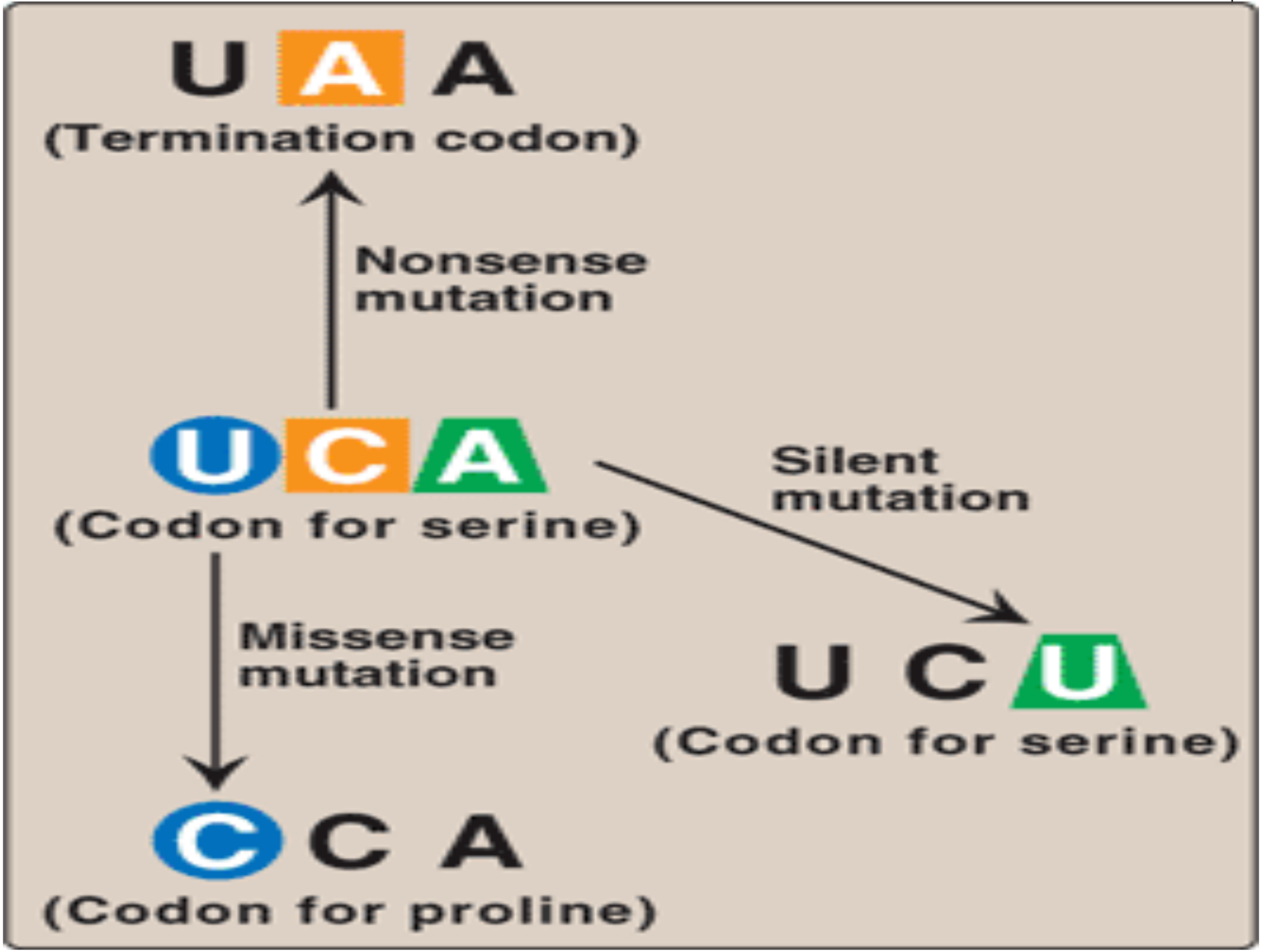
Mutation - Tumour Supressor Gene

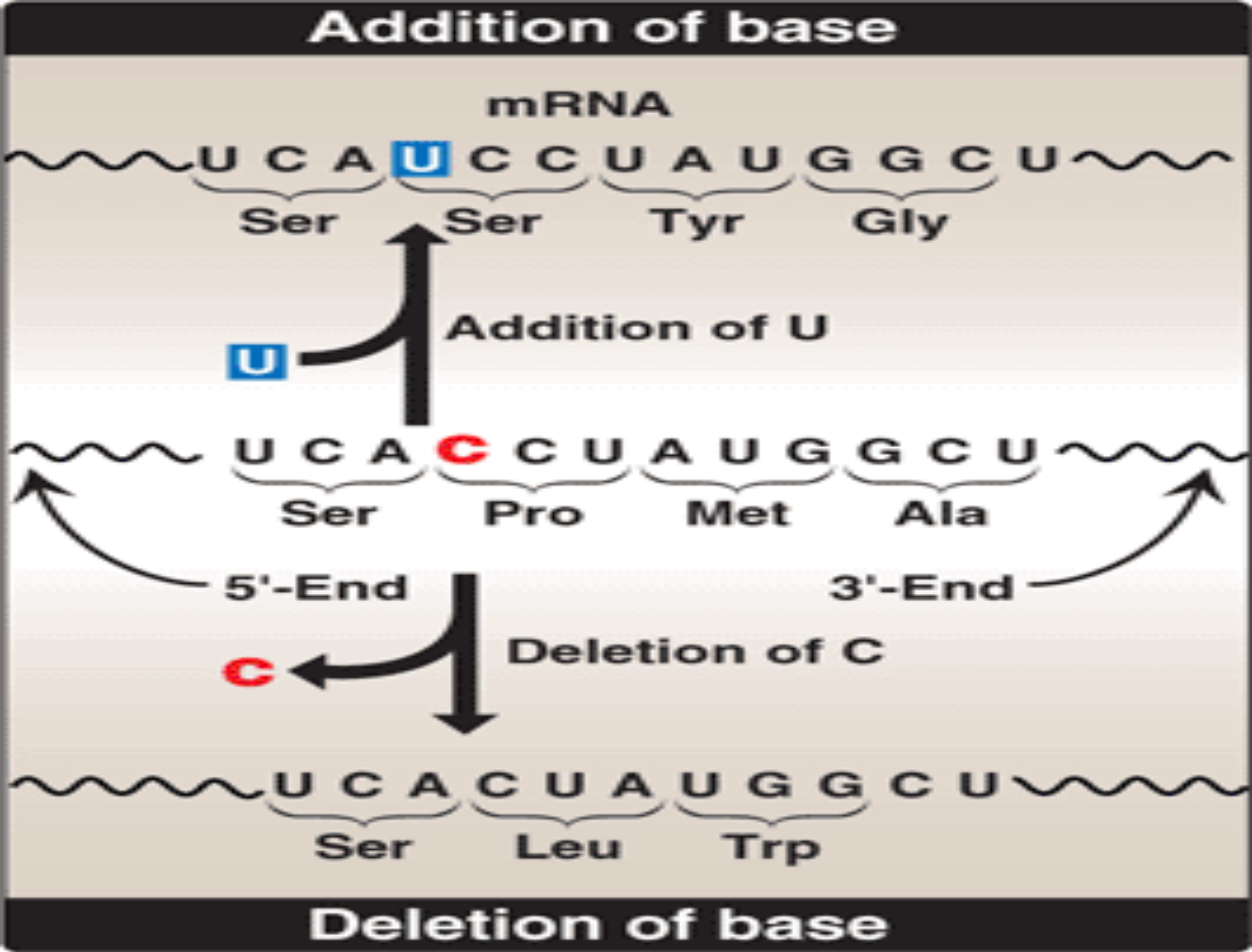
- p53 Gene = p53 protein = 7 domain
- One of Domain Work as
  - DNA Binding Protein (Rich In Arginine)
- p53 = 37% chance of Mutation in Cancer
  - Colon
  - Breast
  - Lungs
- No Synthesis of p53 Proteins
- No Binding with DNA for it’s regulation
- Over Production of NPM1 (Nucleophosmin) gene
- Leukemia

