بسم الله الرحمـٰن الرحيم

(وَفَوْقَ كُلِّ ذِي عِلْمٍ عَلِيمٌ)

Cytology & Molecular Biology | FINAL 17

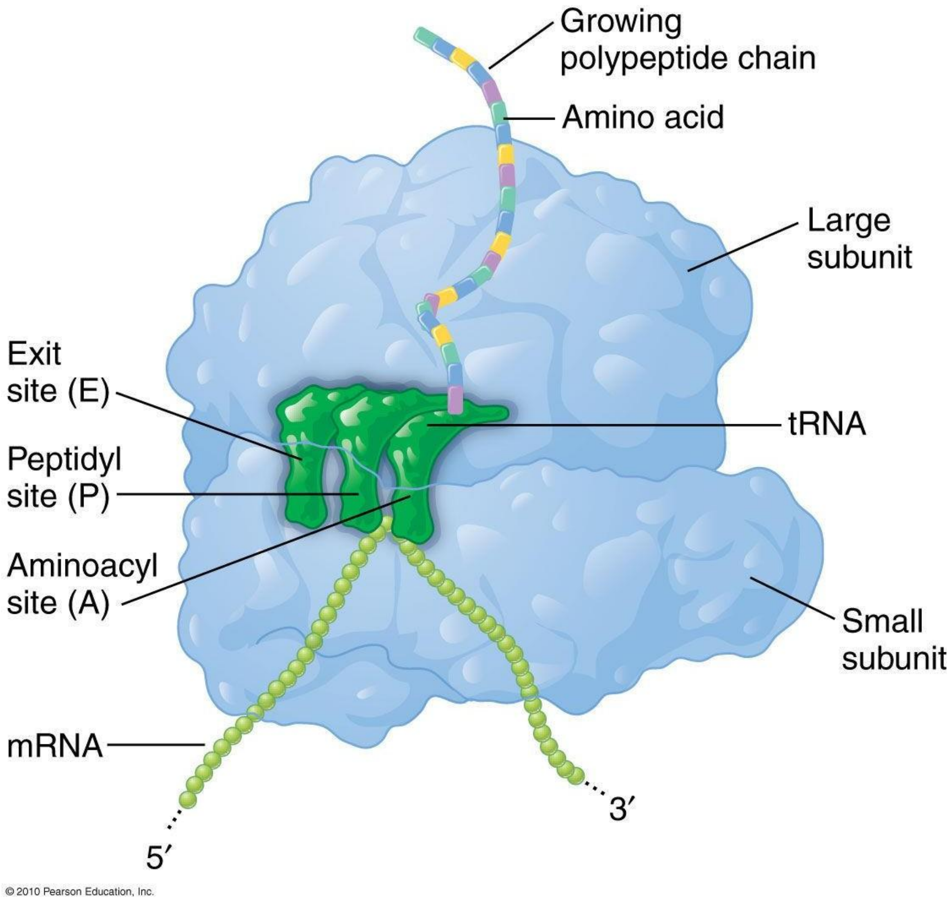
# Translation

# Pt.1

**Written by :** DST
NST

**Reviewed by :** NST

# ❑ General information



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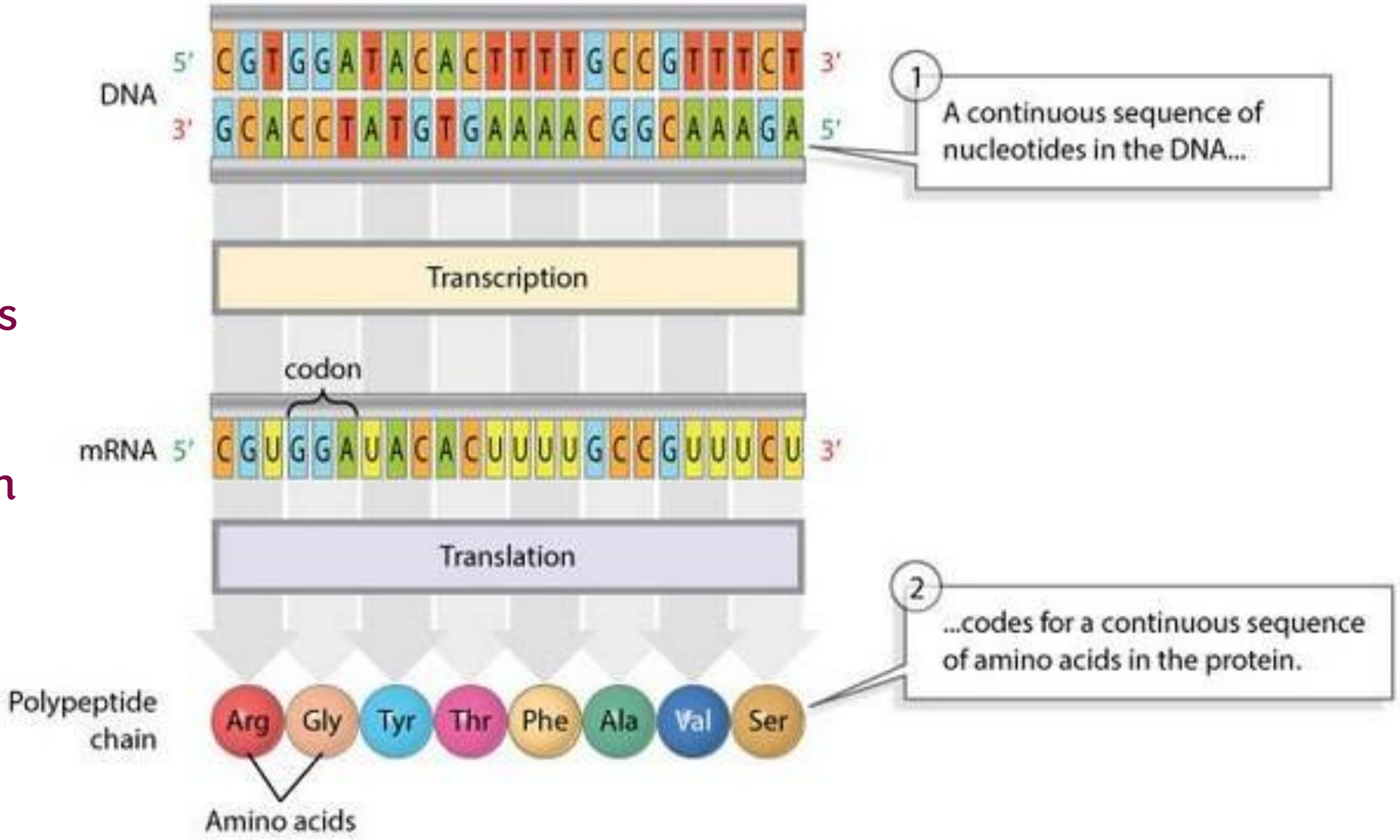
- Translation: The process of making proteins from mRNA.
- Protein synthesis involves interactions between ribosomes with three types of RNA molecules:
  - tRNAs (carry the Amino acids)
  - rRNAs (important for structure, & catalyzes connecting to amino acids)
  - mRNA templates (the main molecule)

# ❑ Colinearity of genes, mRNAs, & proteins

- Co-linearity: In linearity ( they are parallel and accompany each other).
- mRNA has the same nucleotides sequence as the DNA , protein is co-linear with mRNA.
- So, if we have a mutation in a specific region in the DNA, it will reflect on the mRNA and the protein in the same specific region.



