Translation

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Transcription

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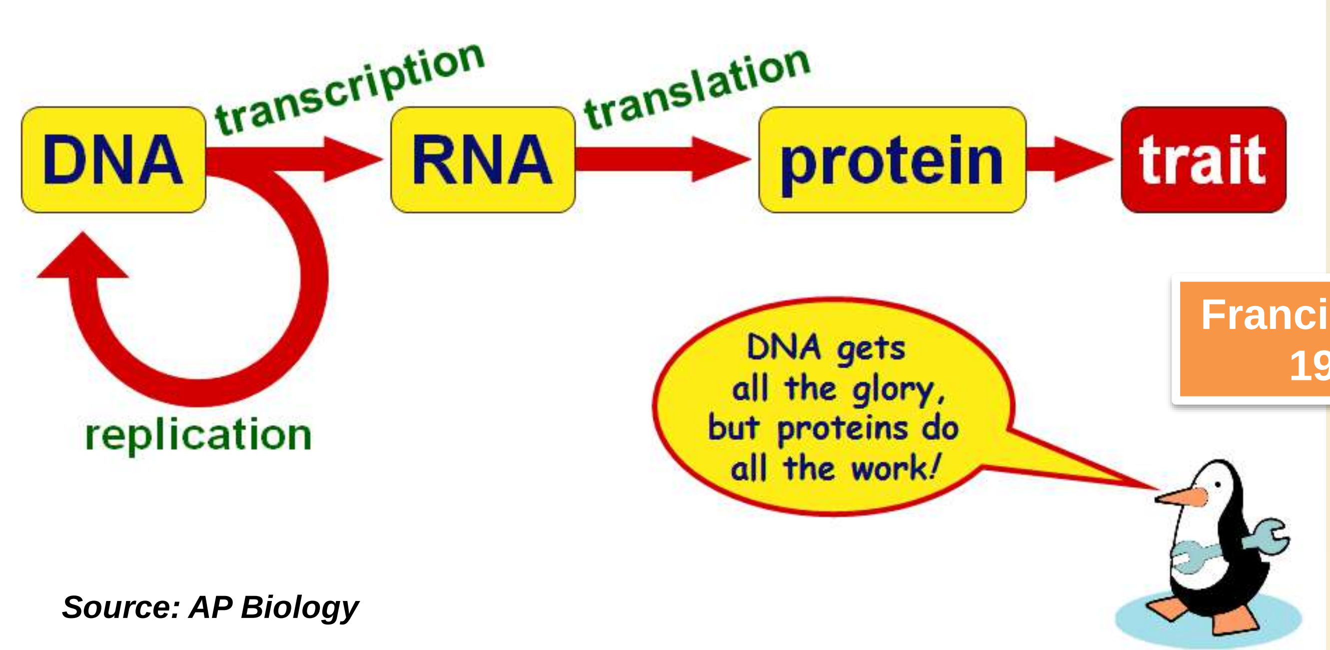
Introduction

- It is the process of synthesis of proteins from messenger RNA transcripts (mRNA) after the process of transcription of DNA to RNA.
- It takes place in the cytoplasm by specialized organelle known as ribosomes.
- There are no endoplasmic reticulum in the prokaryotes and ribosomes are suspended in the cytoplasm, whereas endoplasmic reticulum are present in eukaryotes which harbors ribosomes – translation takes place on rough endoplasmic reticulum (RER) in eukaryotes, whereas translation occurs freely in cytoplasm in the prokaryotes.
- The codons on the mRNA are translated into amino acid sequence which leads to the synthesis of protein.
- Translation requires a variety of cellular components, such as proteins, RNAs and different small molecules.
- It has also three main steps:
    - ***Initiation*** *– Formation of mRNA-ribosome complex*
    - ***Elongation*** *– Formation of polypeptide chain complimentary to the mRNA*
    - ***Termination*** *– Termination of polypeptide chain*

The “Central Dogma”

- ☐ Flow of genetic information in a cell
  - How do we move information from DNA to proteins?



Source: AP Biology

Francis Crick 1958

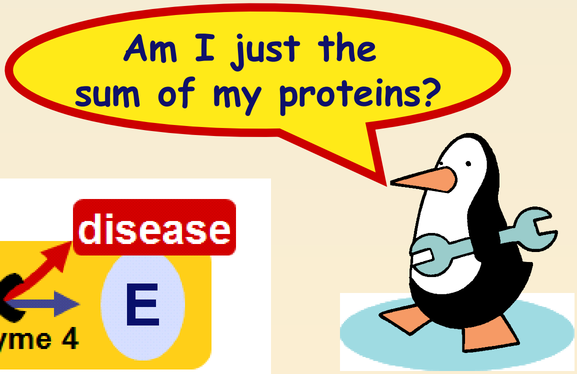
“It states that genetic information is transmitted form DNA to RNA to protein and this information cannot be transferred back from protein to either protein or nucleic acid”.

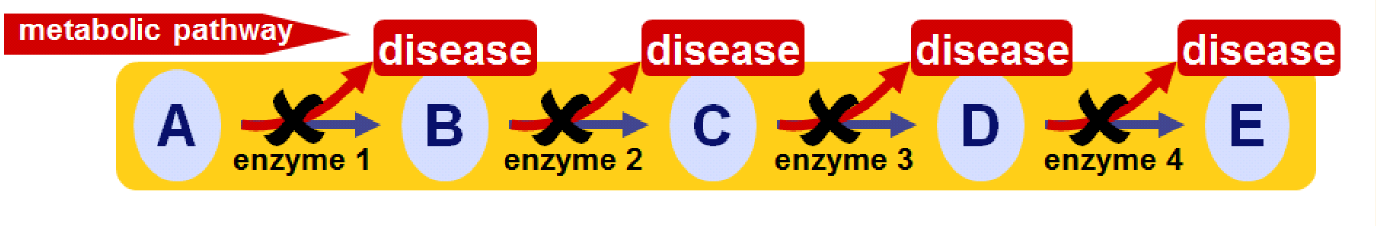
The “Central Dogma”

Inheritance of metabolic disease

- It suggests that genes code for enzymes.
- Each disease, i.e., phenotype, is caused by non-functional gene product, which may be
  - lack of an enzyme
  - Tay Sachs disease - **hexosaminidase A**, causes a fatty substance to collect .
  - Phenylketonuria (PKA) - absence or deficiency of an enzyme called **phenylalanine hydroxylase (PAH)**, responsible for processing the amino acid phenylalanine.
  - Albinism - absence or defect of **tyrosinase**, a copper-containing enzyme involved in the production of melanin.

Proteome - between 80,000 and 400,000 proteins.