Point Mutation

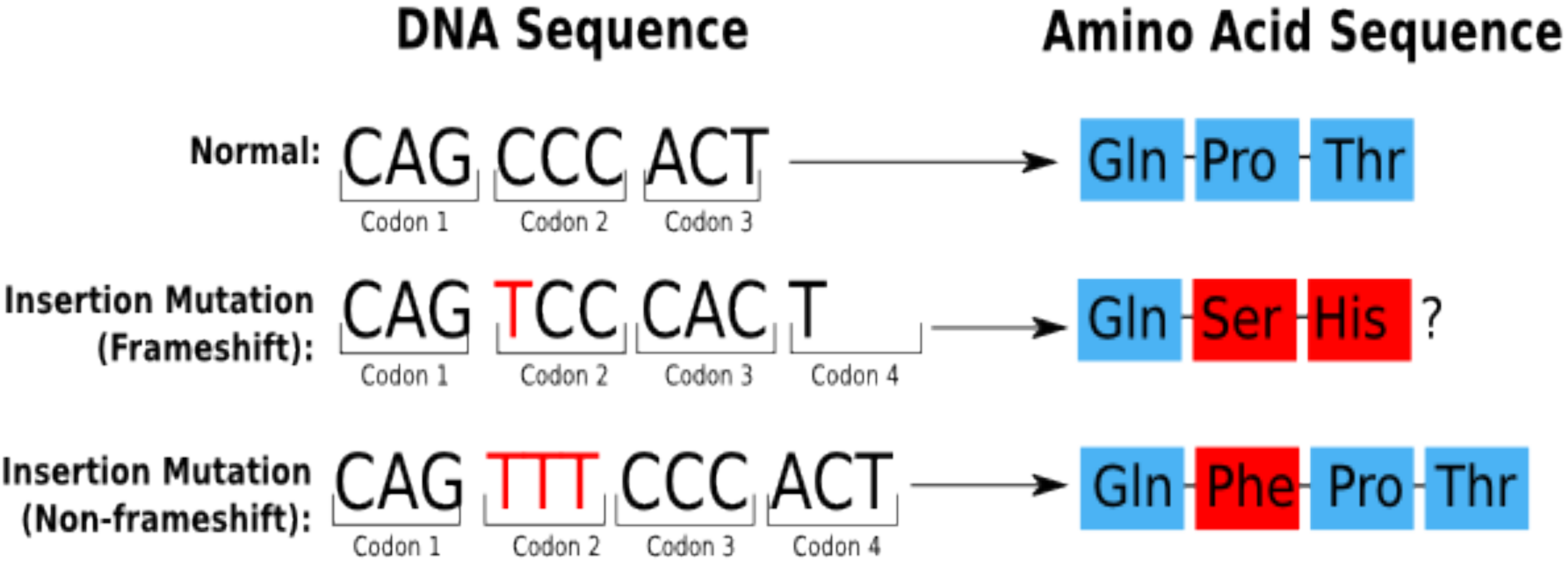


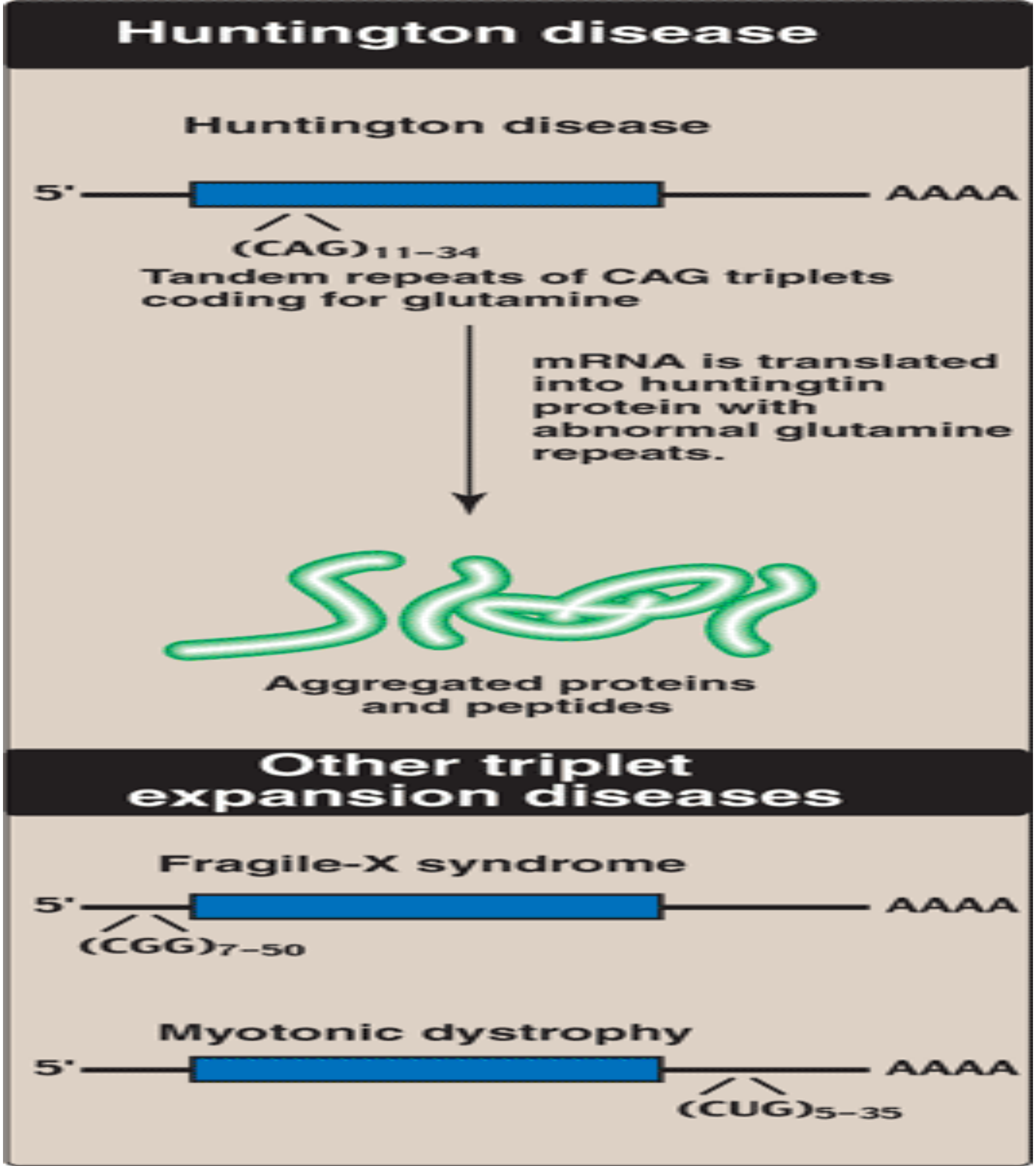
Effect Of Mutation



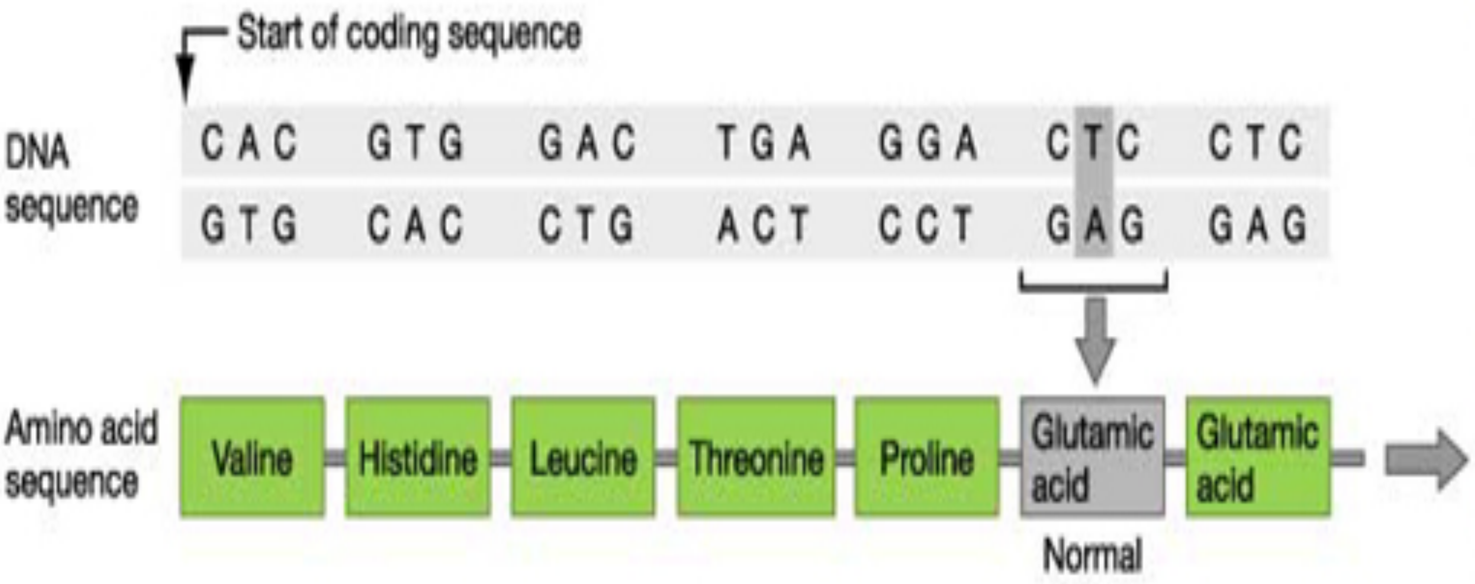

Addition of base
mRNA
U C A U C C U A U G G C U
Ser Ser Tyr Gly
Addition of U
U
U C A C C U A U G G C U
Ser Pro Met Ala
5'-End
3'-End
Deletion of C
C
U C A C U A U G G C U
Ser Leu Trp
Deletion of base

Insertion Type of Mutation




Huntington disease
Huntington disease
5'
AAAA
$(CAG)_{11-34}$
Tandem repeats of CAG triplets coding for glutamine
mRNA is translated into huntingtin protein with abnormal glutamine repeats.
Aggregated proteins and peptides
Other triplet expansion diseases
Fragile-X syndrome
5'
AAAA
$(CGG)_{7-50}$
Myotonic dystrophy
5'
AAAA
$(CUG)_{5-35}$

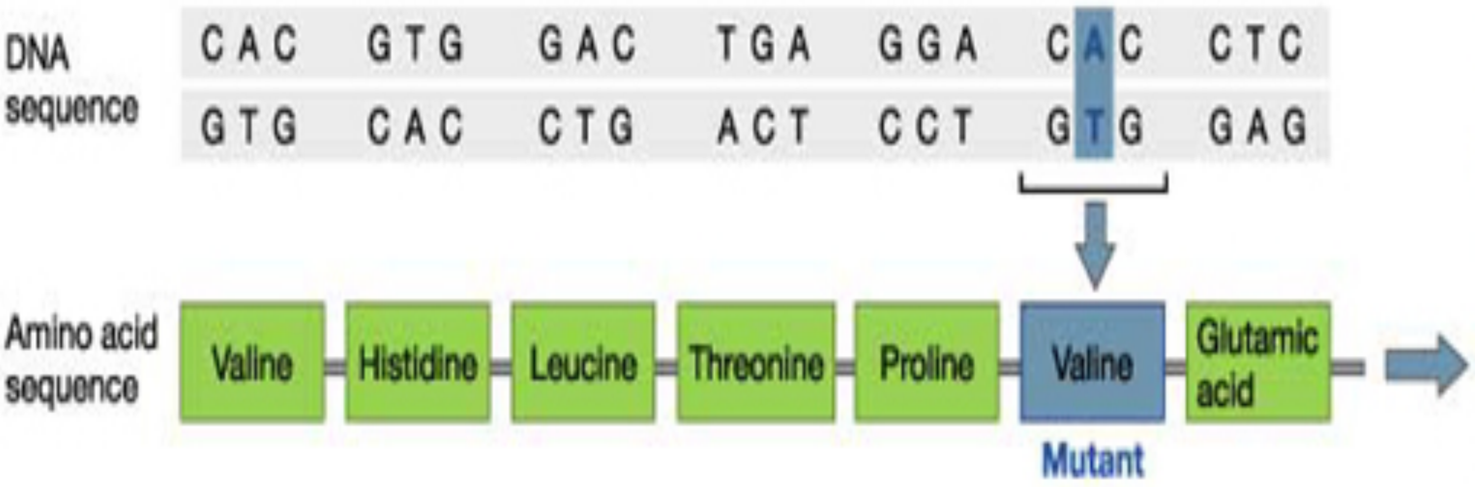
Point Mutation - Mis-Sense



Start of coding sequence

DNA sequence	CAC	GTG	GAC	TGA	GGA	CTC	CTC
	GTG	CAC	CTG	ACT	CCT	GAG	GAG
Amino acid sequence	Valine	Histidine	Leucine	Threonine	Proline	Glutamic acid	Glutamic acid
						Normal	

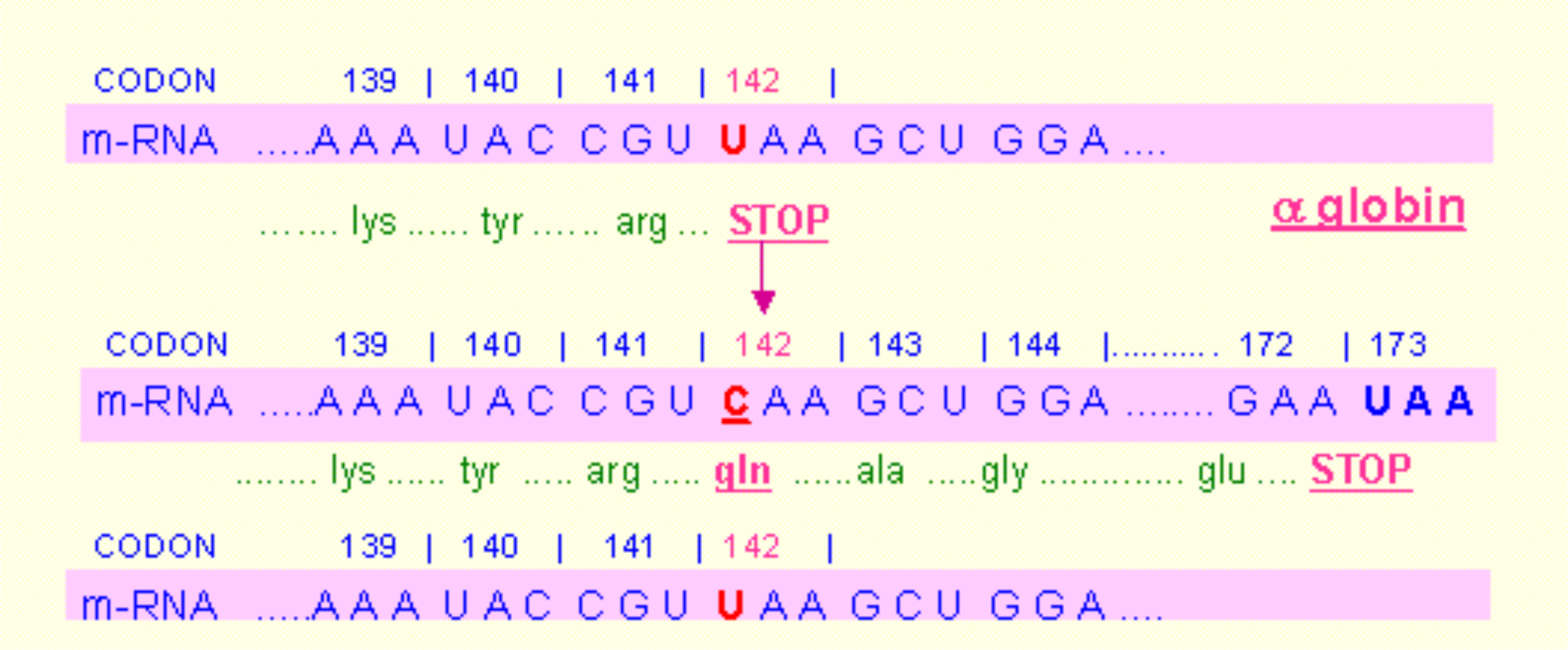
Normal red blood cells



DNA sequence	CAC	GTG	GAC	TGA	GGA	CAC	CTC
	GTG	CAC	CTG	ACT	CCT	GTG	GAG
Amino acid sequence	Valine	Histidine	Leucine	Threonine	Proline	Valine	Glutamic acid
						Mutant	

Sickled red blood cells

What can be problem ?



CODON 139 | 140 | 141 | 142 |

m-RNA .....A A A U A C C G U **U** A A G C U G G A ....