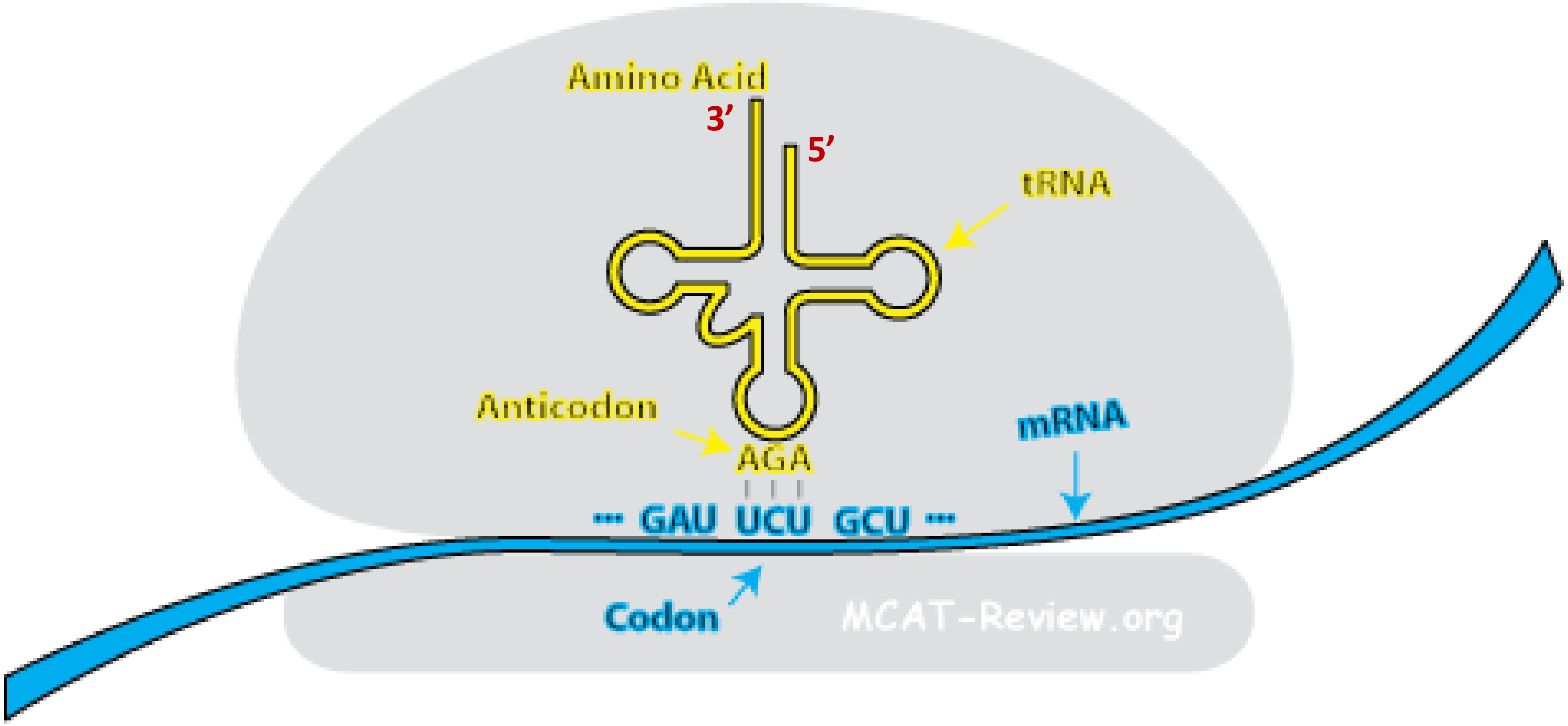
A continuous sequence of nucleotides in the DNA...

...codes for a continuous sequence of amino acids in the protein.

With colinearity, the number of nucleotides in the gene is proportional to the number of amino acids in the protein.

# ❑ mRNA is read by tRNA in triplets

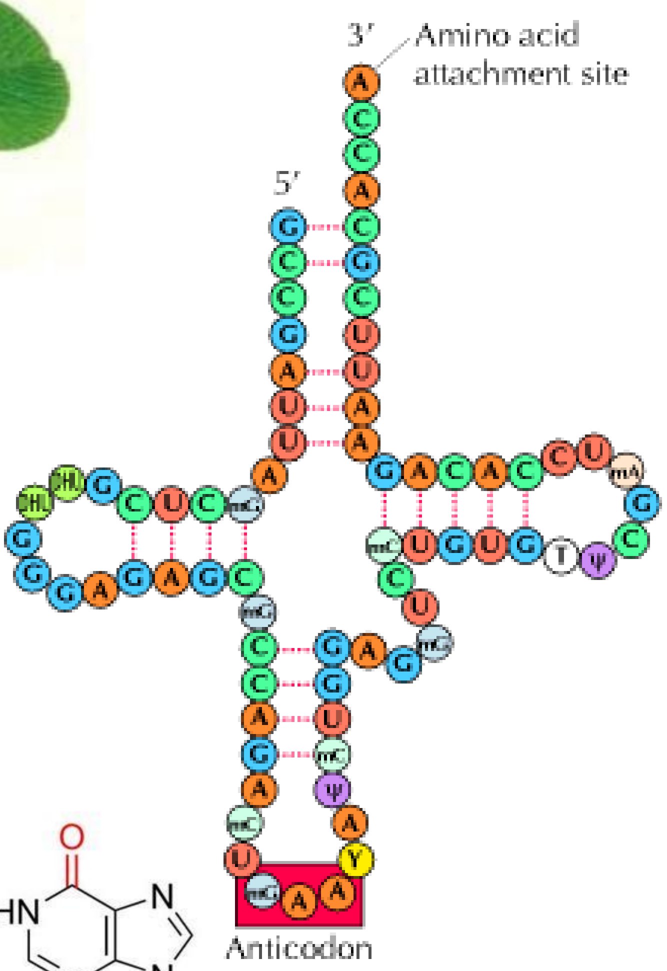
- tRNA reads the mRNA as triplets (codons are made of 3 nucleotides each).