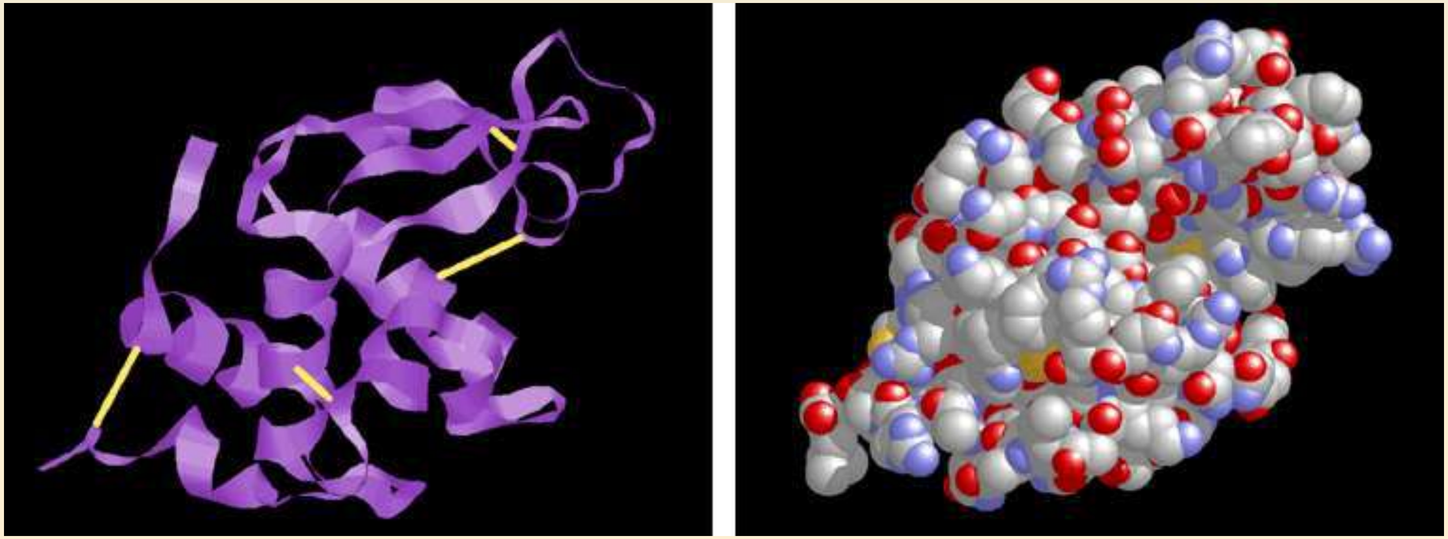




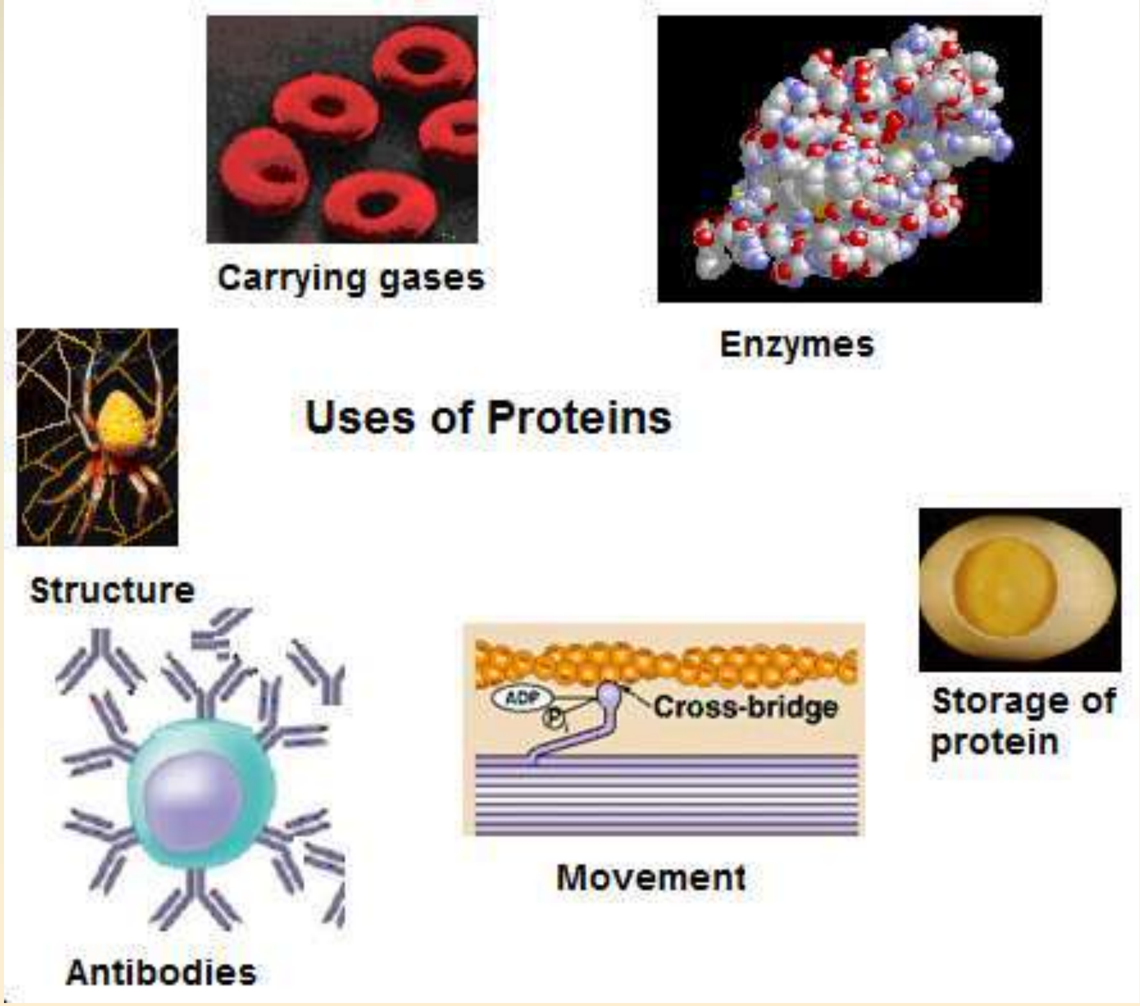
Source: AP Biology

Proteins

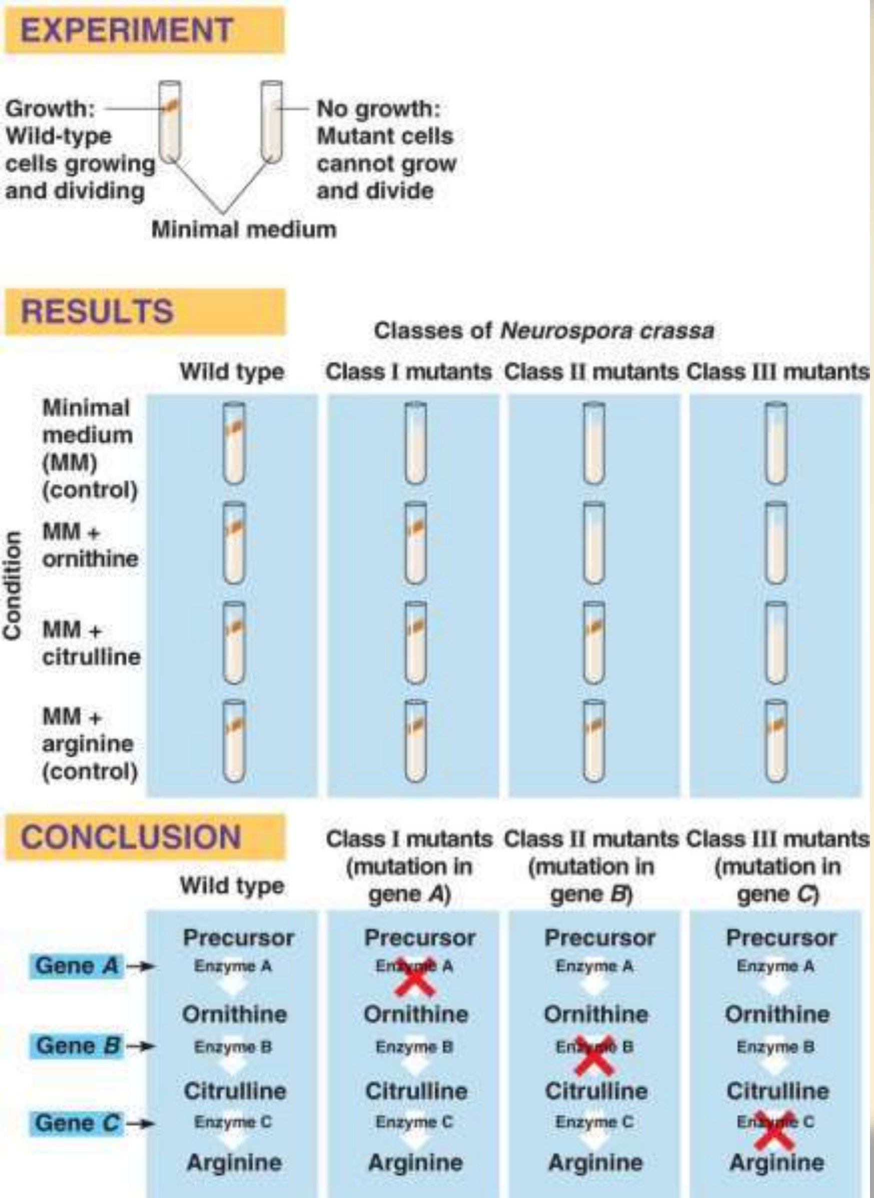
- Proteins are the “workhorse” molecule found in organisms, which determine phenotype of an organism, i.e. what we look like.
- Proteins are made of polypeptide chains that have primary, secondary, tertiary and quaternary structure.
- The polypeptide chains are made of 20 amino acids - an average polypeptide chain is 400 amino acid long (can be shorter than this value).
- *The part of the DNA that codes for a particular polypeptide chain is called as a gene.*



Uses of Proteins



Work of Beadle and Tatum

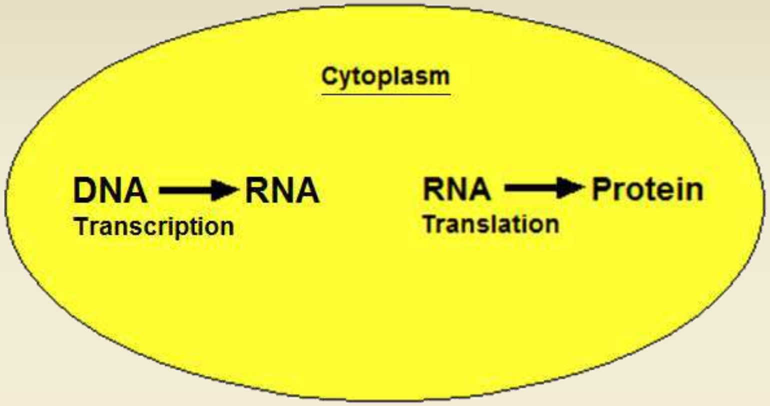


George Beadle and **Edward Tatum** established the link between genes and enzymes in studying bread mold, *Neurospora crassa*.

Conclusion

- One gene produces one enzyme.
- Later it was modified
- One gene produces one protein.
- One gene produces one polypeptide chain.

Overview of Protein Synthesis

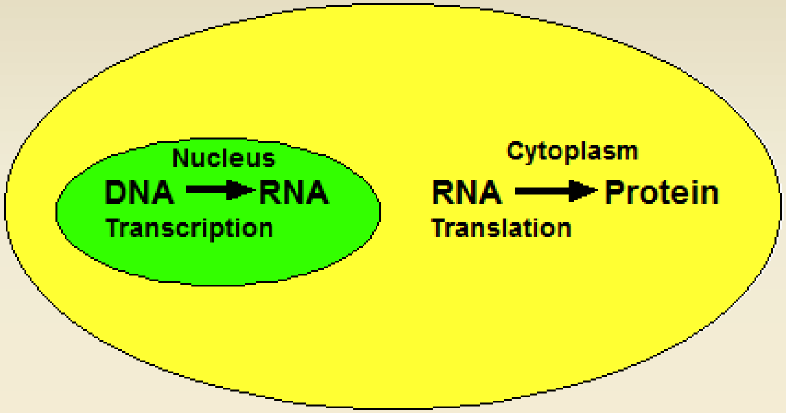


Cytoplasm

DNA → RNA
Transcription

RNA → Protein
Translation

In prokaryotes



Nucleus
DNA → RNA
Transcription

Cytoplasm
RNA → Protein
Translation

In eukaryotes

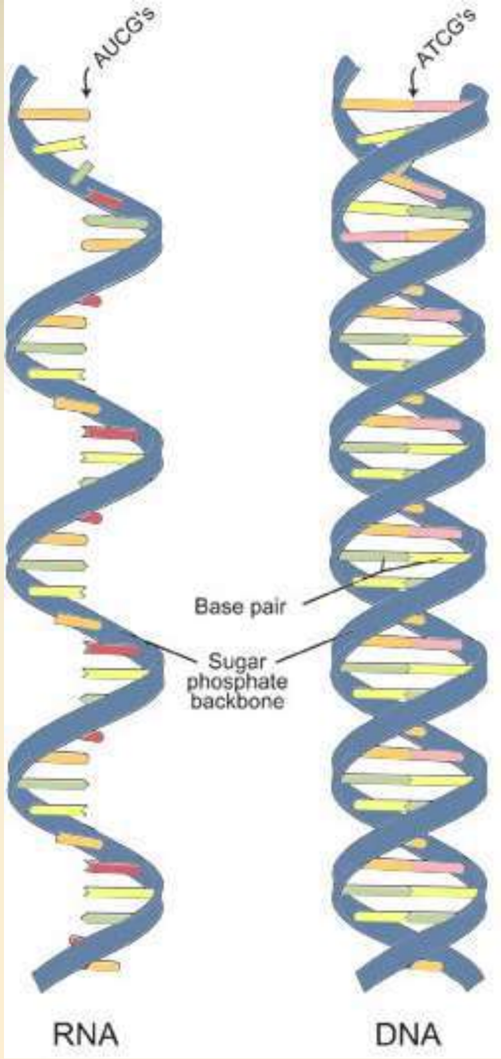
- ❑ DNA is transcribed to mRNA in the cytoplasm in prokaryotes as it has no nucleus, and in the nucleus in eukaryotes.
- ❑ With mRNA and help of other RNA as well as protein molecules, mRNA is translated into specific proteins in the cytoplasm
- ❑ Therefore, RNA is the intermediate between the DNA code and the actual synthesis of a protein

RNAs in the Protein Synthesis

RNA

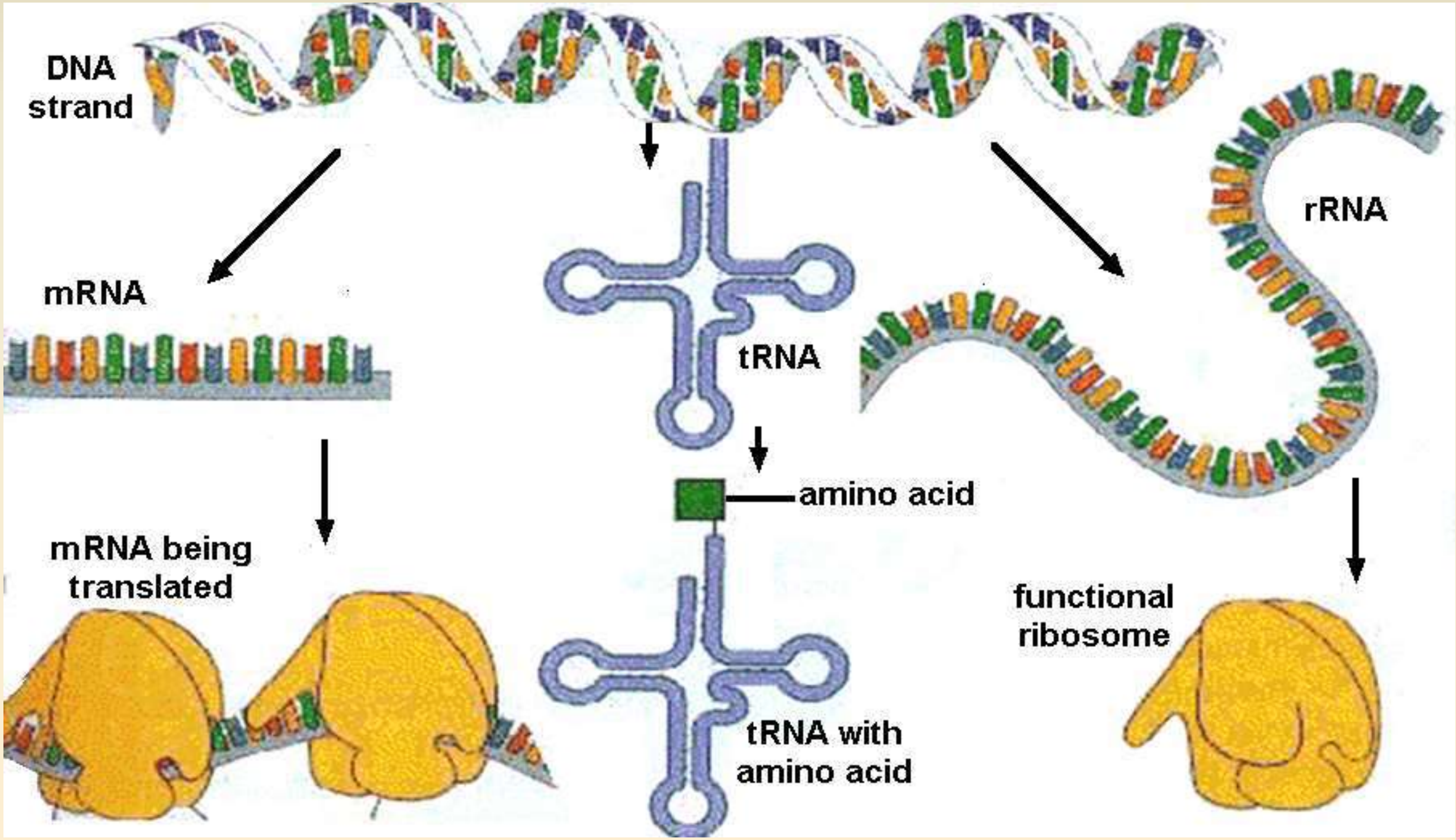
- **ribose sugar**
- **N-bases**
    - **uracil instead of thymine**
    - **U : A**
    - **C : G**
- **single stranded**
- **lots of RNAs**
    - **mRNA, tRNA, rRNA, siRNA…**

DNA → **transcription** → **RNA**



RNAs in the Protein Synthesis

Types of RNA in protein synthesis

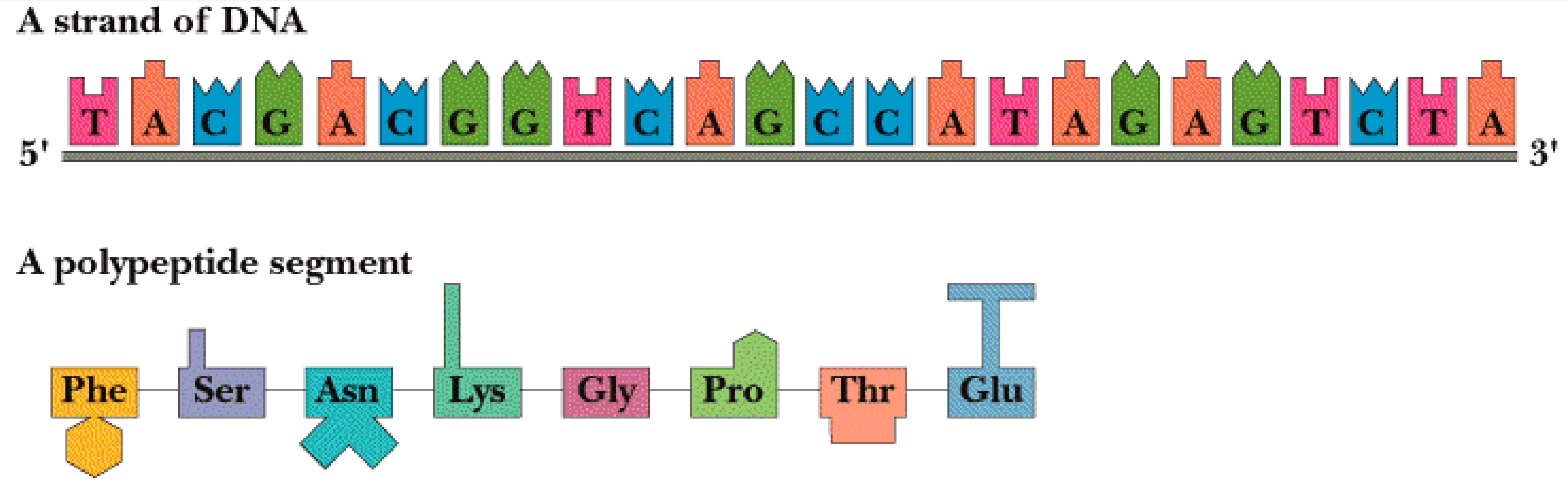


RNAs in the Protein Synthesis

3 types of RNA help in protein synthesis

Messenger RNA (mRNA)

- It carries code from DNA to ribosomes. It actually acts as a transporter of genetic information to protein synthesis machinery.
- It is specific for a particular protein.