.... lys ...... tyr ...... arg ... STOP

α globin

CODON 139 | 140 | 141 | 142 | 143 | 144 |.......... 172 | 173

m-RNA .....A A A U A C C G U **C** A A G C U G G A .... G A A **U A A**

.... lys ...... tyr ..... arg ..... gln ......ala .....gly .... glu .... STOP

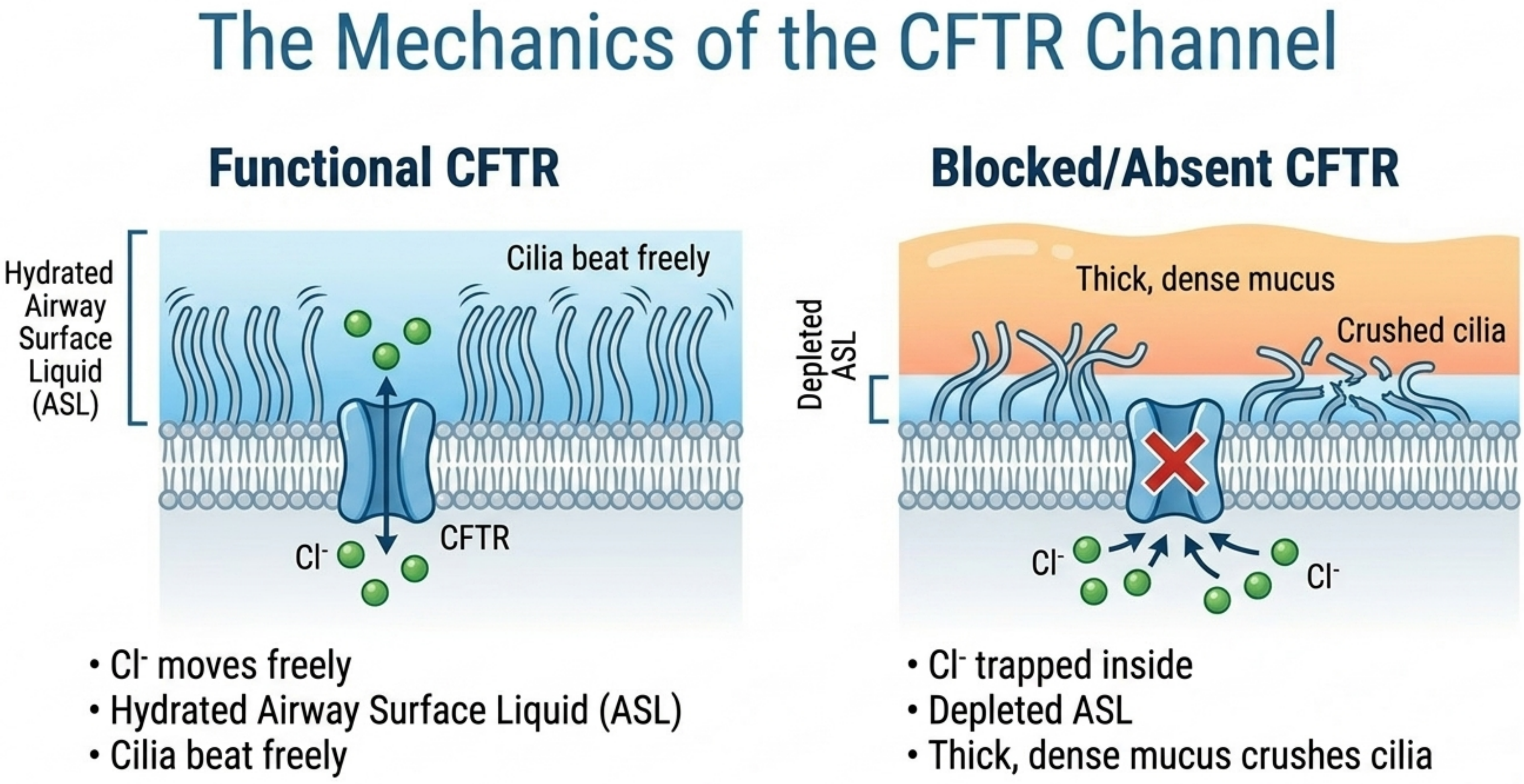
CODON 139 | 140 | 141 | 142 |

m-RNA .....A A A U A C C G U **U** A A G C U G G A ....

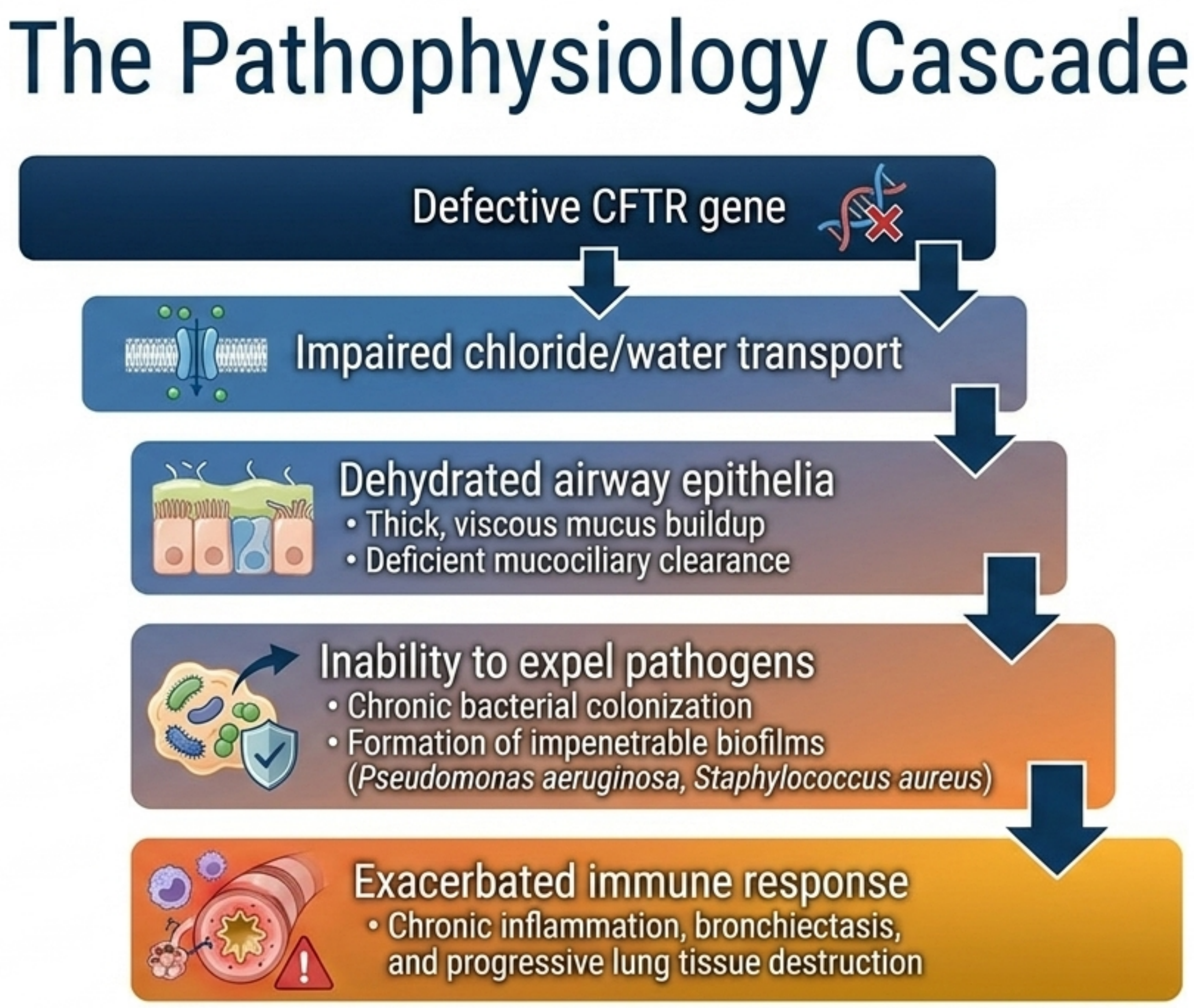
Deletion Type of Mutation

Deletion of “CTT” code from CFTR Gene

CFTR = Cystic Fibrosis Transmembrane Conductance Regulator



Cystic Fibrosis



The Pathophysiology Cascade

Defective CFTR gene

Impaired chloride/water transport

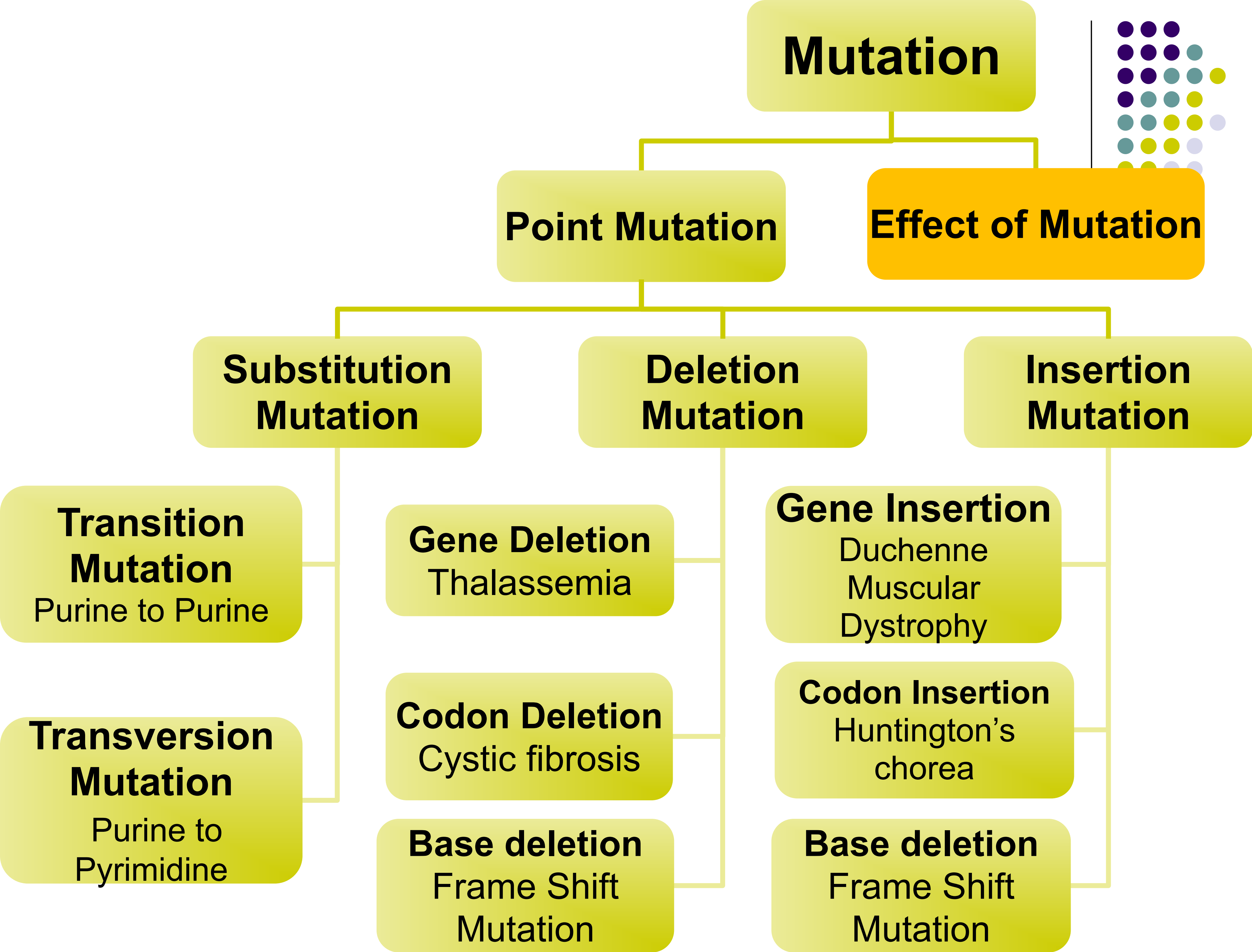
Dehydrated airway epithelia
- Thick, viscous mucus buildup
- Deficient mucociliary clearance

Inability to expel pathogens
- Chronic bacterial colonization
- Formation of impenetrable biofilms (*Pseudomonas aeruginosa, Staphylococcus aureus*)

Exacerbated immune response
- Chronic inflammation, bronchiectasis, and progressive lung tissue destruction

Clinical Feature in Cystic Fibrosis

- GIT
- Respiratory
- Fallopian Tube
- Seminal Vesicles
- Pancreatic duct
- Billiary System