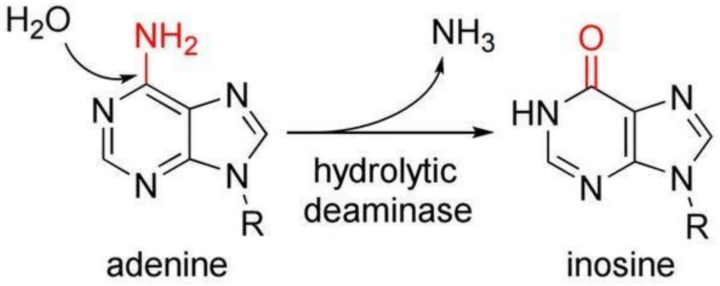


# ❑ tRNA structure

- tRNAs are short single-stranded RNA molecules (80 bases long).
- “Charged” or “activated” tRNA carries one amino acid at the 3’-end.
- Amino Acid carried by the tRNA is determined by :
  1. Triplet of nucleotides ( anticodon ), which is complementary to the codon of mRNA.
  2. Internal sequence (special code inside the tRNA).
- tRNAs contain stem loop structures, modified bases, and unusual bases (example: inosine).
- In addition to the 4 nitrogenous bases we know, tRNA has additional modified base, for example (inosine).

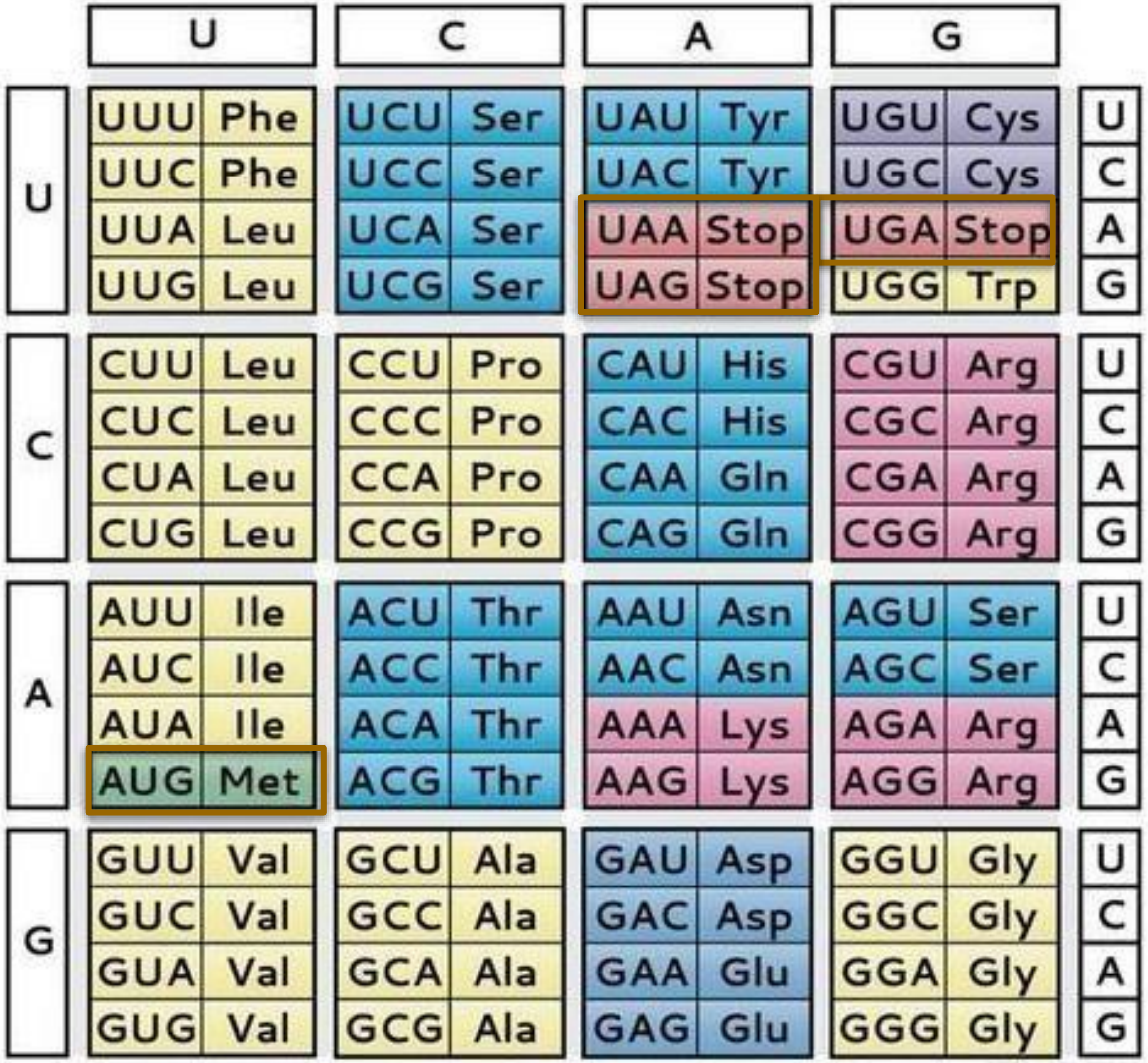
tRNA structure looks like a clover leaf





(DO NOT MEMORIZE THE WHOLE TABLE)

## Genetic Codon Chart



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

Translation START codon

Translation STOP codon

Positively charged amino acids

Negatively charged amino acids

Hydrophobic amnio acids

Hydrophilic non-charged amino acids