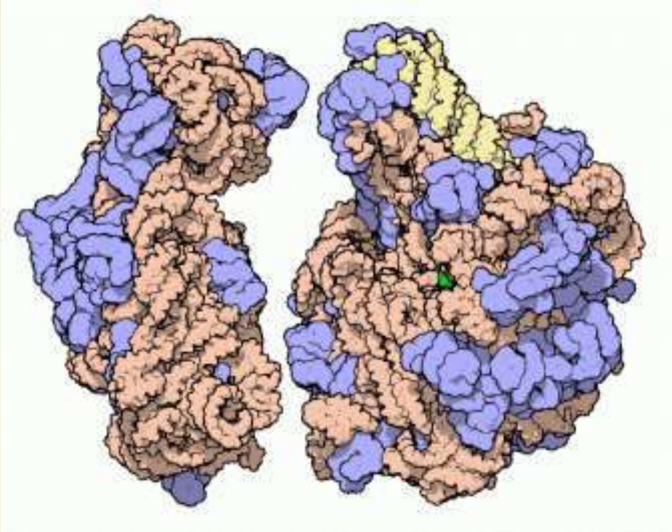


RNAs in the Protein Synthesis

3 types of RNA help in protein synthesis

RIBOSOMAL RNA (rRNA)

- Made in nucleolus in eukaryotes, while it is made in the cytoplasm in prokaryotes.
- It has 2 subunits (large & small)
- It combines with proteins to form ribosomes
- Prokaryotic ribosomes are of different size than eukaryotic ribosomes (30S and 50S subunits in prokaryotes and 40S and 60S subunits in eukaryotes).
- Medically significant – some antibiotics target bacterial ribosomes in the host



Ribosomal subunits – RNA in orange and yellow and proteins in blue.

Source: https://pdb101.rcsb.org/motm/10

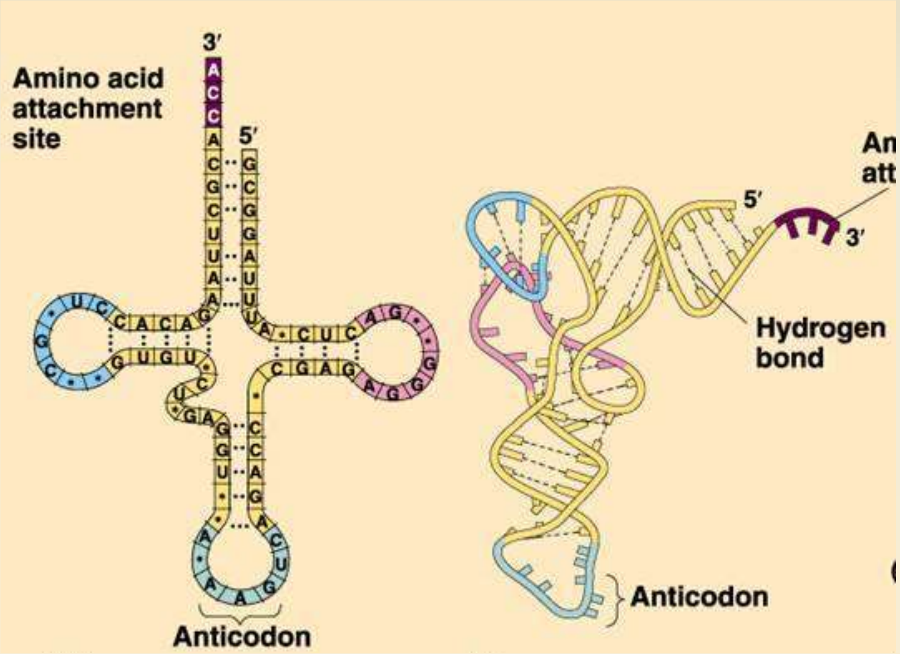
Endosymbiotic theory: It states that some of the organelles in eukaryotic cells were once prokaryotic microbes.

RNAs in the Protein Synthesis

3 types of RNA help in protein synthesis

Transfer RNA (tRNA)

- Anticodon sequence are present.
- **Anticodon** sequence matches **codon** on mRNA to add correct amino acid during protein synthesis.
- **Aminoacyl-tRNA synthetase** enzyme attaches a specific amino acid using energy from ATP.



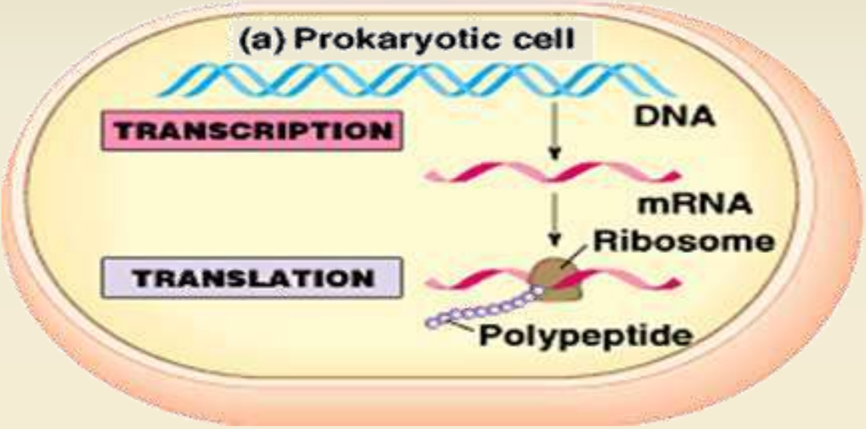
http://www-math.mit.edu/~lippert/18.417/lectures/01_Intro/

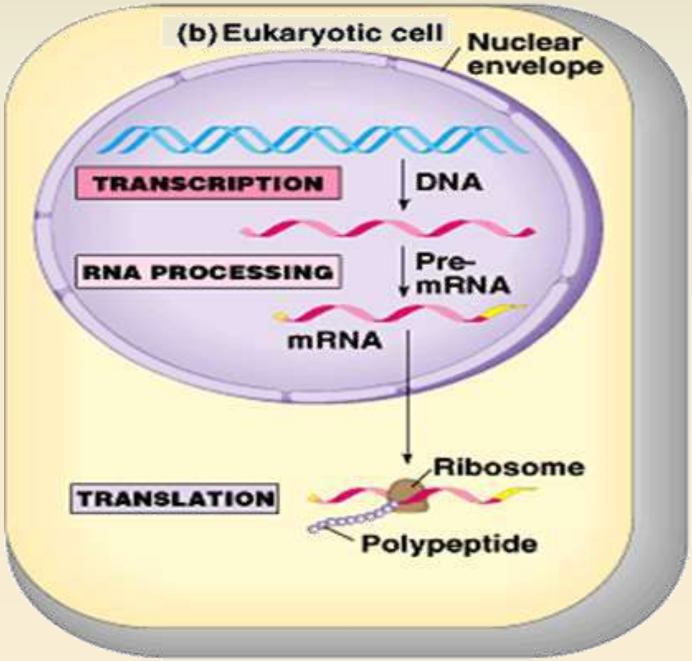
What is the anticodon for the codon AUG?

UAC

Protein Synthesis in Prokaryotes and Eukaryotes

Difference between Protein Synthesis in Prokaryotes and Eukaryotes

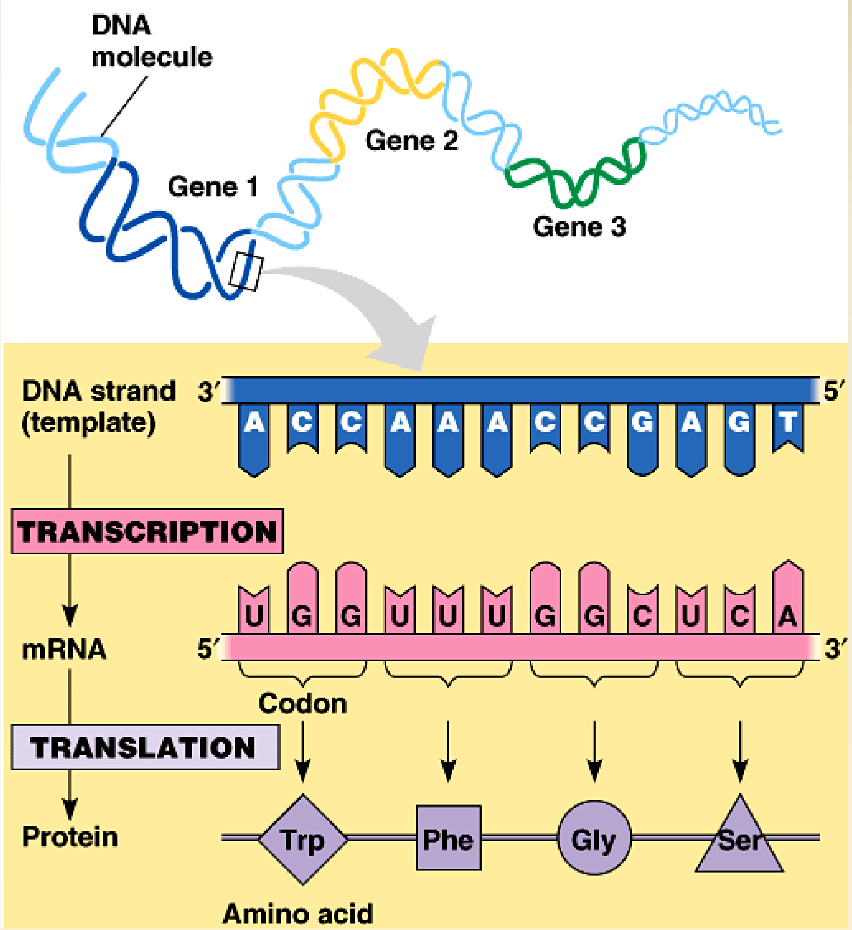




- Prokaryotes do not have introns like eukaryotes.
- There is no or very little RNA processing in prokaryotes.
- Transcription and translation can be simultaneous in prokaryotes.

Protein synthesis requires genetic information as genetic code contained in the DNA.

Genetic Code



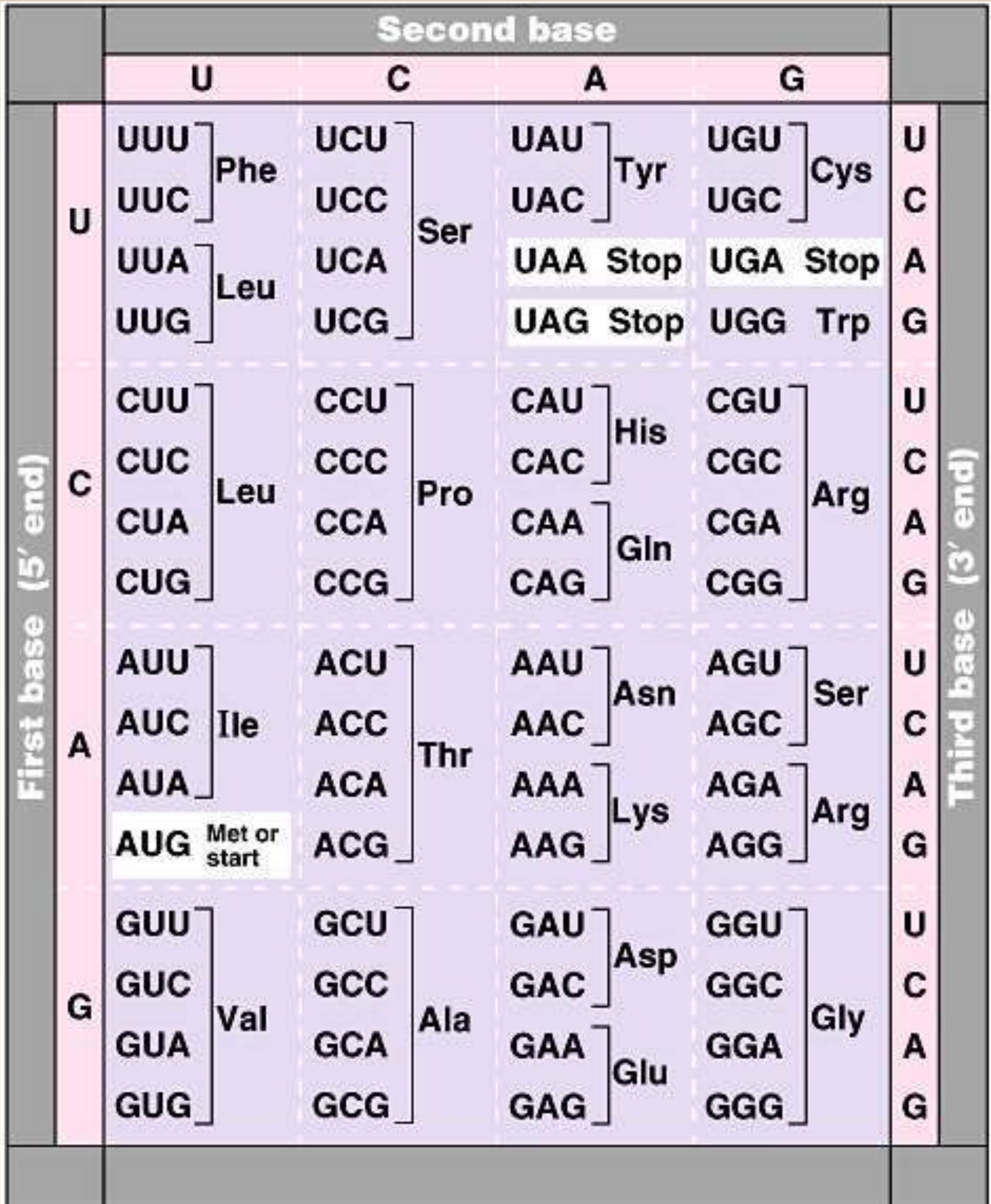
Amino acids are coded by triplets of DNA nucleotides, called codons.