Mutation

Point Mutation

Effect of Mutation

Substitution Mutation

Transition Mutation
Purine to Purine

Transversion Mutation
Purine to Pyrimidine

Deletion Mutation

Gene Deletion
Thalassemia

Codon Deletion
Cystic fibrosis

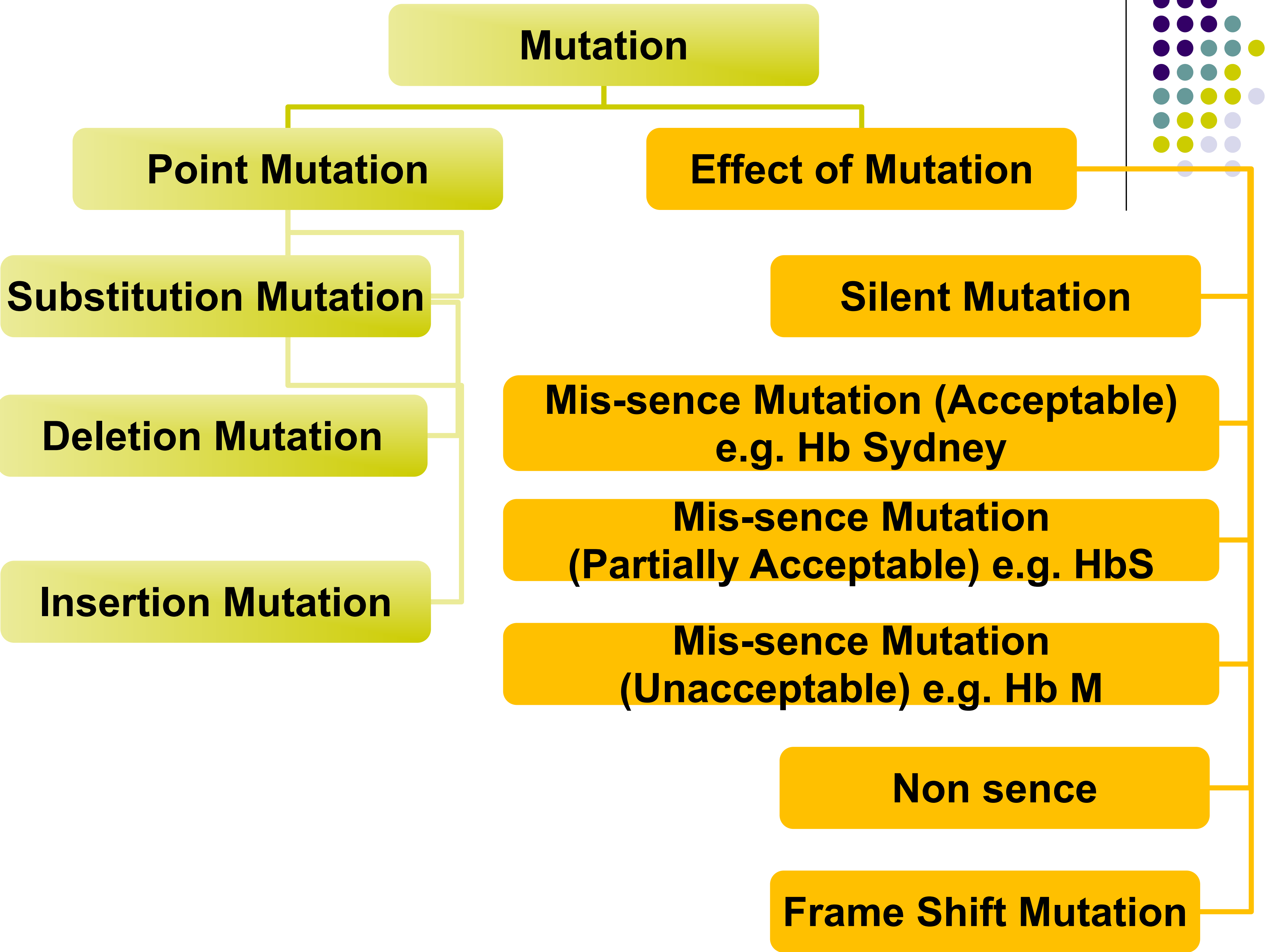
Base deletion
Frame Shift Mutation

Insertion Mutation

Gene Insertion
Duchenne Muscular Dystrophy

Codon Insertion
Huntington’s chorea

Base deletion
Frame Shift Mutation



Mutation

- Point Mutation
  - Substitution Mutation
  - Deletion Mutation
  - Insertion Mutation
- Effect of Mutation
  - Silent Mutation
  - Mis-sence Mutation (Acceptable) e.g. Hb Sydney
  - Mis-sence Mutation (Partially Acceptable) e.g. HbS
  - Mis-sence Mutation (Unacceptable) e.g. Hb M
  - Non sence
  - Frame Shift Mutation

Substitution Mutation

- Transition
  - Purine replace by Purine
  - Pyrimidine replace by Pyrimidine
- Transversion
  - Purine replace by Pyrimidine
  - Pyrimidine replace by Purine
  - E.g. Sickle cell anaemia
  - GAG (glutamic acid)= GUG (valine)

Translation
(Protein Synthesis)

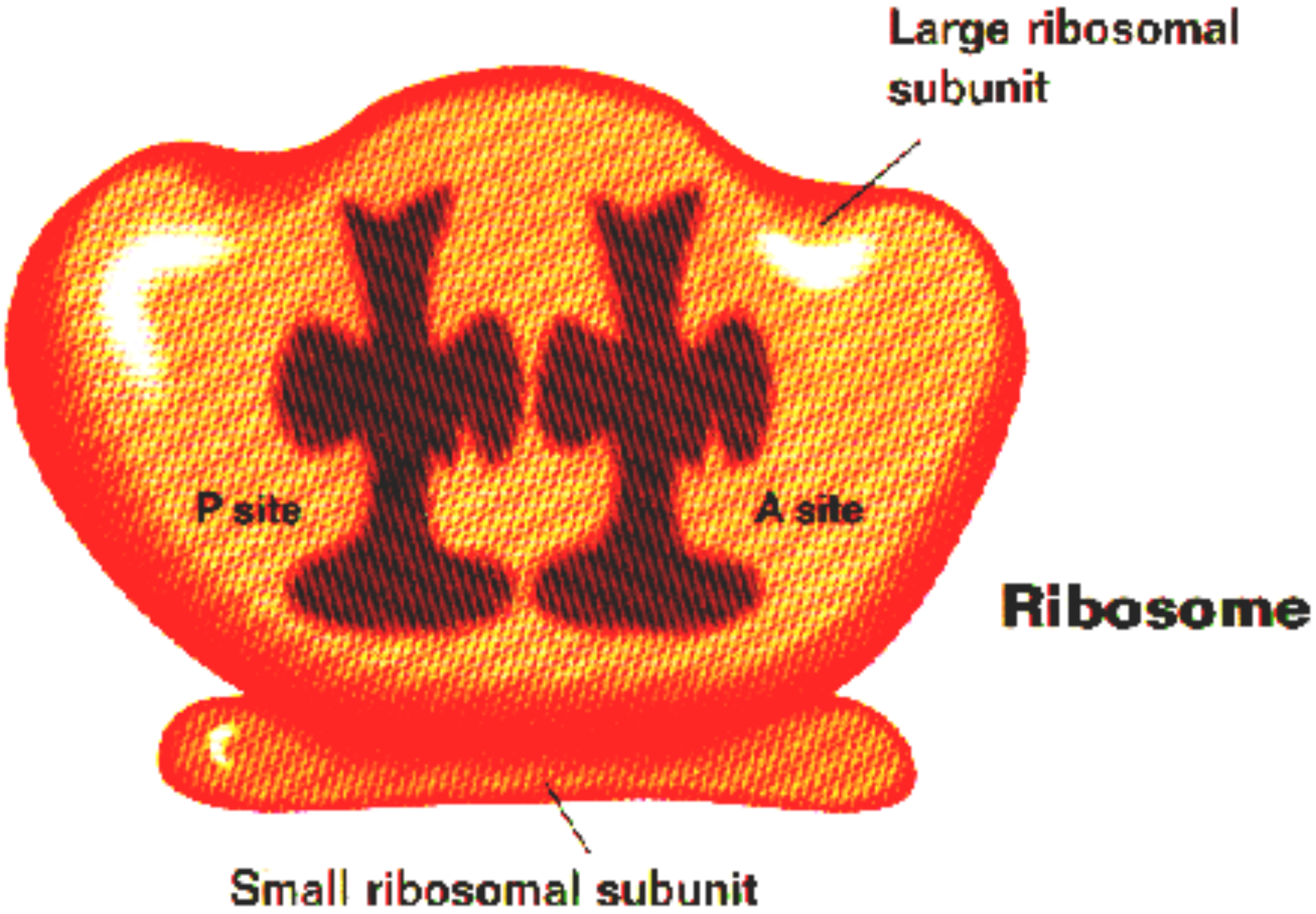
Translation

- Steps:
  - Intiation
  - Elongation
  - Termination
  - Post - Translation

Translation Process

- Requires
  - Ribosomes (50s + 30s)
  - r-RNA
  - t-RNA
  - m-RNA
  - Amino acid
- Ribosome
  - Made of protein and r-RNA (Nucleo-protein)
  - Has internal sites for 2 t-RNA molecules.
  - Two subunit
    - Prokaryotic 50S + 30S subunits = form a 70S.
    - Eukaryotic 60S + 40S subunits = form an 80S.

Ribosome


Large ribosomal subunit
P site
A site
Ribosome
Small ribosomal subunit

Translation

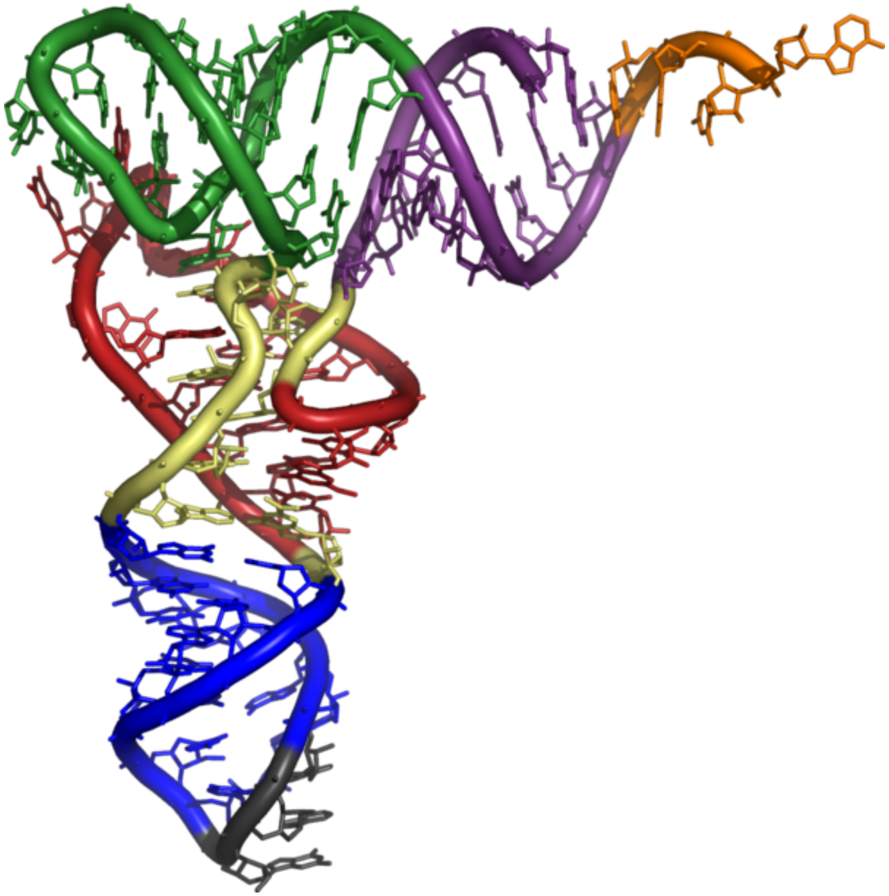
- **Initiation**
  - Ribosomal subunits **assemble** on mRNA
  - r-RNA aids in binding of mRNA
- **Elongation**
  - **t-RNAs** with appropriate anticodon loops **bind to complex**
  - have **amino acid attached** (done by other enzymes)
  - **Amino acids transfer** form t-RNA 2 to t-RNA 1
  - Process repeats
- **Termination**
  - t-RNA with **stop codon** binds into ribosome
  - No amino acid attached to t-RNA
  - Complex falls apart