There are 64 codons.

61 code for amino acids, 3 code for STOP, and one codes for START and also for Methionine.

Marshall Nirenberg and Heinrich Matthaei determined the first codon for an amino acid, which was UUU that coded for the amino acid phenylalanine, by creating mRNA entirely of uracil.

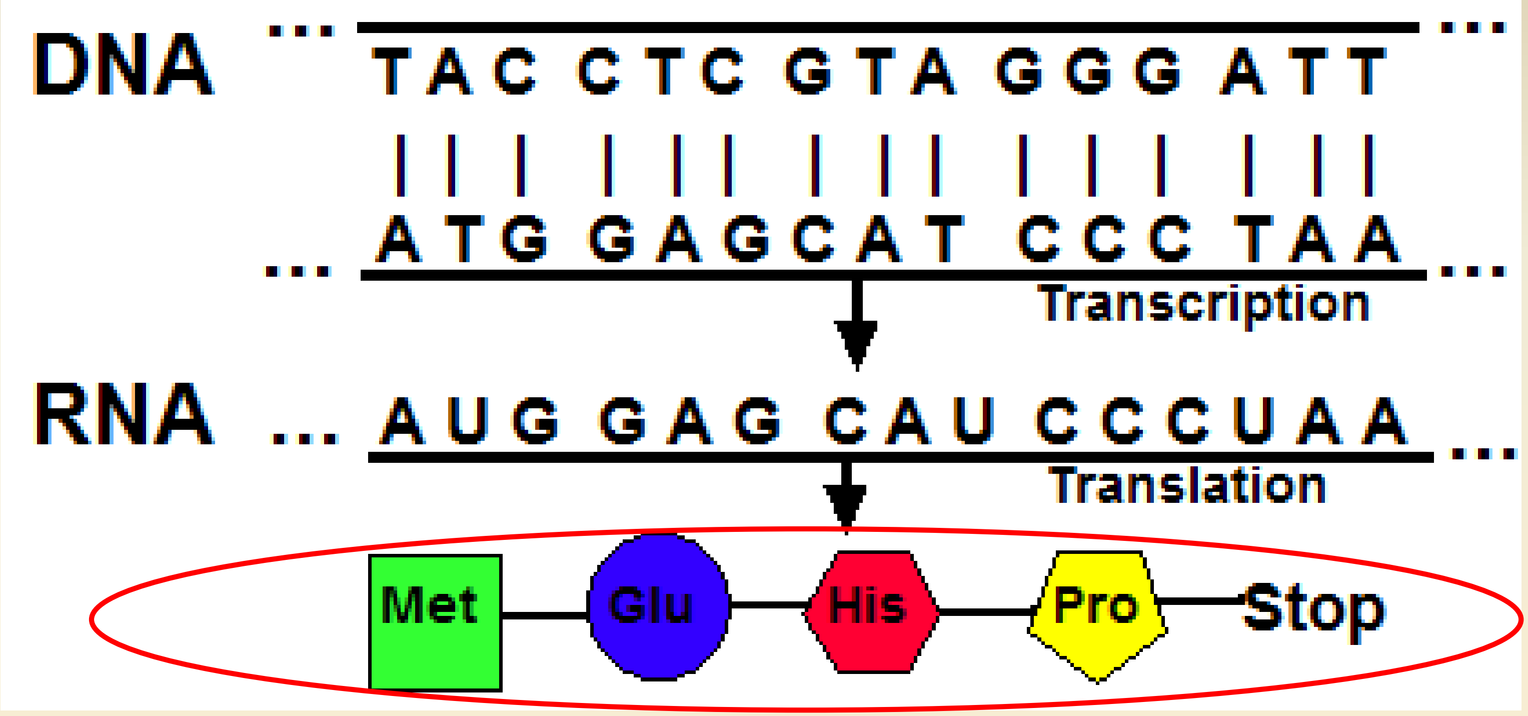
Genetic Code



First base (5′ end)	Second base				Third base (3′ end)
	U	C	A	G	
U	UUU Phe	UCU Ser	UAU Tyr	UGU Cys	U
	UUC	UCC	UAC	UGC	C
	UUA Leu	UCA	UAA Stop	UGA Stop	A
	UUG	UCG	UAG Stop	UGG Trp	G
C	CUU Leu	CCU Pro	CAU His	CGU Arg	U
	CUC	CCC	CAC	CGC	C
	CUA	CCA	CAA Gln	CGA	A
	CUG	CCG	CAG	CGG	G
A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U
	AUC	ACC	AAC	AGC	C
	AUA	ACA	AAA Lys	AGA Arg	A
	AUG Met or start	ACG	AAG	AGG	G
G	GUU Val	GCU Ala	GAU Asp	GGU Gly	U
	GUC	GCC	GAC	GGC	C
	GUA	GCA	GAA Glu	GGA	A
	GUG	GCG	GAG	GGG	G

- ❑ The code has redundancy (GGU, GGC, GGA, and GGG); all code for the amino acid glycine.
- ❑ Each codon only codes for one amino acid.
- ❑ The code is a universal code meaning almost all cells use the same code. A eukaryotic gene can be expressed in a prokaryotic cell.
- ❑ Code for ALL life (common origin for all life..

Translation of Codons into a Polypeptide

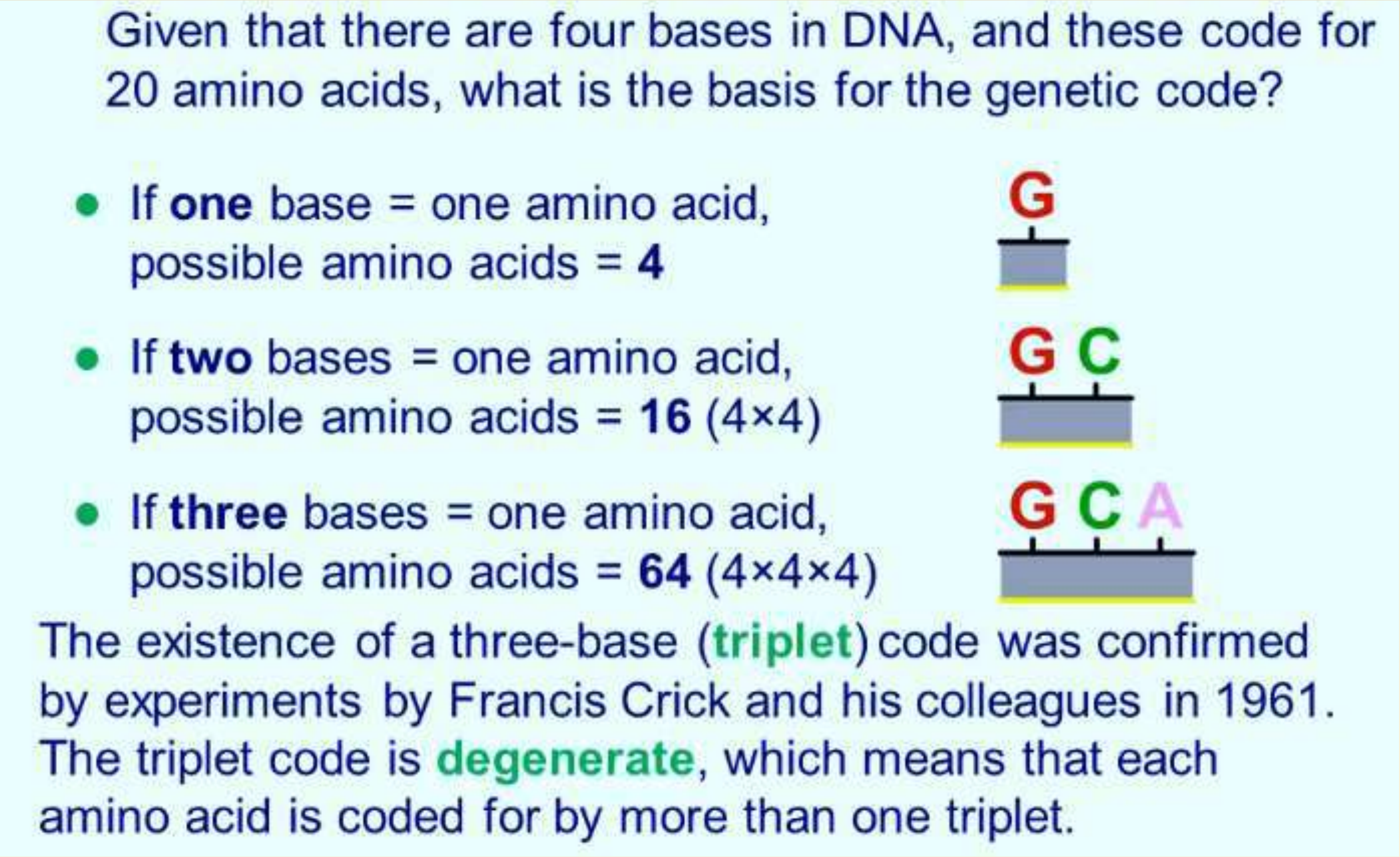


The gene designates that the following peptide chain be made with the amino acids in this particular order.

- **Start codon**
  - AUG

- **Stop codon**
  - UGA, UAA, UAG

Why is genetic code triplate?

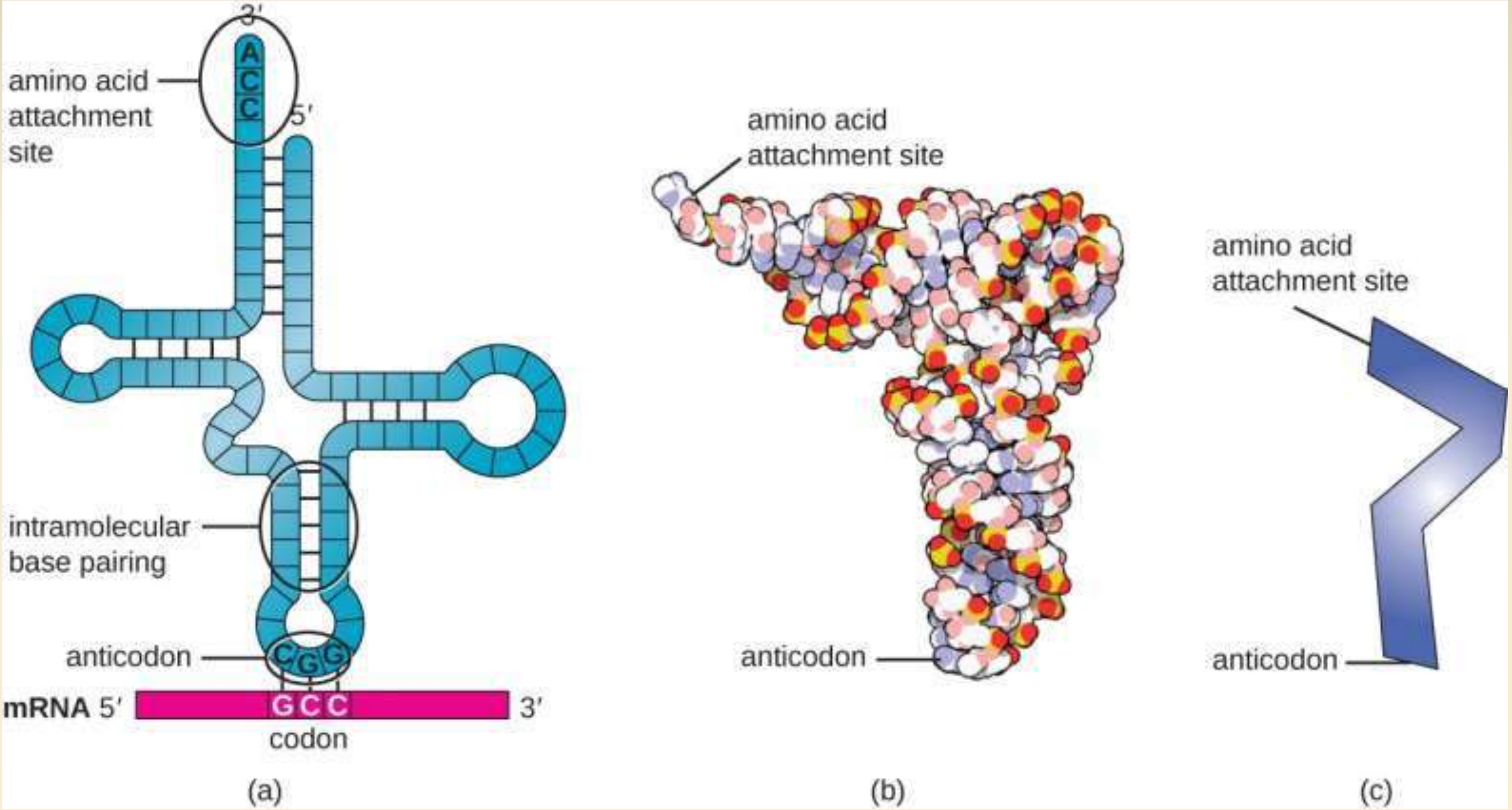


Given that there are four bases in DNA, and these code for 20 amino acids, what is the basis for the genetic code?