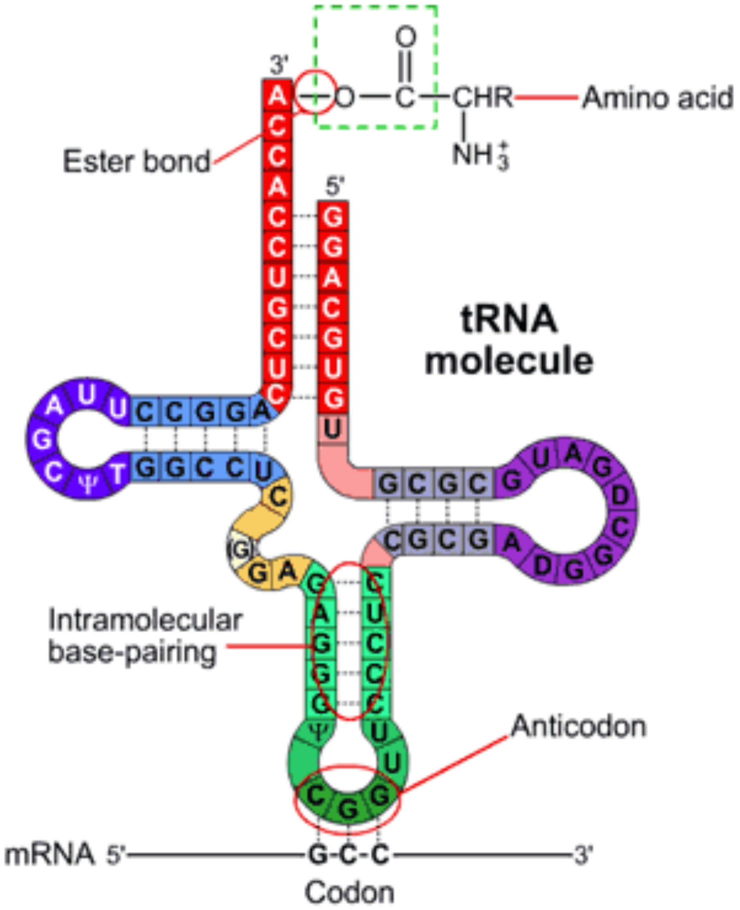
A – P site on ribosome

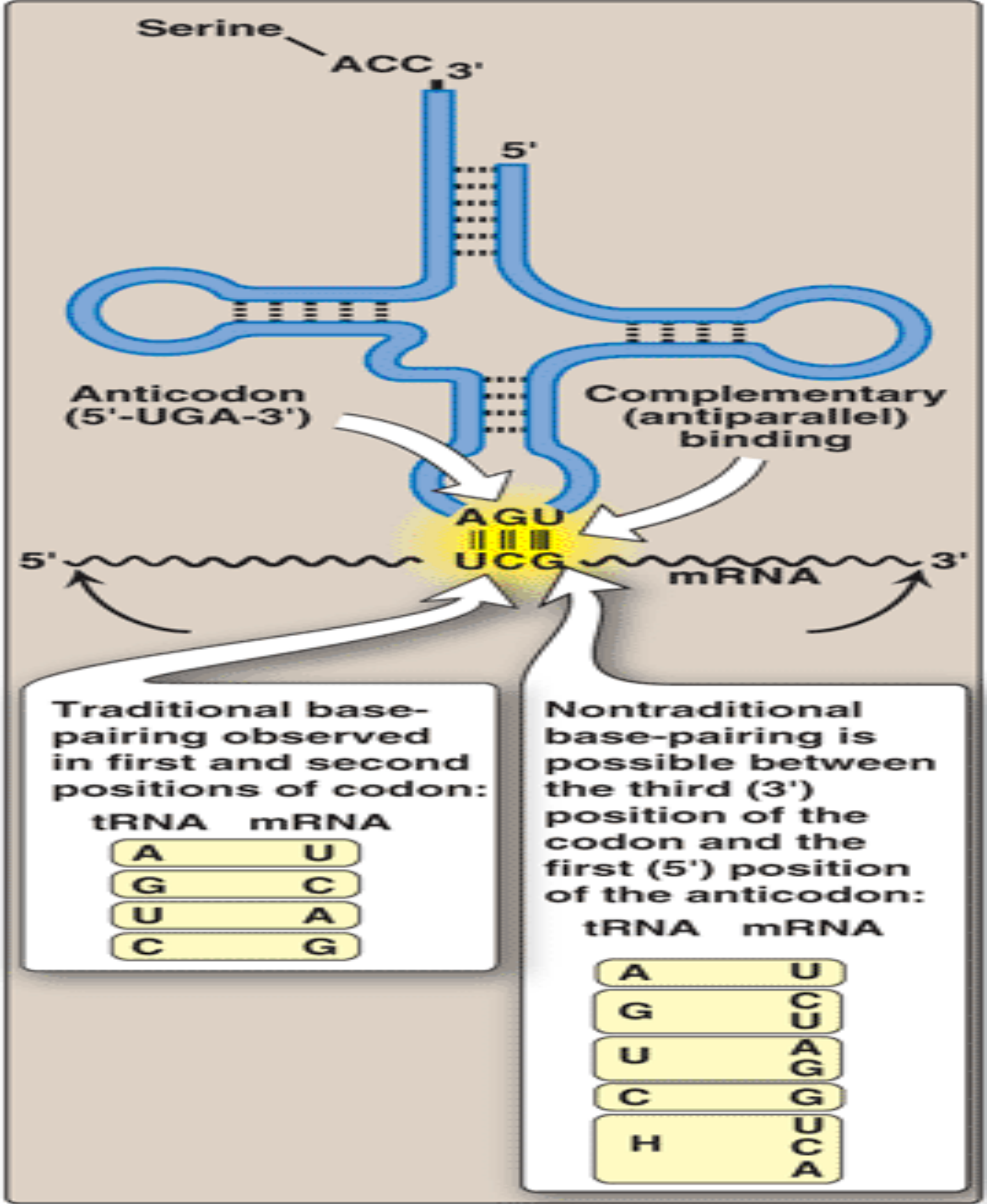
- Ribosome has two binding sites for t-RNA

  — **P** **&** **A** sites —
- Together, they cover two neighboring codons.
- **P-site** binds
  - codon is occupied by **Peptidyl t-RNA**.
  - This t-RNA carries the **chain of amino acids** that has already been synthesized.
- **A site** binds
  - incoming **Aminoacyl-tRNA** as directed by the codon.
  - This codon **specifies the next amino acid** to be added to the growing peptide chain.

Transfer RNA







Traditional base-pairing observed in first and second positions of codon:

tRNA	mRNA
A	U
G	C
U	A
C	G

Nontraditional base-pairing is possible between the third (3') position of the codon and the first (5') position of the anticodon:

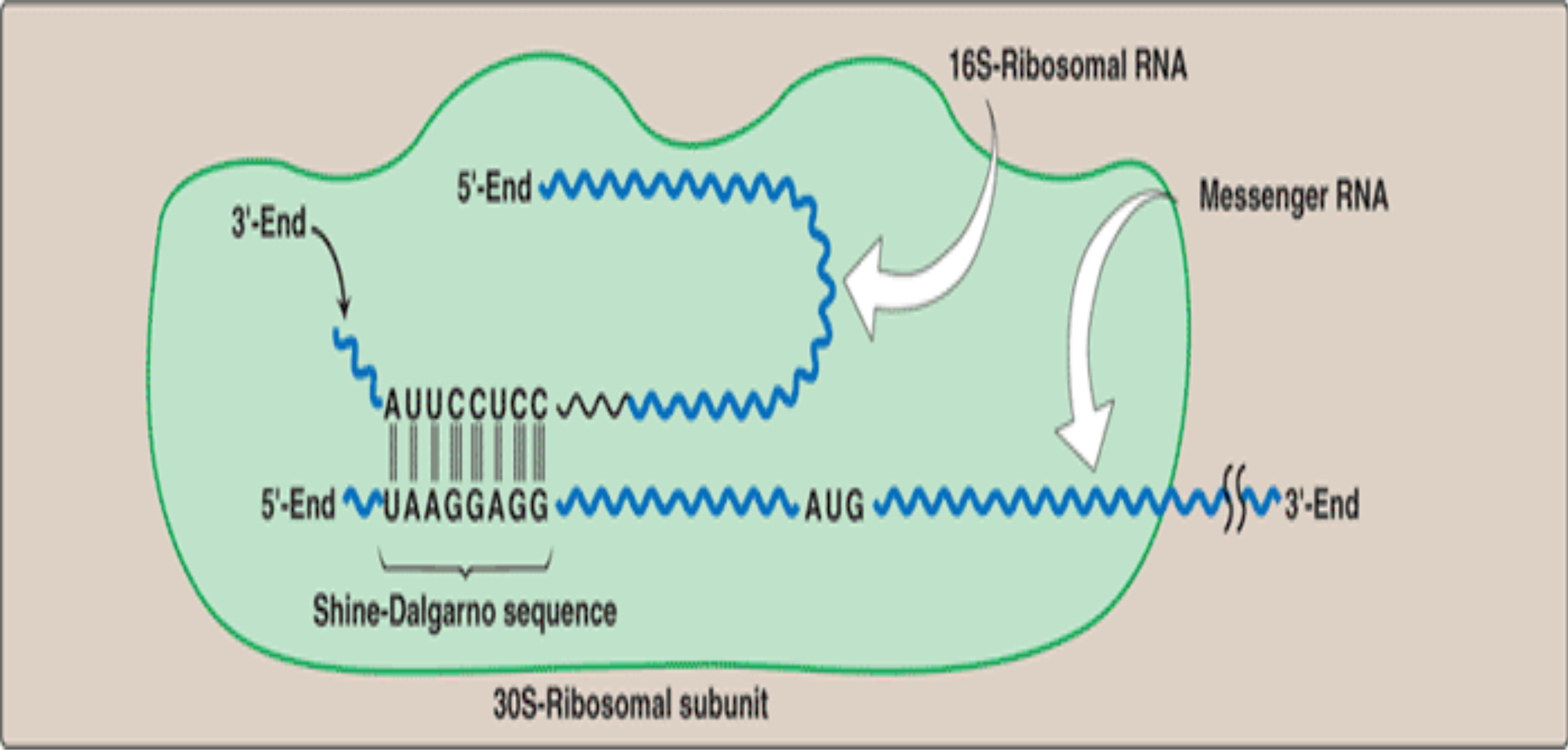
tRNA	mRNA
A	U
G	C U
U	A G
C	G
H	U C A

Aminoacyl-tRNA synthetases

- Required for attachment of amino acids to their corresponding t-RNA.
- Carboxyl group of an amino acid to the 3′-end of t-RNA.
- Require ATP.
- Extreme specificity
- High fidelity of translation of the genetic message.
- Enzyme have **“proofreading” or “editing”** activity

Initiation

- Involves the assembly of the components
- Components include
  - **Two ribosomal** subunits.
  - **m-RNA** to be translated.
  - **Aminoacyl t-RNA** specified by the first codon
  - **GTP**
  - **Initiation factors**
    - In Prokaryotes, Initiation factors (**IF-1, IF-2, IF-3**)
    - In eukaryotes, more than 10 (designated eIF).



Complementary binding between prokaryotic mRNA Shine-Dalgarno sequence and 16S rRNA.

- **Shine - Dalgarno (SD) sequence**
  - Purine rich sequence (e.g. 5′-UAAGGAGG-3′)
  - 6 - 10 bases upstream of the initiating AUG codon
  - Near m-RNA 5′-end.
  - 16S r-RNA of the 30S ribosomal subunit has complementary base pair at 3′-end.
  - Facilitating the binding of the 30S ribosomal subunit on the mRNA

  - **In eukaryotes**
  - the 40S ribosomal subunit binds to the cap structure at the 5′-end of the mRNA
  - By eIF-4 and moves down the mRNA until it encounters the initiator AUG.
  - This “scanning” process requires ATP.

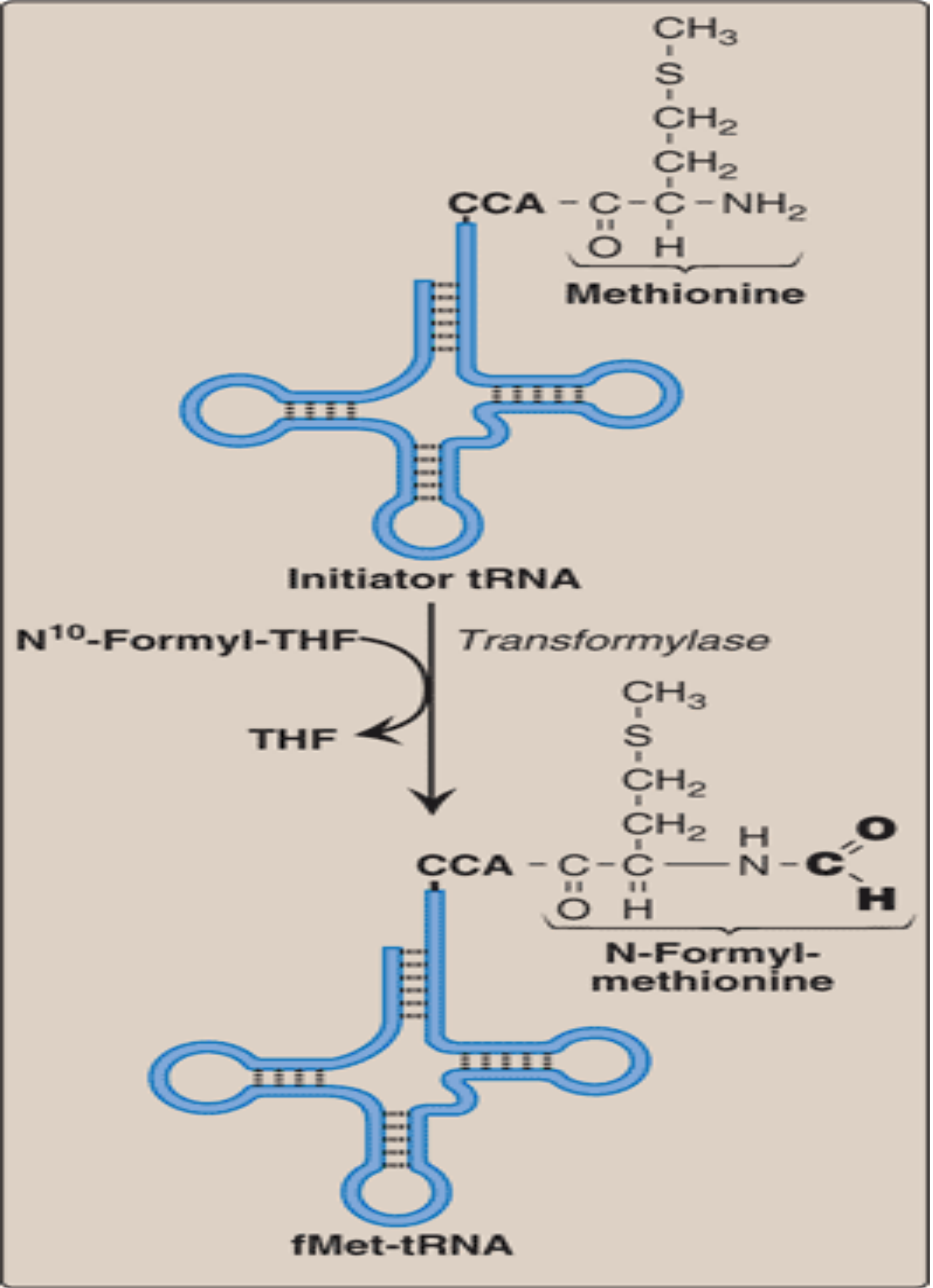
Initiation codon

- AUG is recognized by initiator t-RNA.
- Recognition is facilitated by IF-2 (bound to GTP).