- If **one** base = one amino acid, possible amino acids = **4**
- If **two** bases = one amino acid, possible amino acids = **16** (4×4)
- If **three** bases = one amino acid, possible amino acids = **64** (4×4×4)

The existence of a three-base (**triplet**) code was confirmed by experiments by Francis Crick and his colleagues in 1961. The triplet code is **degenerate**, which means that each amino acid is coded for by more than one triplet.

How are the codons matched to amino acid?

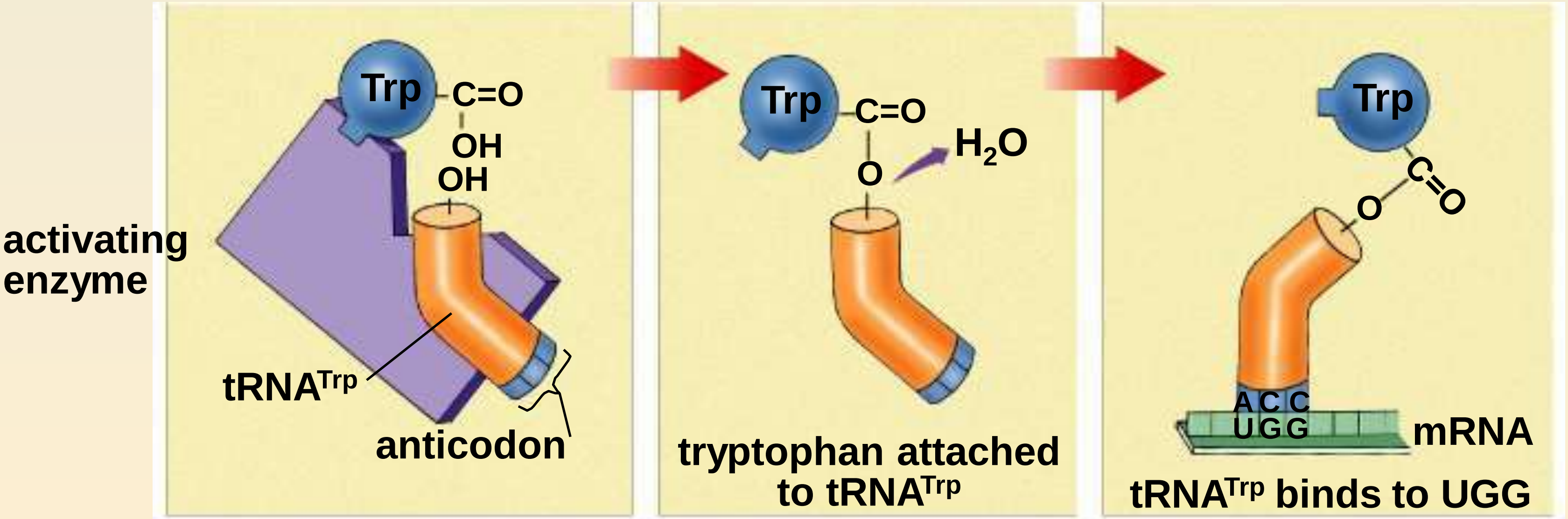


Charging of tRNA by an enzyme called aminoacyl tRNA synthetase also called tRNA-ligase (one aminoacyl tRNA synthetase is present for each standard amino acid, i.e., 20 aminoacyl tRNA synthetase are present in most of the cell).

Charging of tRNA

Charging of tRNA is accomplished by an enzyme <u>aminoacyl tRNA synthatse</u>

- **<u>Aminoacyl tRNA synthetase</u>**
  - **enzyme which bonds amino acid to tRNA**
  - **bond requires energy**
    - **ATP → AMP**
    - **bond is unstable, so it can release amino acid at ribosome easily**

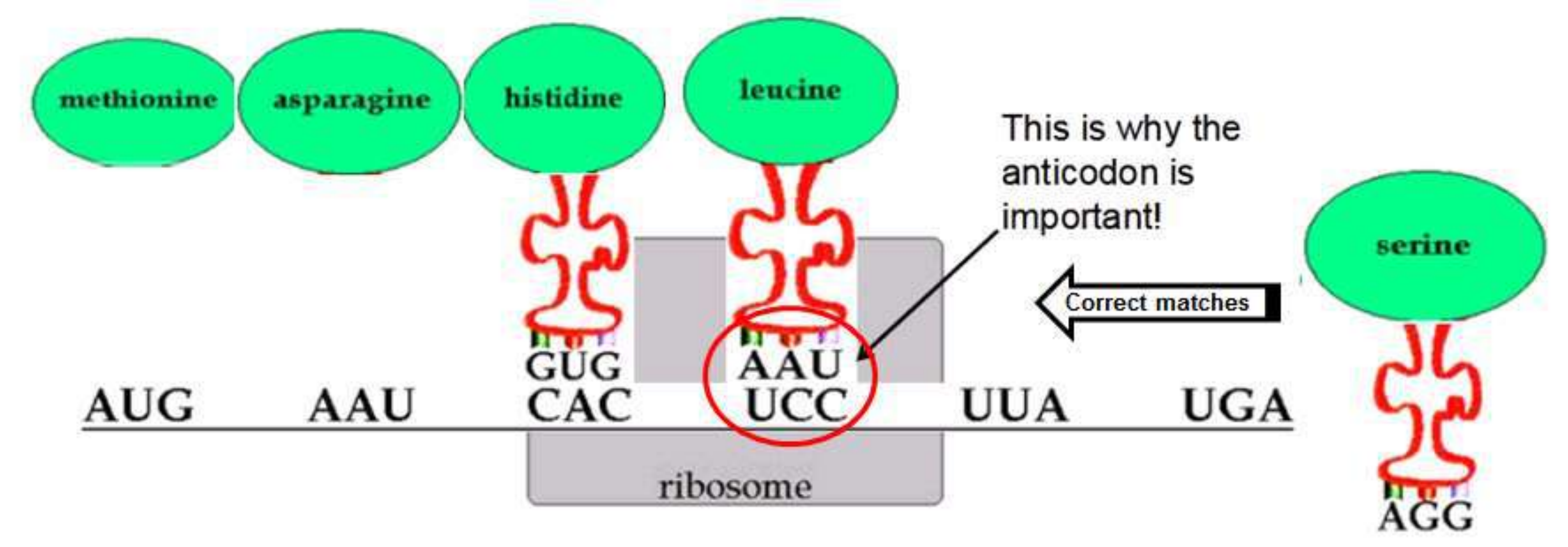


tryptophan attached to $tRNA^{Trp}$

$tRNA^{Trp}$ binds to UGG condon of mRNA

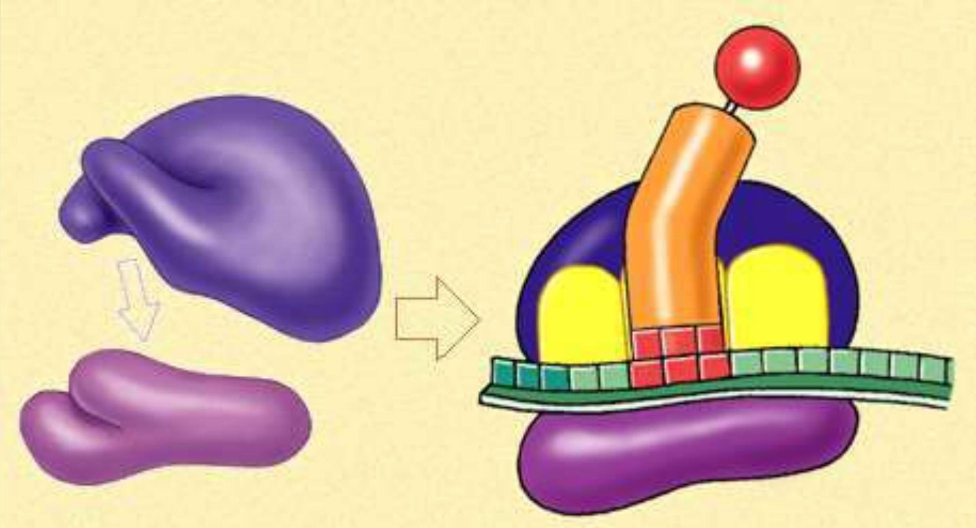
Ester bond between amino acid and tRNA

How are the codons matched to amino acid?



- ***Each codon represents a particular amino acid, and each codon is recognized by a specific tRNA.***
- ***Only codon specific anticodon containing tRNA interacts with codon, otherwise tRNA of wrong anticodon cannot interact with codon site.***

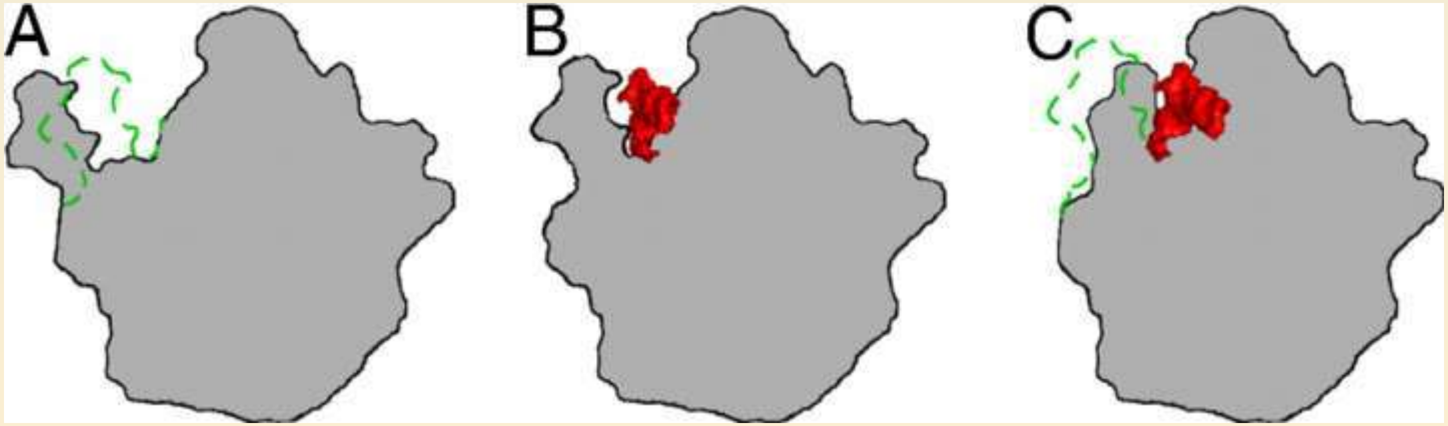
Ribosomes



- ❑ Ribosomes are a complex of ribosomal RNA (rRNA) and proteins.
- ❑ It is composed of two sub-units of unequal size;
  - ➢ Large subunit
  - ➢ small subunit
- ❑ It facilitates coupling of tRNA anticodon to mRNA
- ❑ It has many sites meant for specialized function, which are:
  - → **A site (aminoacyl-tRNA site)**
    - *It holds tRNA carrying next amino acid to be added to the polypeptide chain.*
  - → **P site (peptidyl-tRNA site)**
    - *It holds tRNA carrying growing polypeptide chain.*
  - → **E site (exit site)**
    - *It ensures empty tRNA leaves ribosomes from exit site*

Ribosomes & L1 Stalk

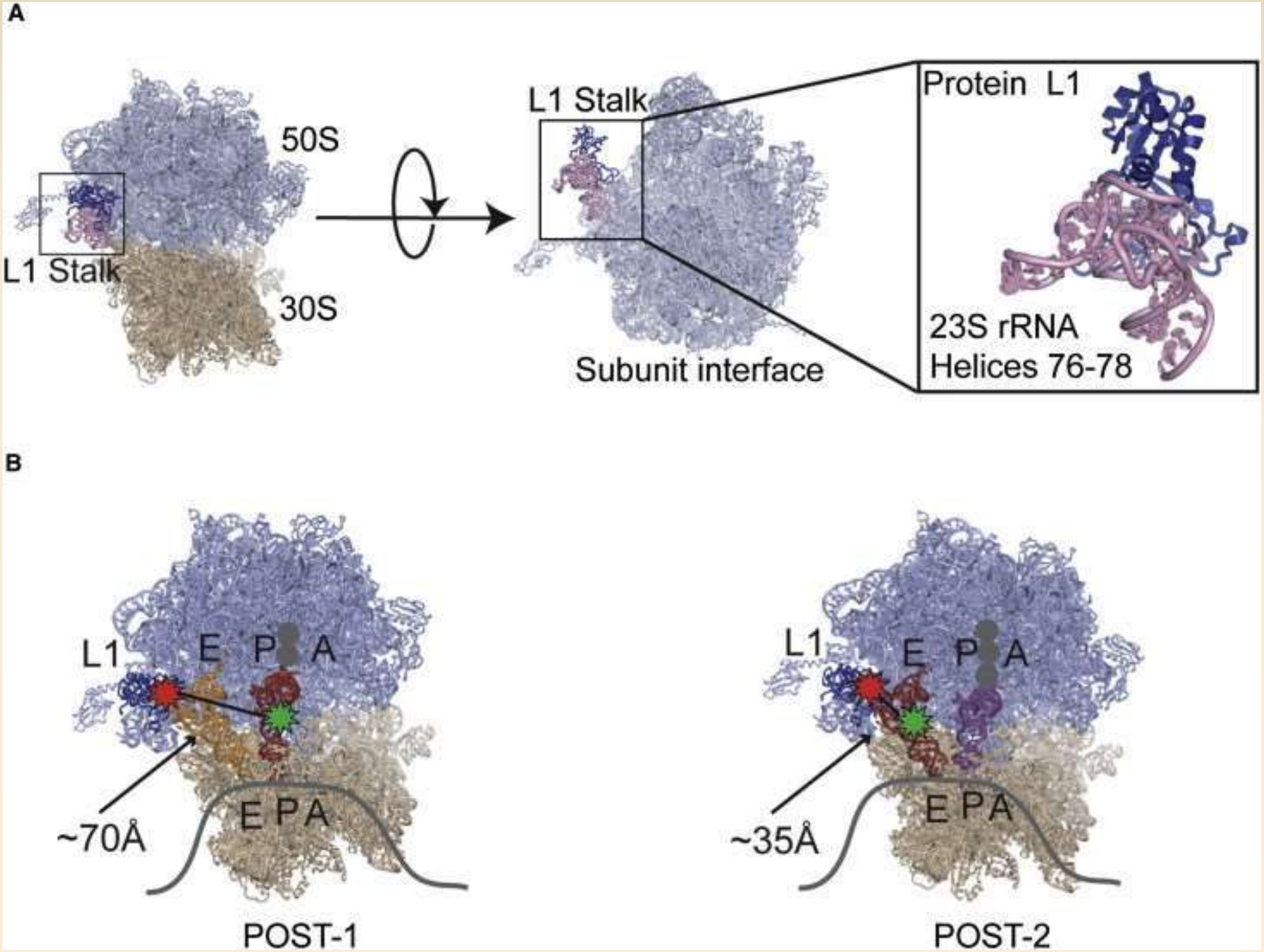
- ☐ The L1 stalk is a mobile domain of the large ribosomal subunit E site that interacts with the elbow of deacylated tRNA during protein synthesis.
- ☐ It is implicated in directing tRNA movement during translocation through the ribosome.
- ☐ L1 stalk can move by 90 degree independently of intersubunit rotation and its mobility facilitates binding, movement, and release of deacylated tRNA by remodeling the structure of the 50S subunit E site between 3 distinct conformations, corresponding to the E/E vacant, P/E hybrid, and classical states.



(*A*) Open state of the L1 stalk with vacant E site; (*B*) half-closed state of the L1 stalk with deacylated tRNA in the classical E/E state; (*C*) fully closed state of the L1 stalk with tRNA in the hybrid P/E state.

Cornish et. al., PNAS 2009; 106 (8) 2571-2576.

Ribosomes & L1 Stalk



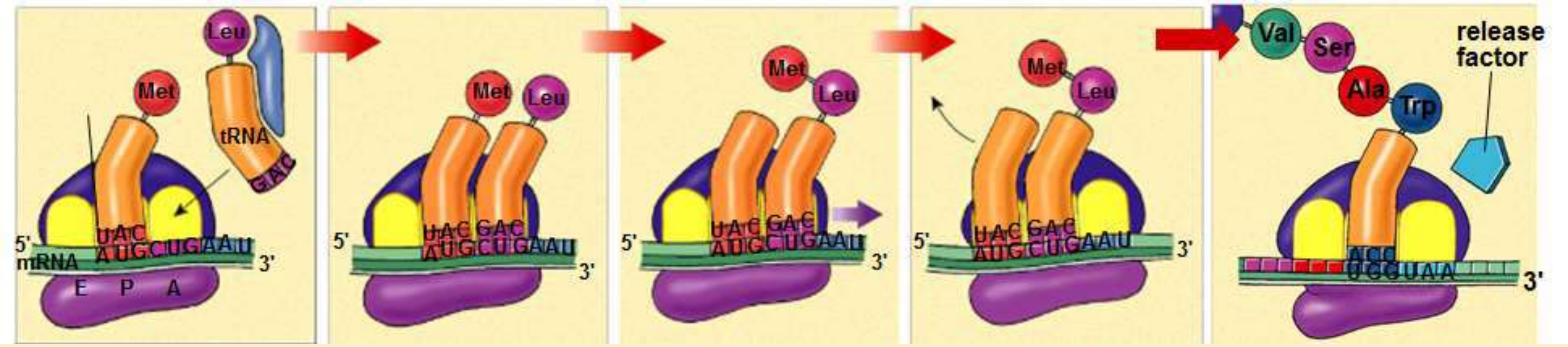
Fei et. al. Molecular Cell 2008; 30(3): 348-359.

- Interaction of tRNA with L1 site results in rotation of L1-tRNA complex to 90◦.
- Rotation results in changes in distance of complex at different sites of ribosomes and is required for movement of mRNA and tRNA in the ribosomes.
- It plays a crucial role in elongation.

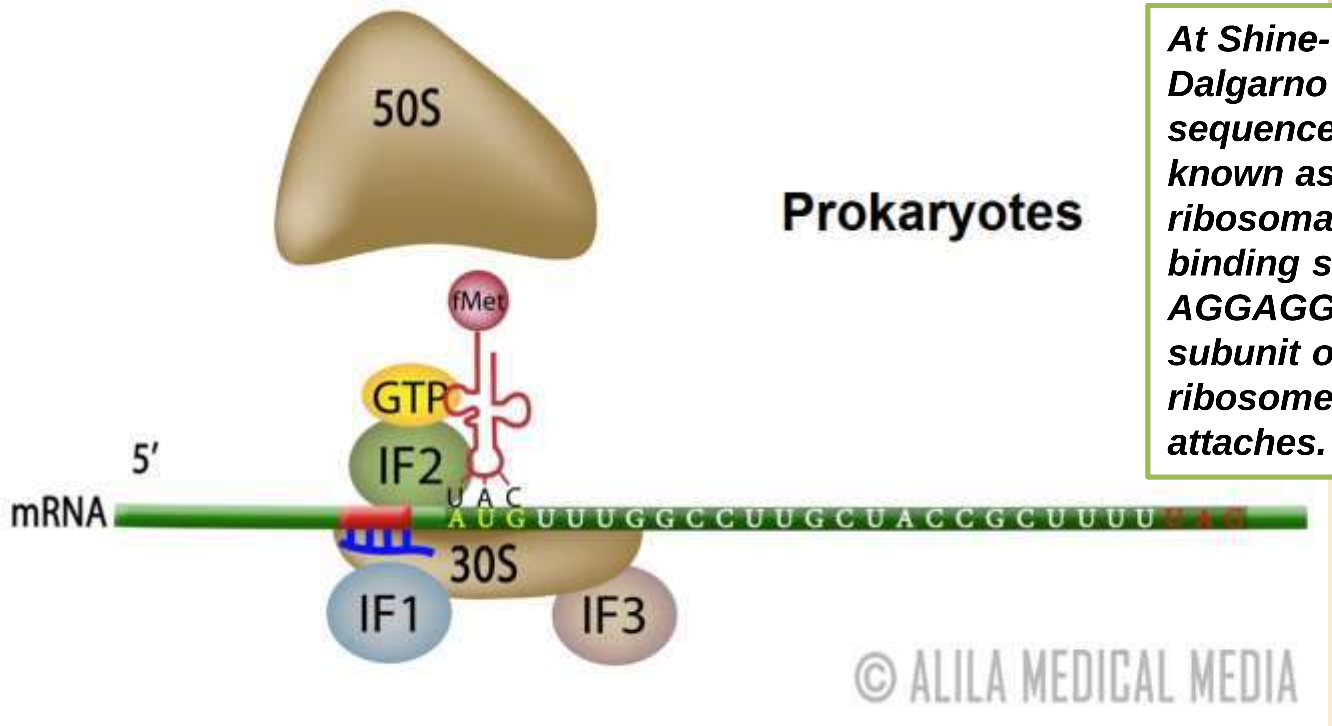
Protein Synthesis

Three steps

- **Initiation**
  - It brings together mRNA, ribosomal subunits and initiator tRNA.
- **Elogation**
  - In this phase, adding of amino acids take place based on codon sequence.
- **Termination**
  - Here codon ends and translation stops



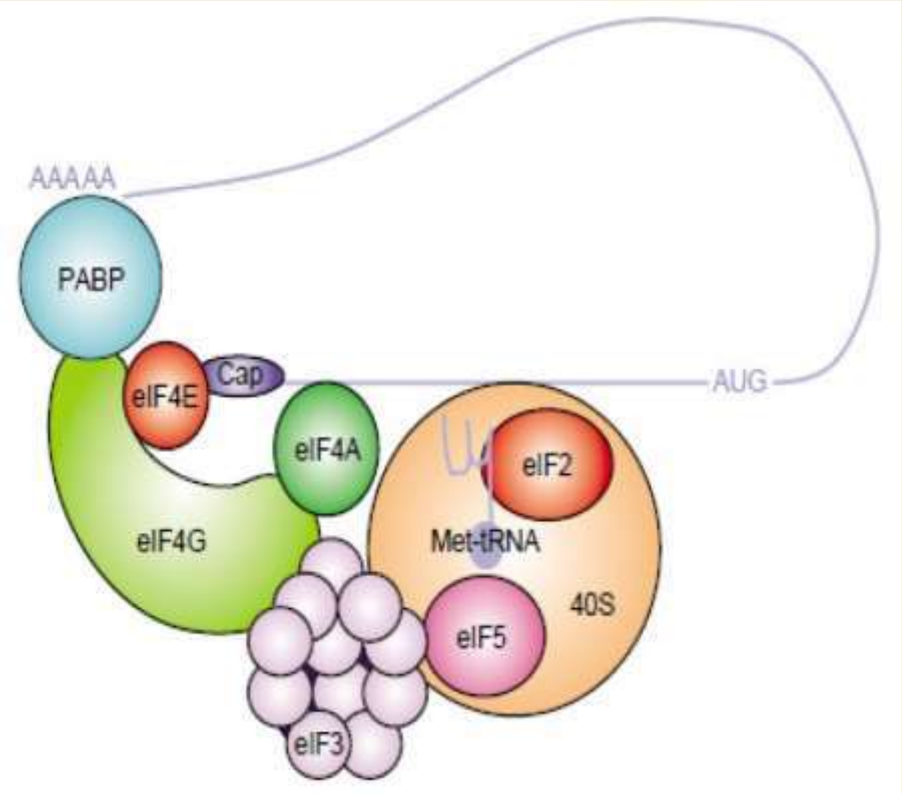
Initiation of Translation



At Shine-Dalgarno sequence (also known as the ribosomal binding site AGGAGG), small subunit of ribosome attaches.

In prokaryotes, protein synthesis begins with the formation of an initiator complex which involves the small 30S ribosome, the mRNA template, 3 initiation factors that helps the ribosome assemble correctly, guanosine triphosphate (GTP) that acts as a energy source, and a special initiator tRNA carrying N-formyl-methionine (fMet-tRNA^{fMet})

Initiation of Translation



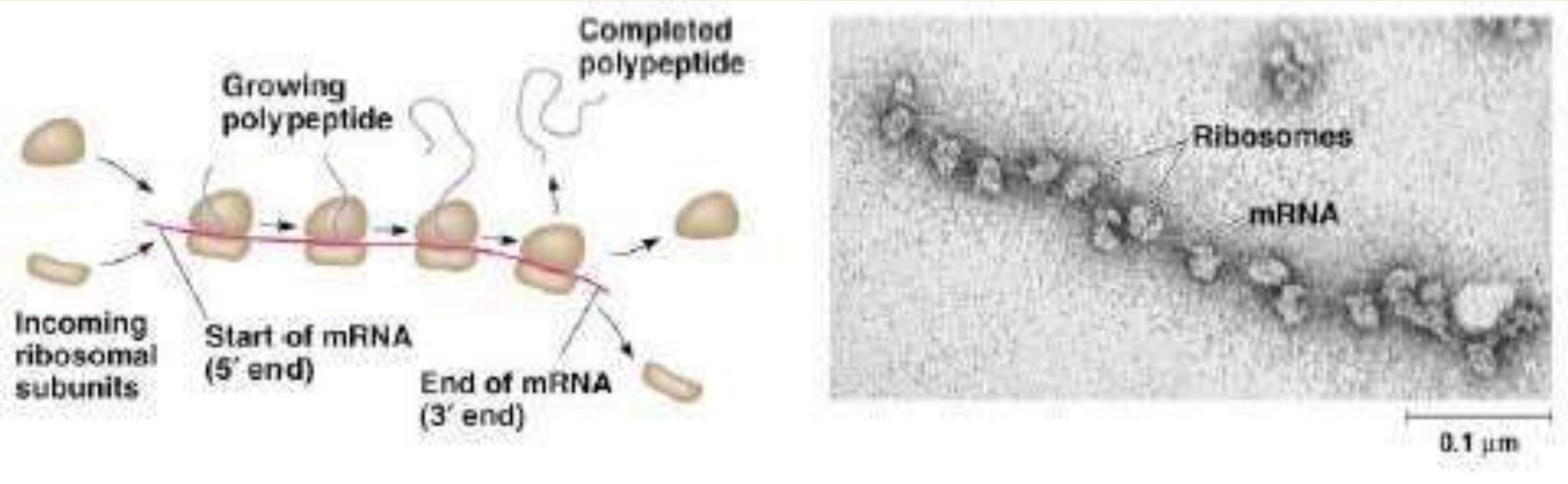
ETS-related transcription factor **(Elf)**

- In eukaryotes, capped mRNAs are recruited by the eIF4F complex (it has two subunits; eIF4E and eIF4G – eIF4E is the cap binding protein, while eIF4G is a “scaffolding” protein which interacts with several initiator factors, such as poly (A) binding protein (PABP), eIF4A (a DEAD box helicase for unwinding secondary structures) and eIF3 (a multisubunit that binds to the 40S ribosome).
- Once the mRNA is bound to the 40S ribosome, the ribosome and associated factors scan along the mRNA until an initiation codon is encountered.
- Then 60S ribosomal subunit binds upon eIF5-meiated GTP hydrolysis of the ternary complex.