- Initiator t-RNA enters the ribosomal P site
- GTP is hydrolyzed to GDP.

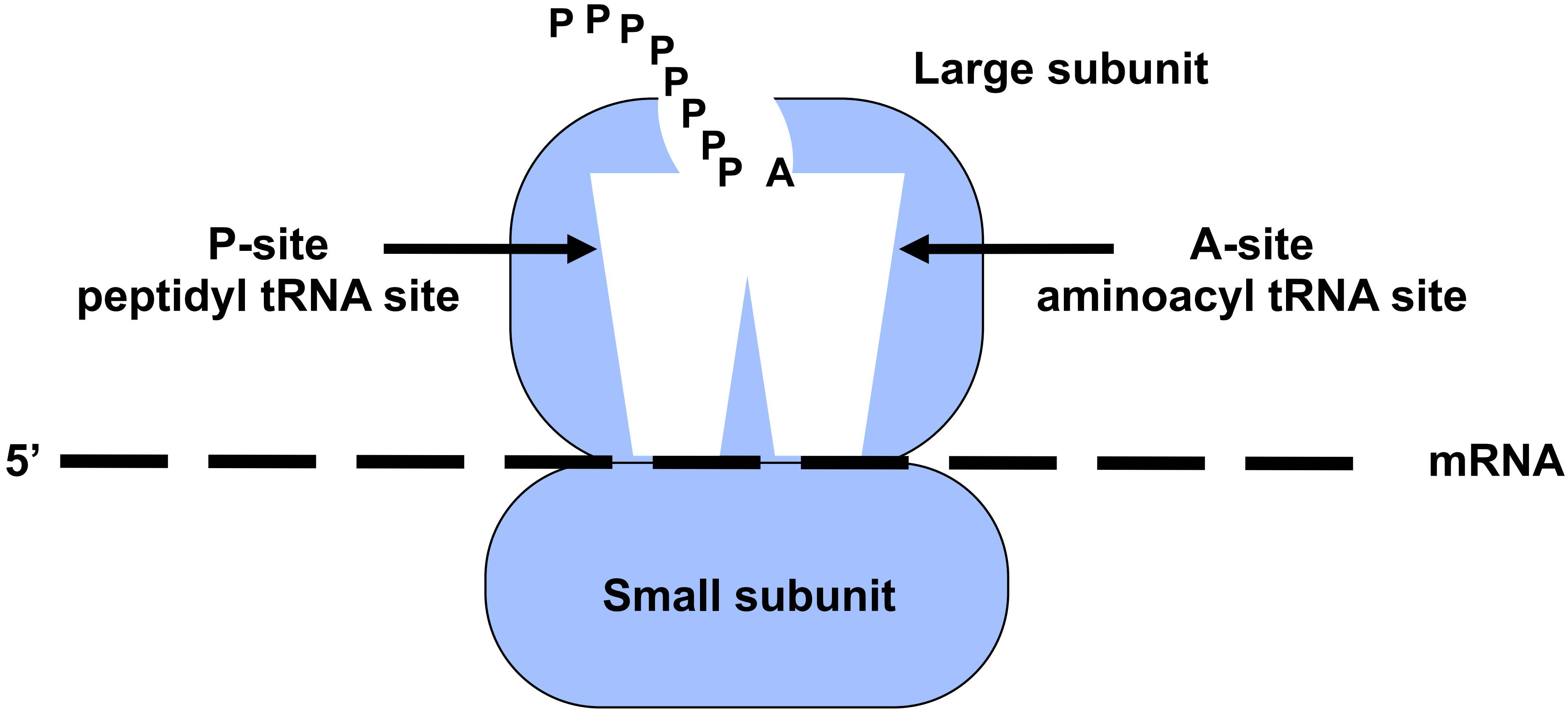
- Initiator t-RNA carries N-formylated methionine.
- N10-formyl tetrahydrofolate as the carbon donor.

- In eukaryotes, the initiator tRNA carries a methionine that is not formylated.



Generation of the initiator N-formylmethionyl-tRNA (fMet-tRNA)

Ribosome structure



Large subunit

P-site
peptidyl tRNA site

A-site
aminoacyl tRNA site

5’

mRNA

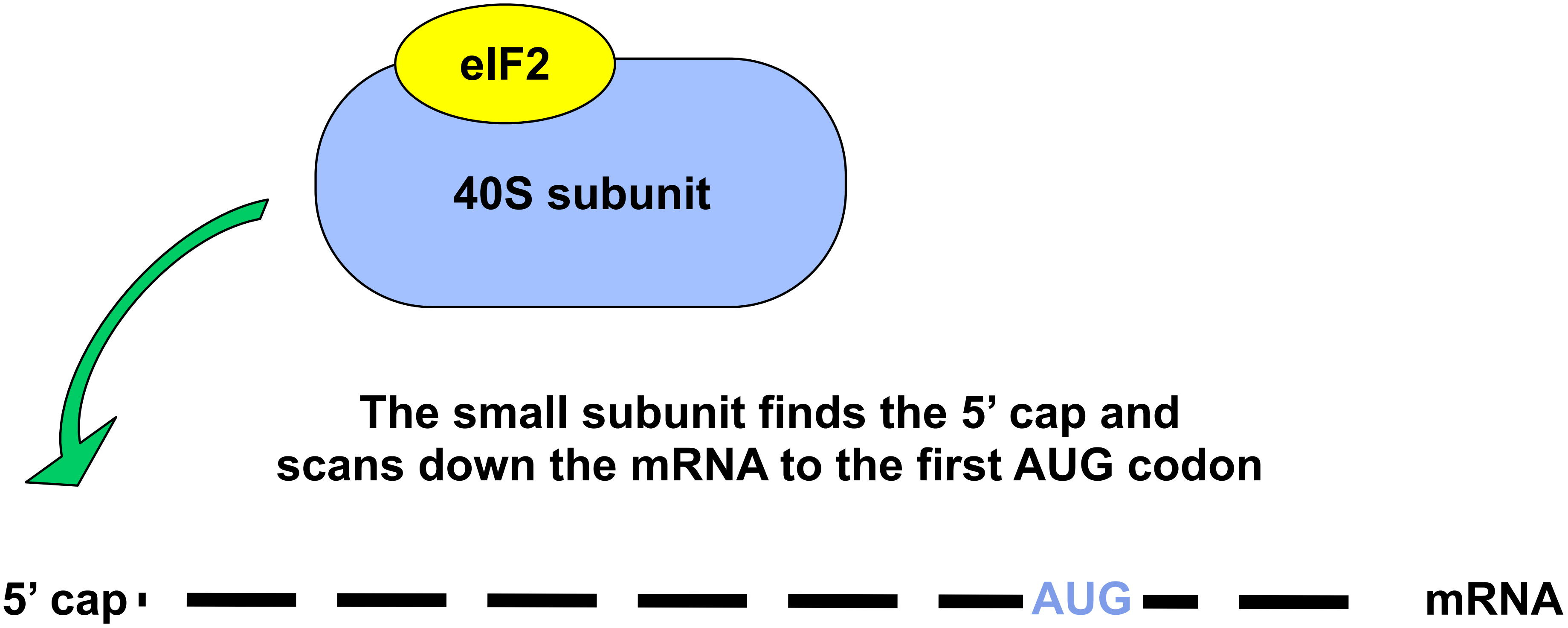
Small subunit

Ribosome with bound tRNAs and mRNA

Initiation of protein synthesis: mRNA binding

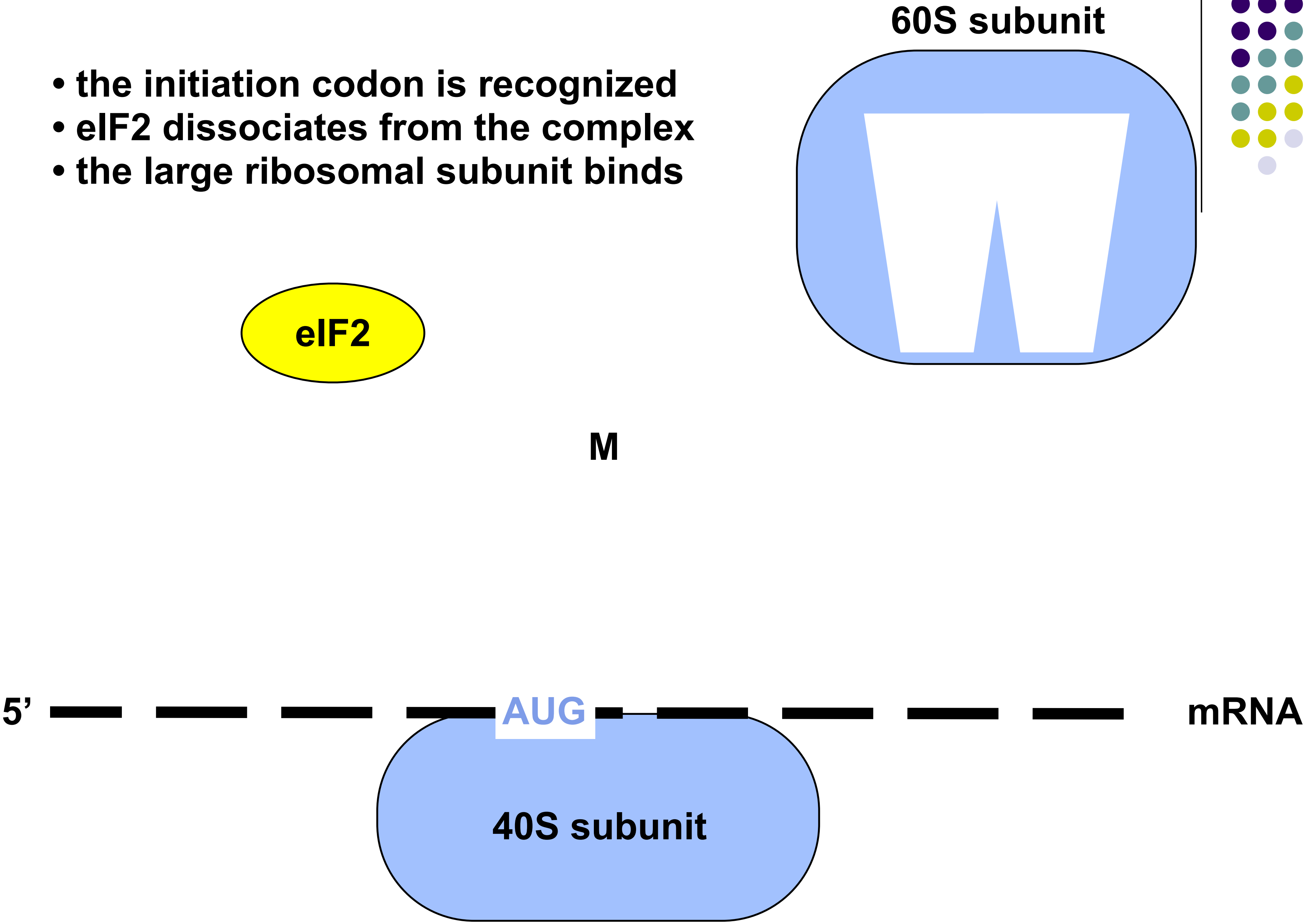
M

Initiator tRNA bound to the small ribosomal subunit with the eukaryotic initiation factor-2 (eIF2)