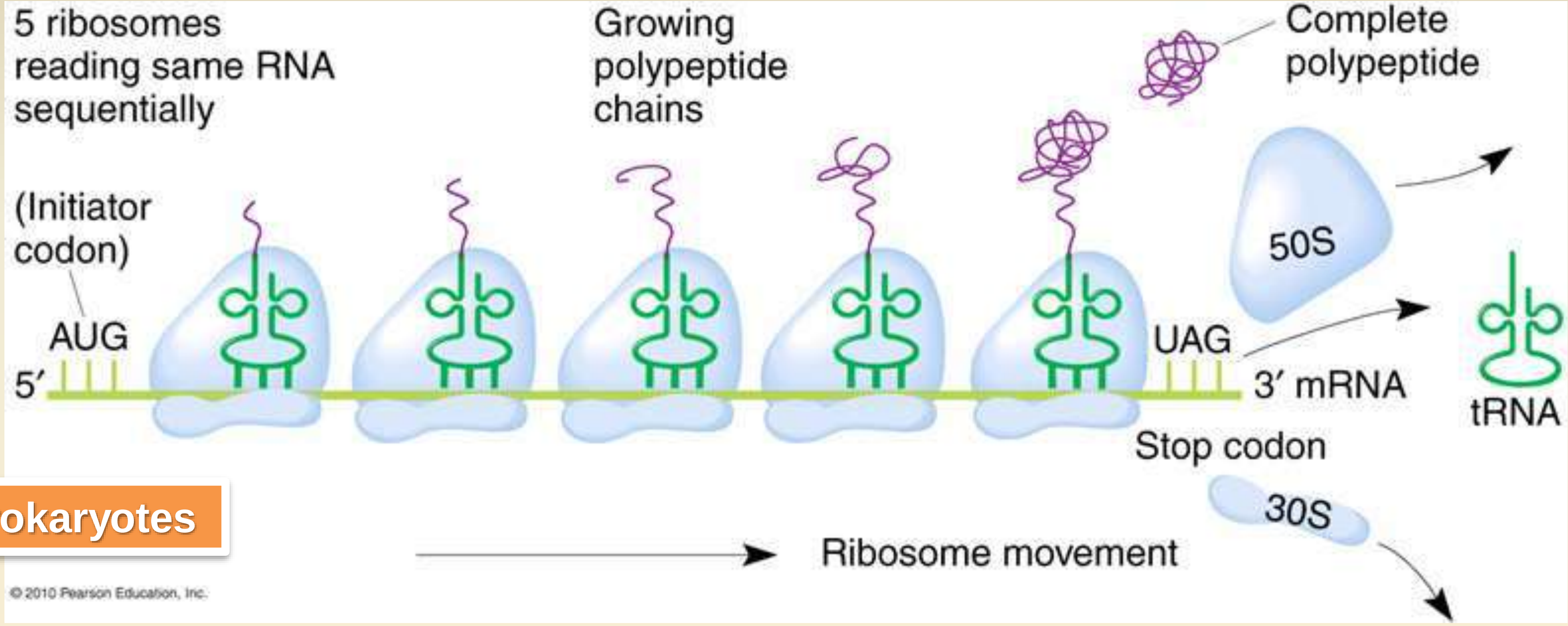
Souii et. al. International Journal of Molecular Sciences 2013; 14(3):4525-44

Elongation of Polypeptide Chain

- **Polyribosomes (Polysomes)**
  - **Numerous ribosomes translate same mRNA at same time**
  - **3-D folding (1’, 2’, 3’ structure)**
  - **Chaparonins:** provide essential kinetic assistance to protein folding by binding non-native proteins.



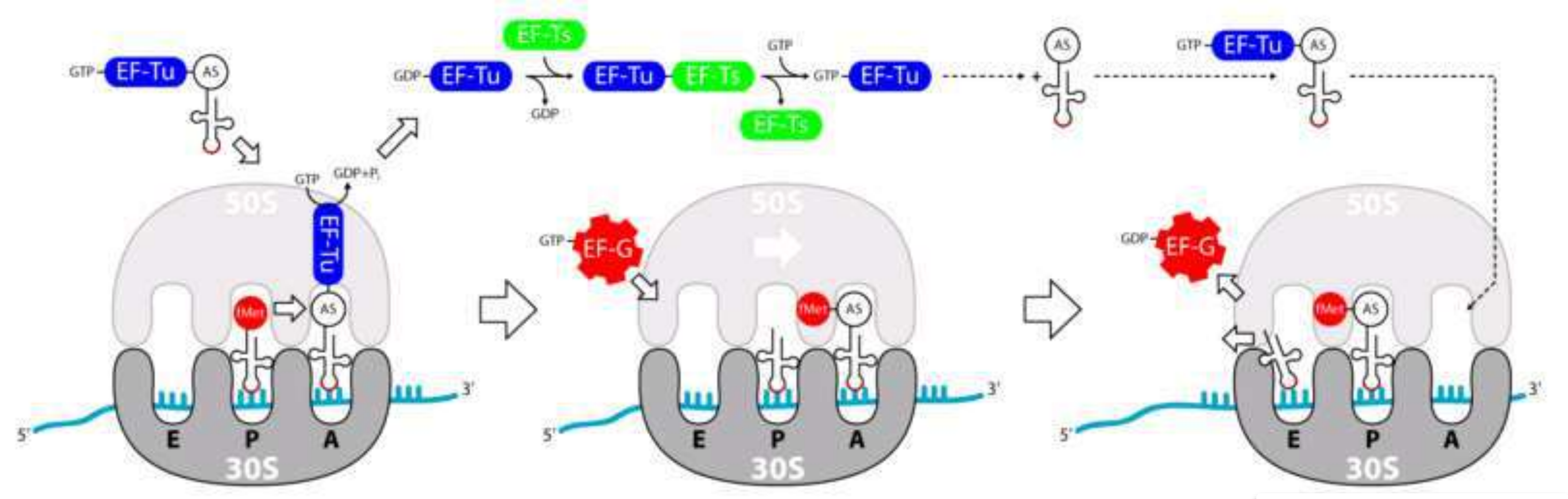
Elongation of Polypeptide Chain



Prokaryotes

- ❑ Elongation starts with the occupation of metthionyl-tRNA to the ribosome P – site after recognizing a start codon on mRNA bound to small ribosomal subunit.
- ❑ The large subunit then joins the small subunit, and a second tRNA is recruited.
- ❑ As the mRNA moves relative to the ribosome, successive tRNAs move through the ribosome and the polypeptide chain is formed.
- ❑ In this way, elongation proceeds with charged tRNAs sequentially entering and leaving the ribosome as each new amino acid is added to the polypeptide chain.

Elongation of Polypeptide Chain



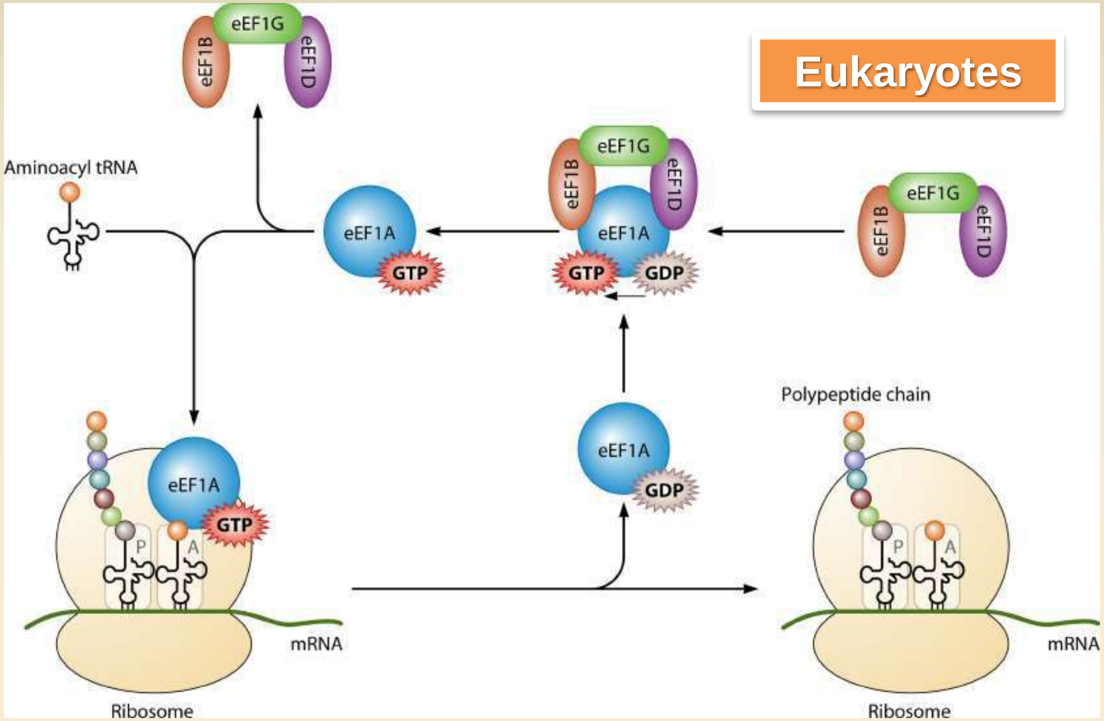
Souii et. al. International Journal of Molecular Sciences 2013; 14(3):4525-44

Prokaryotes

- This movement of a tRNA from A to P to E site is induced by conformational changes that advance the ribosome by 3 bases in 3′ direction.
- The energy for each step, such as binding of a new aminoacyl-tRNA to the A site and for its translocation to the P site after formation of the peptide bond along the ribosome is donated by elongation factors that hydrolyze GTP.
- Peptide bonds form between the amino group of the amino acid attached to the A-site tRNA and the carboxyl group of the amino acid attached to the P-site tRNA by an enzyme peptidyl transferase ntegrated into large subunit..

Elongation of Polypeptide Chain

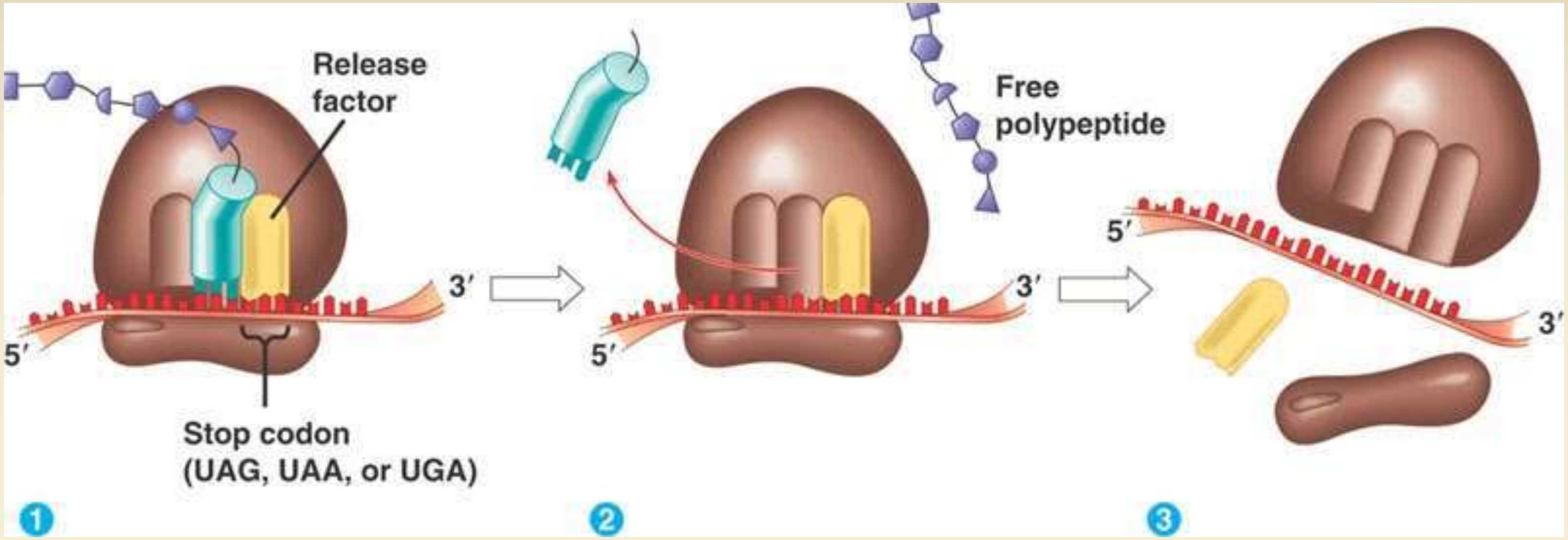
- ☐ In most eukaryotes, elongation is facilitated by two elongation factors (eEF1 and eEF2) which is active after making complex with GTP. Fungi also requires eEF3.
- ☐ eEF-1 is a multimer and mediates the binding of the cognate aminoacyl-tRNA to the ribosome, while eEF2, a monomer, catalyzes the movement of the ribosome relative to the mRNA.