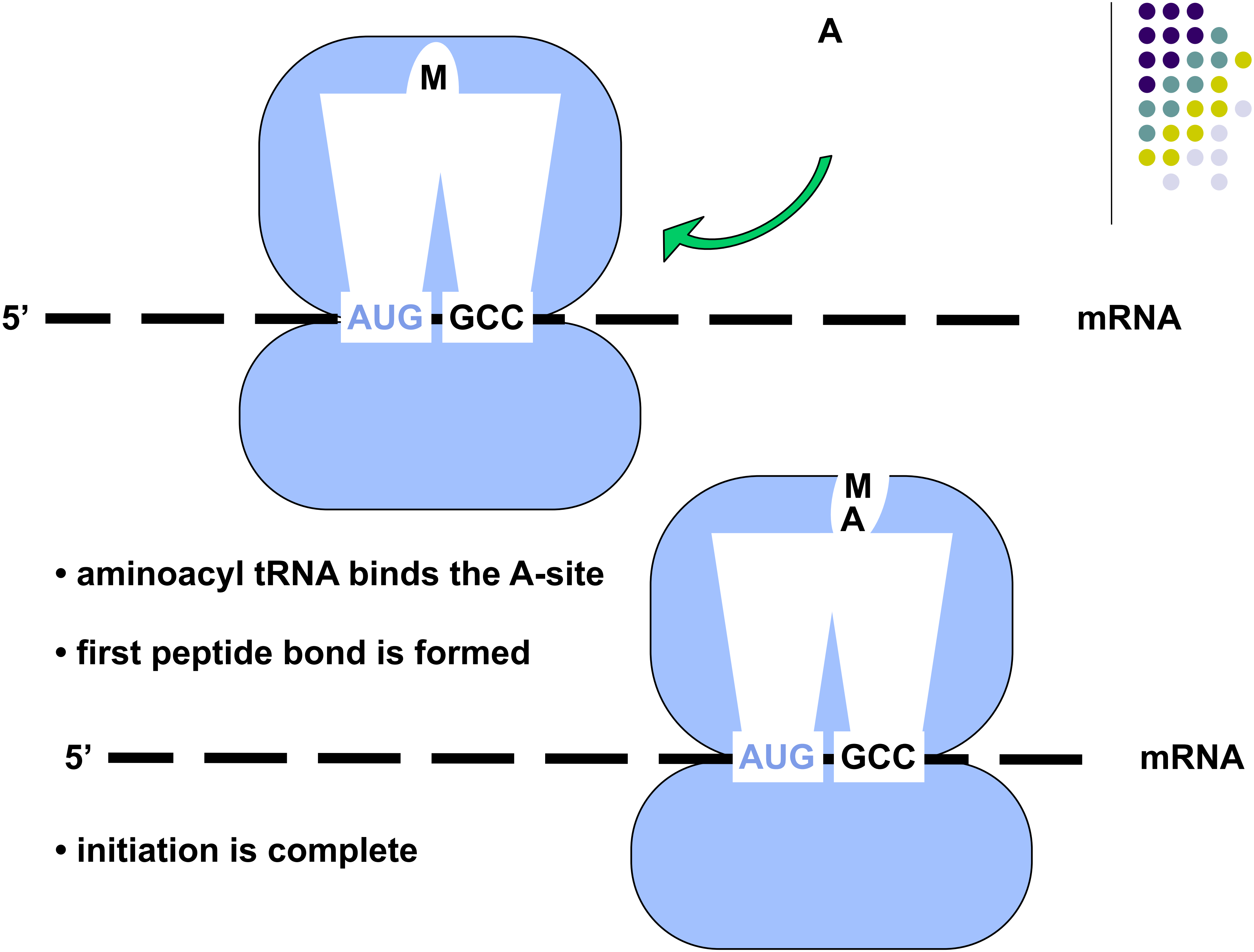
The small subunit finds the 5’ cap and scans down the mRNA to the first AUG codon

- the initiation codon is recognized
- eIF2 dissociates from the complex
- the large ribosomal subunit binds



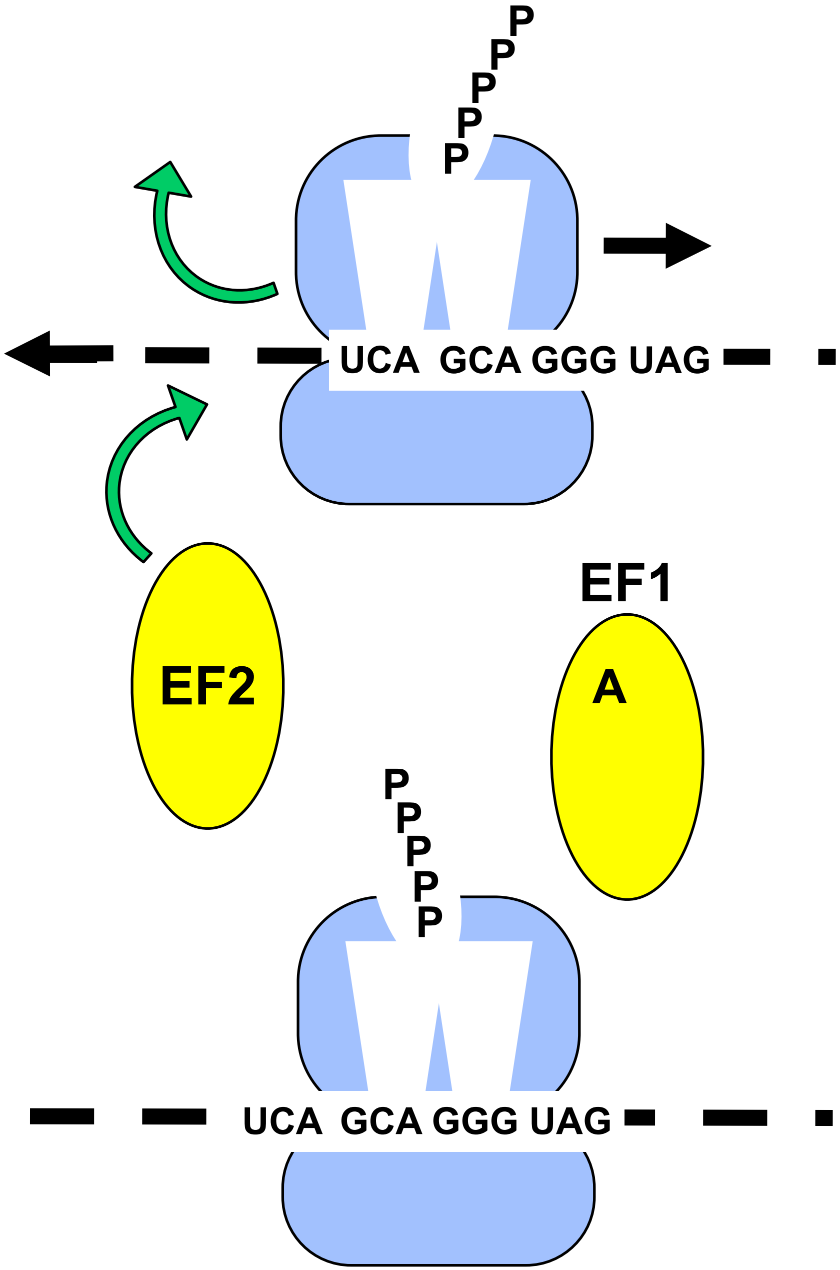
Elongation

- Addition of amino acids to the carboxyl end of the growing chain.
- Ribosome moves from the 5′-end to the 3′-end of mRNA
- New aminoacyl-tRNA for next triplet codon appears in ribosomal A site
- Facilitated by EF-Tu, EF-Ts & EF-G & requires GTP.
- After the peptide bond has been formed, the ribosome moves to next triplet codon toward the 3′-end of the mRNA. = **Translocation**
- This causes movement of the **uncharged tRNA** into the ribosomal **E site** and movement of the peptidyl-tRNA into the P site.



- aminoacyl tRNA binds the A-site
- first peptide bond is formed
- initiation is complete

Elongation

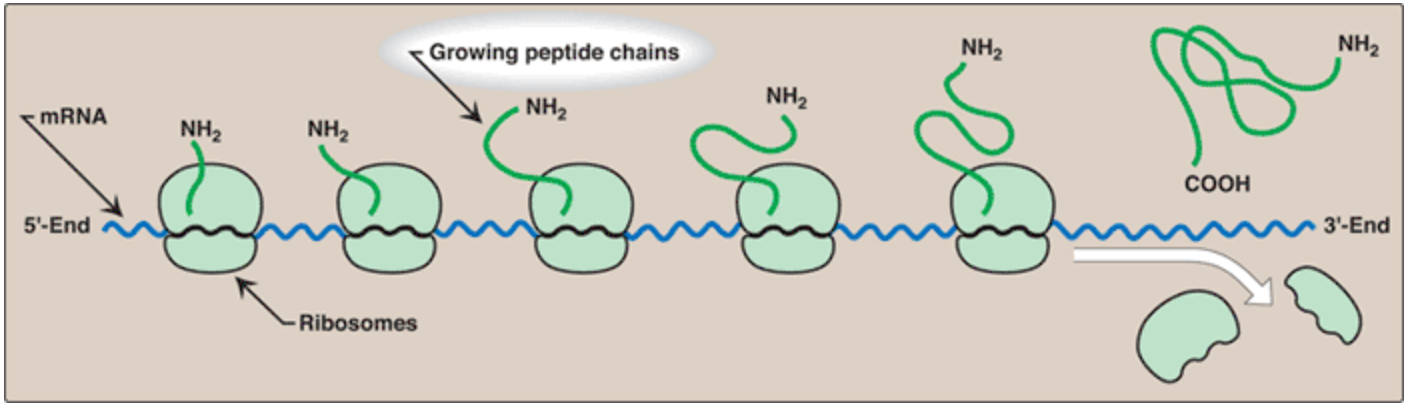


- the uncharged tRNA dissociates
  from the P-site

- **translocation =**
  the ribosome shifts one codon along mRNA, moving peptidyl tRNA from the A-site to the P-site.
  requires EF2

- **next aminoacyl tRNA** then binds within the **A-site**;
  tRNA binding requires EF1

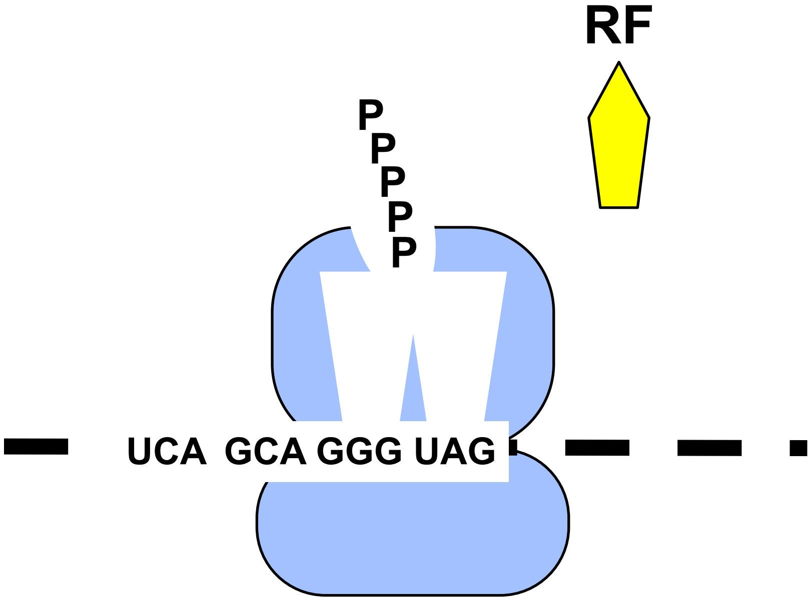
- **energy for elongation is provided by the hydrolysis of two GTPs:**
  - one for translocation
  - one for aminoacyl tRNA binding


Growing peptide chains
mRNA
NH2
NH2
NH2
NH2
NH2
NH2
5'-End
3'-End
COOH
Ribosomes

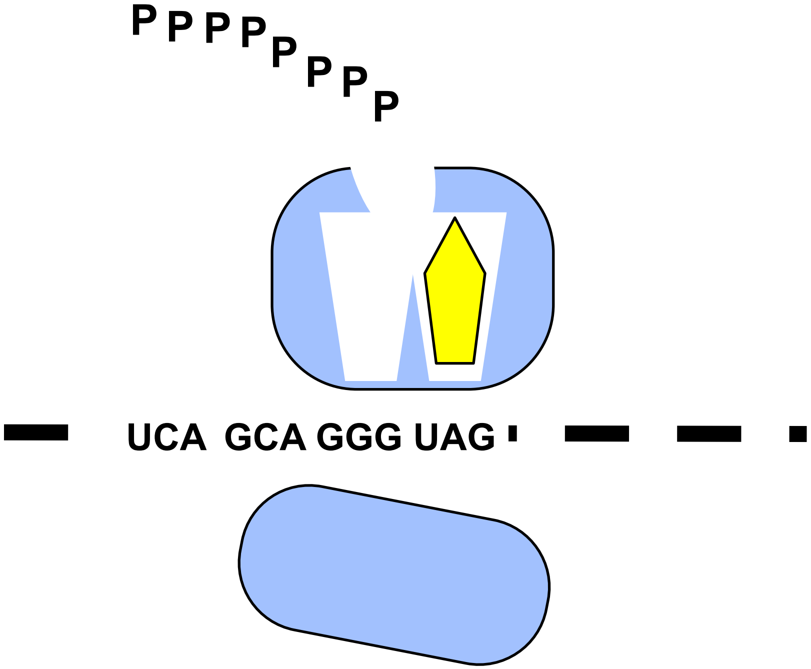
Termination

- Termination occurs when one of the three termination codons moves into the A site.
- Termination codons are recognized in by
  - **RF-1 = UAA and UAG**
  - **RF-2 = UAA and UGA**
- RF induces peptidyltransferase to hydrolyze the bond linking the peptide to the tRNA at the A site, causing the nascent protein to be released from the ribosome.
- **RF-3** (bound to GTP) cause **release of RF-1 or RF-2** as GTP is hydrolyzed.