Li et. al. Microbiol. Mol. Biol. Rev. 2013, 77(2):253.

- ☐ Eukaryotic elongation factor 1A (eEF1A)-GTP delivers an aminoacylated tRNA to the A site of the ribosome. Thereafter, GTP is hydrolyzed when codon-anticodon recognition occurs.
- ☐ Then eEF1A-GDP is released from the ribosome. Rest movement aminoacylated tRNA on 3 sites on ribosomes are same as that of prokaryotes.

Termination of Translation

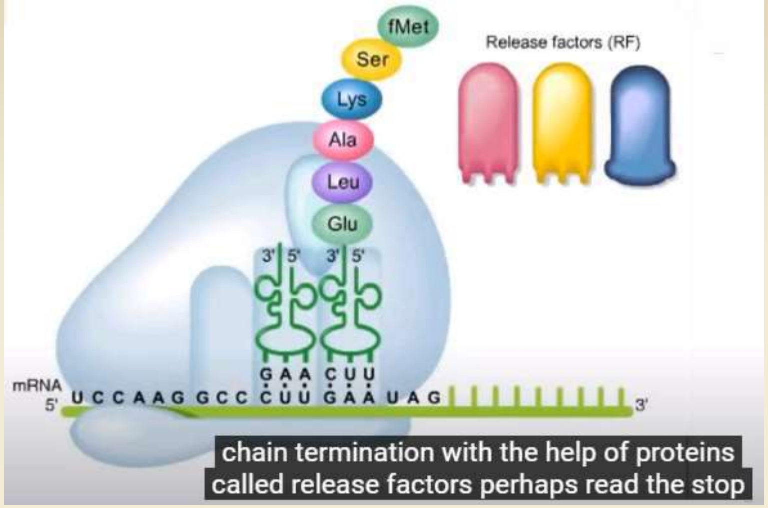


Step 1 **–** After the amino acids needed to make the protein required are properly bonded to each other a release factor binds to the complex when a stop codon enters the A site.

Step 2 **–** The release factor then disconnects the polypeptide from the tRNA in the P site.

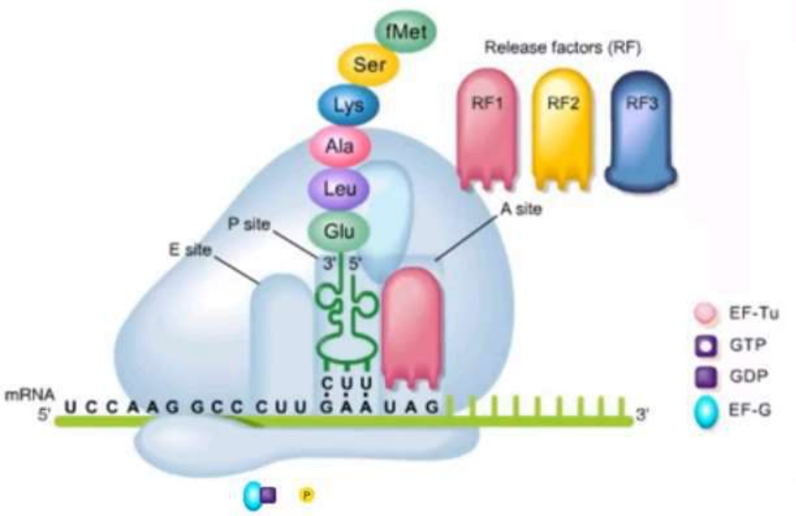
Step 3 **–** The remaining components mRNA, ribosomal subunit, and the protein are released and the process of translation ends.

Termination of Translation in Prokaryotes



chain termination with the help of proteins
called release factors perhaps read the stop

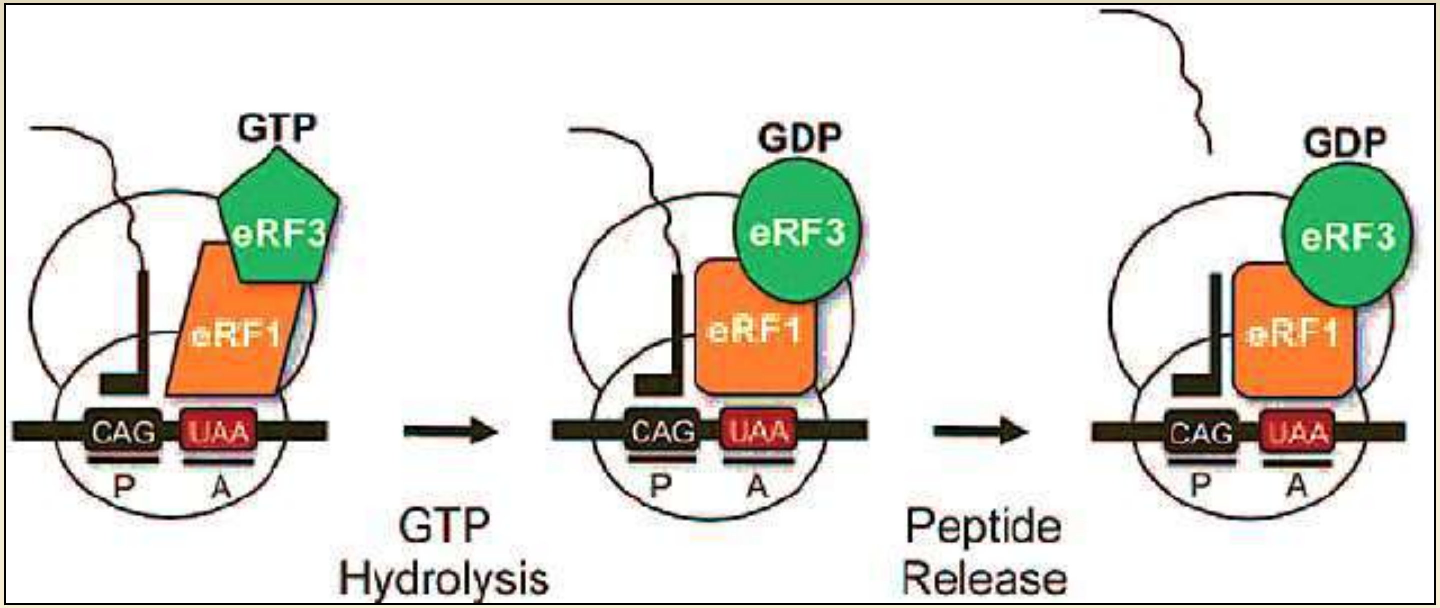
The ribosome recognizes polypeptide chain termination with the help of proteins called release factors (RF), RFs read the stop codon and initiate a series of specific termination events.



E. Coli has 3 Rfs; Rf1, Rf2 and Rf3. Rf1 recognizes UAA and UAG, while Rf2 recognizes UAA and UGA. Rf3 does not recognizes any stop codons, but stimulates the subsequent termination events.

Elongation and ribosome translocation results in a stop codon entering the vacant A site. RF1 or RF2 binds to the stop codon which triggers peptidyl transferase to cleave the now complete polypeptide from its tRNA located in the P site of the ribosome.

Termination of Translation in Eukaryotes



Keeling et. al. Critical Reviews in Biochemistry and Molecular Biology 2012; 47(5):444-63.

A complex comprised of eRF1 and eRF3 mediate translation termination. eRF1 recognizes any of the three stop codons (UAA, UAG, UGA) in the ribosomal A site. GTP hydrolysis by eRF3 assists: (i) stop codon recognition by eRF1, and (ii) eRF1 accommodation into the peptidyl transferase center so polypeptide release can occur.

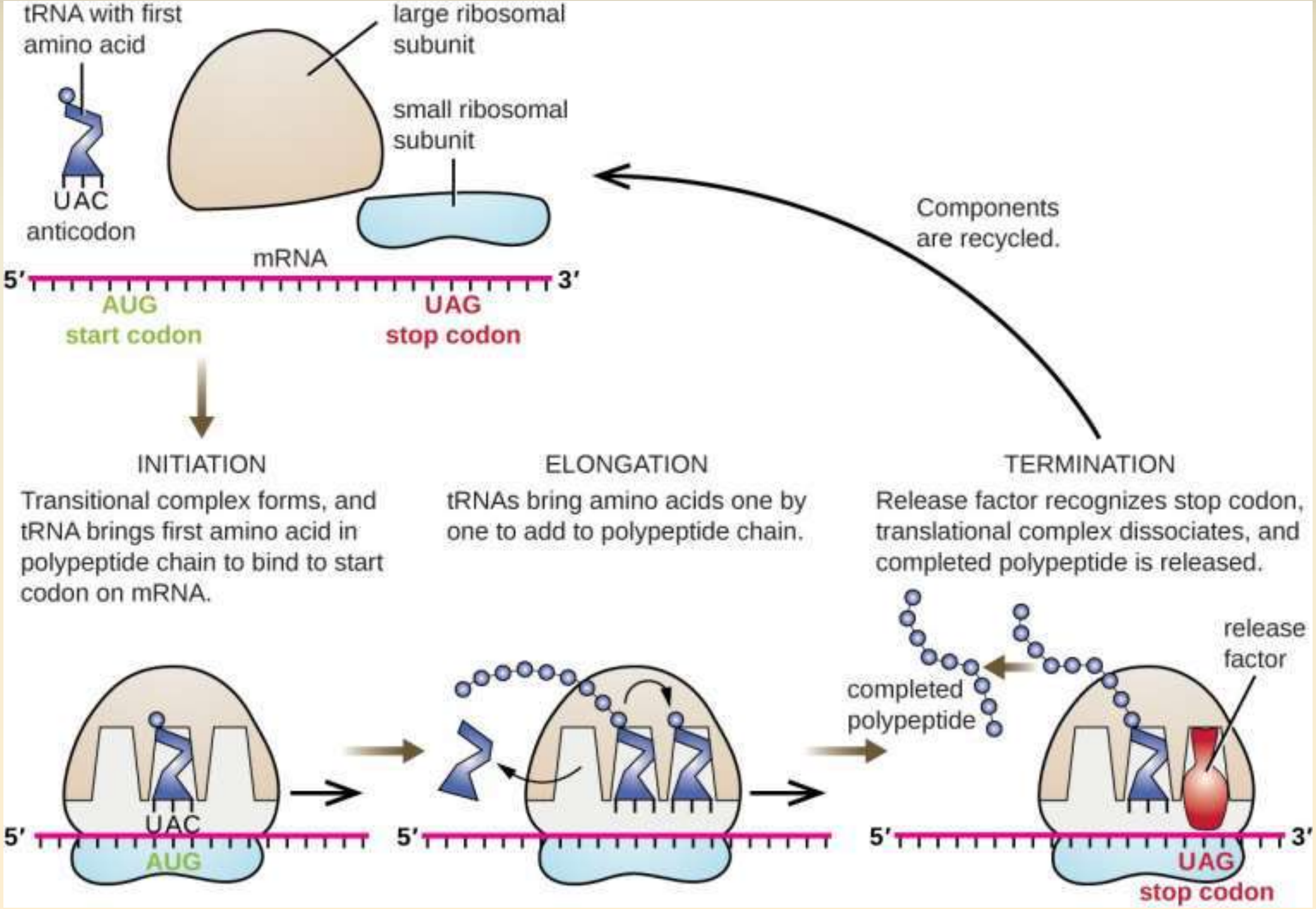
Regulation of Translation

- It refers to the control of the levels of protein synthesized from its mRNA.
- In eukaryotes, regulation of protein synthesis can occur by modification of DNA or at the level of transcription within the nucleus, processing of mRNA in the nucleus, or translation in the cytoplasm.

Regulation at the translational level: It occurs during the initiation of elongation reactions, such as,

- **Heme** stimulates the synthesis of globin by preventing the phosphorylation and consequent inactivation of eIF-2, a factor involved in the initiation of protein synthesis.
- **Interferon** stimulates the phosphorylation of eIF-2, causing inhibition of initiation.
- **Iron-response elements** (IREs) in mRNA for ferritin (an iron storage protein) and the transferrin receptor regulate translation of the respective mRNAs. These elements either destabilize the mRNA (transferrin receptor) or allow translation of the mRNA (ferritin) when iron levels are high.

Overview of Translation



Overview of Translation

Comparison of translation in Prokaryotes and Eukaryotes (& Archea)		
Ribosomes	70S ▪ 30S (small subunit) with 16S rRNA subunit ▪ 50S (large subunit) with 5S and 23S rRNA subunits	80S ▪ 40S (small subunit) with 18S rRNA subunit ▪ 60S (large subunit) with 5S, 5.8S and 28S rRNA subunits
Amino acid carried by initiator tRNA	fMet	Met
Shine-Dalgarno sequence in mRNA	Present	Absent
Simultaneous transcription and translation	Yes	No

In prokaryotes, Met-tRNA is modified by the addition of a formyl group and it is fMet-tRNA in prokaryotes.

Brainteaser

Do the same DNA sequences lead to the same proteins in all organisms?

- No, due to differential mRNA splicing identical DNA sequences may lead to non-identical proteins.
- There are about 150 known cases of deviations from the universal genetic code with 1 or 2 codons being re-assigned to different amino acids; typically in small (organelle) genomes, but occasionally in nuclear genomes as well.

Further reading

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- Griswold A. 2008. Genome Packaging in Prokaryotes: the Circular Chromosome of *E. coli*. Nature Education 1(1):57.
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