Termination



- when translation reaches the stop codon, RF binds within the A-site, recognizing the stop codon



- RF catalyzes the hydrolysis of the completed polypeptide from the peptidyl tRNA, and the entire complex dissociates

Post-translation modification

Trimming

- Many proteins are initially made as initially made as large, precursor molecules that are not functionally active.
- Precursor proteins are cleaved in the endoplasmic reticulum or the Golgi apparatus, others are cleaved in developing secretory vesicles.
- Zymogens are inactive secreted enzymes (including the proteases required for digestion).
- They become activated through cleavage when they reach their proper sites of action.
- E.g. Pancreatic zymogen, trypsinogen, becomes activated to in the small intestine.

Post-translation modification

Covalent Alterations

1. **Phosphorylation** :
    - **On hydroxyl groups** of serine, threonine, tyrosine.
    - **increase or decrease the functional activity** of the protein.
2. **Glycosylation :**
    - **Proteins of a plasma membrane.**
    - Carbohydrate attached to serine or threonine hydroxyl groups (O-linked) or the amide nitrogen of asparagine (N-linked).
3. **Hydroxylation :**
    - **Proline and lysine** residues = **collagen**

Post-translation modification

Covalent Alterations

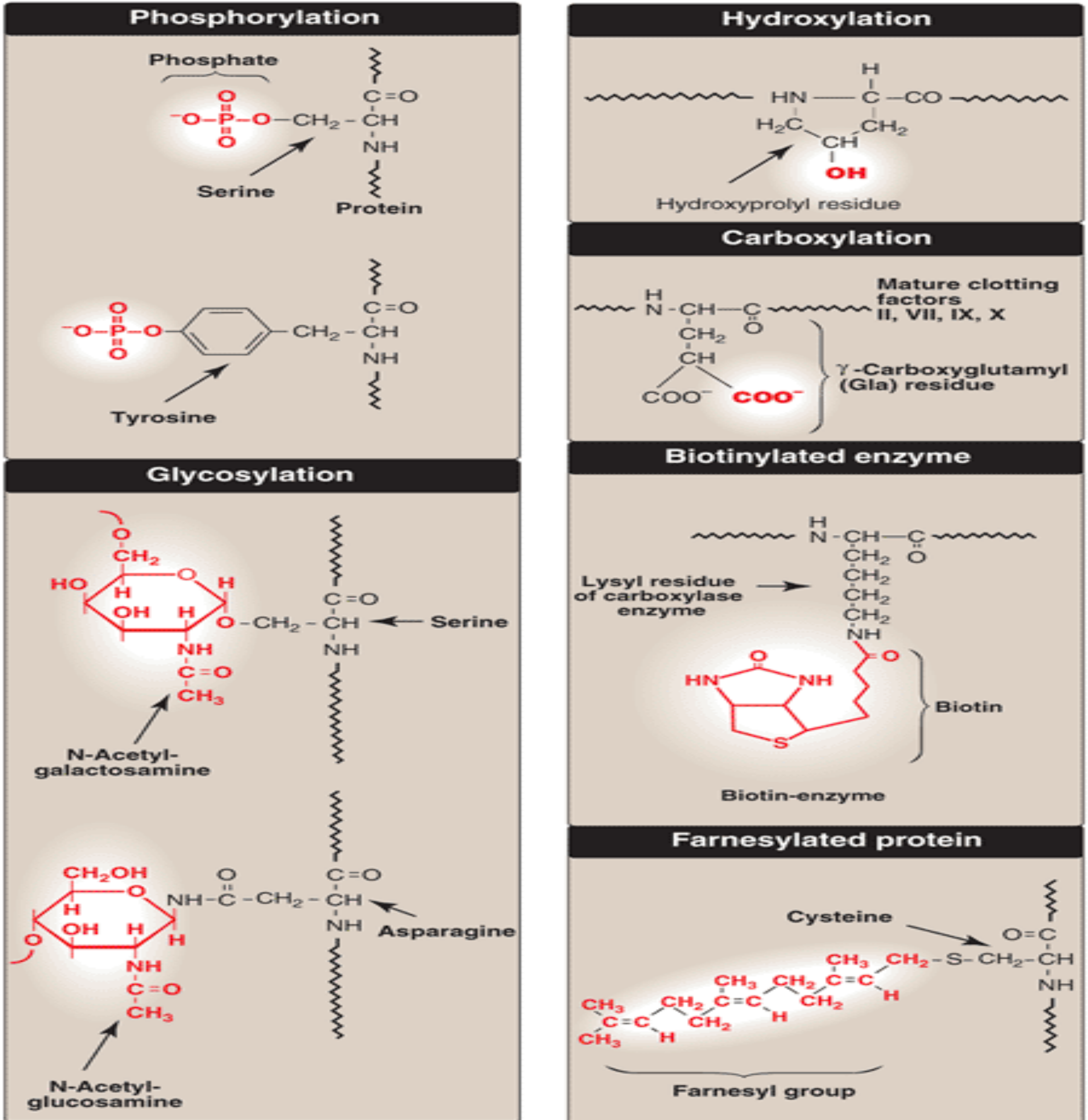
1.Other covalent modification :

- **Vitamin K–dependent carboxylation** of Glutamate residues of **clotting factors.**

- **Biotin** = ε-amino groups of lysine residues of biotin-dependent enzymes
  = carboxylation reactions.
  e.g. **pyruvate carboxylation**

- Attachment of lipids, such as farnesyl groups, can help anchor proteins in membranes.

- Acetylated


Phosphorylation
Phosphate
Serine
Protein
Tyrosine
Glycosylation
Serine
N-Acetyl-galactosamine
Asparagine
N-Acetyl-glucosamine
Hydroxylation
OH
Hydroxyprolyl residue
Carboxylation
Mature clotting factors II, VII, IX, X
γ-Carboxyglutamyl (Gla) residue
COO⁻
Biotinylated enzyme
Lysyl residue of carboxylase enzyme
Biotin
Biotin-enzyme
Farnesylated protein
Cysteine
Farnesyl group

Post-translation modification

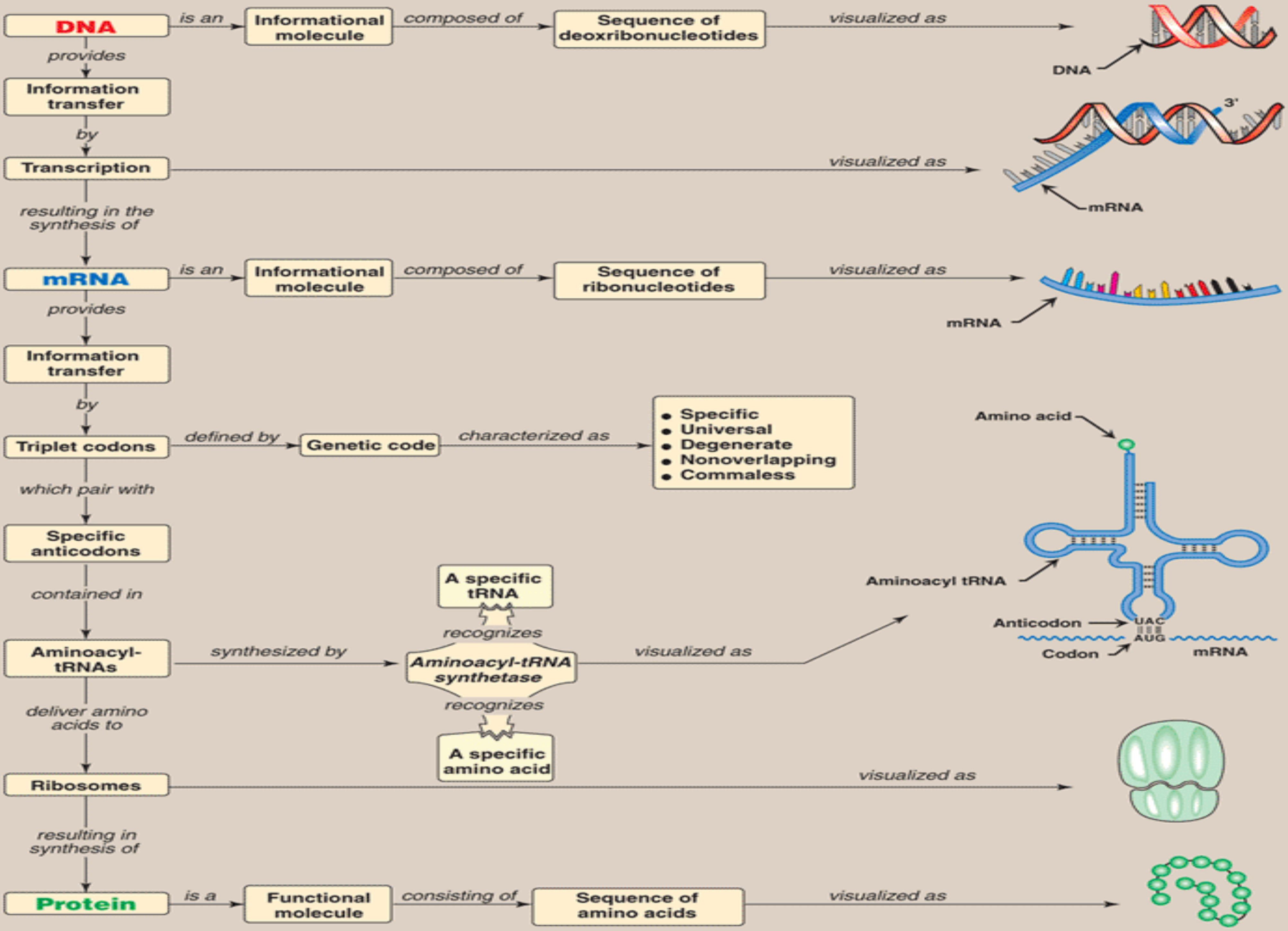
Protein degradation

- Defective Protein, for rapid turnover are often marked for destruction by **ubiquitination**
- The attachment of a small, highly conserved protein, called **ubiquitin.**
- Proteins marked in this way are rapidly degraded by a cellular component known as the **“proteasome”.**

Inhibitor of Translation

Inhibitor (Antibiotic)	
Erythromycin	*50 s ribosomal subunit*
Clindamycin	*50 s ribosomal subunit*
Tetracycline	30 s ribosomal subunit
Puramycin	**Amino-acyl t-RNA**
Chloramphenicol	**Peptidyl Transferase**
Diphtheria Toxin	***eEF-2***

Flow of genetic information



DNA *is an* Informational molecule *composed of* Sequence of deoxribonucleotides *visualized as*

DNA *provides* Information transfer *by* Transcription *visualized as*

Transcription *resulting in the synthesis of* **mRNA**

mRNA *is an* Informational molecule *composed of* Sequence of ribonucleotides *visualized as*

mRNA *provides* Information transfer *by* Triplet codons

Triplet codons *defined by* Genetic code *characterized as*

- Specific
- Universal
- Degenerate
- Nonoverlapping
- Commaless

Triplet codons *which pair with* Specific anticodons *contained in* Aminoacyl-tRNAs

Aminoacyl-tRNAs *synthesized by* *Aminoacyl-tRNA synthetase* *visualized as*

Aminoacyl-tRNA synthetase *recognizes* A specific tRNA

Aminoacyl-tRNA synthetase *recognizes* A specific amino acid

Aminoacyl-tRNAs *deliver amino acids to* Ribosomes *visualized as*

Ribosomes *resulting in synthesis of* **Protein**

Protein *is a* Functional molecule *consisting of* Sequence of amino acids *visualized as*

Thanks