Cysteine

- tRNA reads mRNA as triplets (codons).
- We have 64 probability of different triplets (codons) to encode 20 amino acids.
- These codons are at the mRNA not the tRNA.
- Amino acids cluster in groups ( hydrophobic amino acids, hydrophilic amino acids, etc…), so its not random, which reduces the impact of mutations.
- ➢ AUG codes for methionine and it's the first codon in the translation.
- ➢ UAA / UAG / UGA => stop codons.

((:

UGA = يما جوعان انا
UAG = يما انا جوعان
UAA = يما انا افطرت

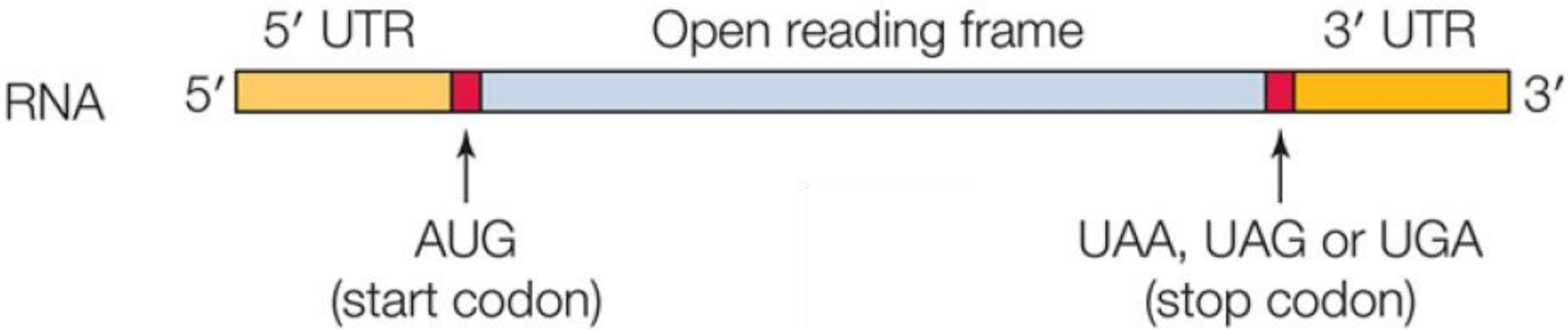
# ❑ Features of the genetic codon

All 64 possible codons of the genetic code and the amino acid specified by each, as read in the 5′→3′ direction from the mRNA sequence.

Sixty-one codons specify an amino acid.

Three STOP codons (UAA, UAG, and UGA) do not encode any amino acid.

The genetic code for mitochondrial mRNA (mtDNA) is typical of the universal code except for a few variants.

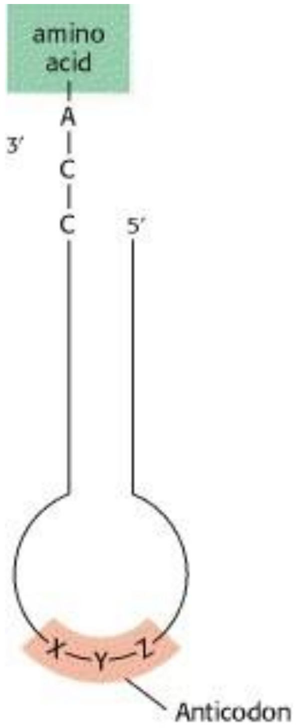


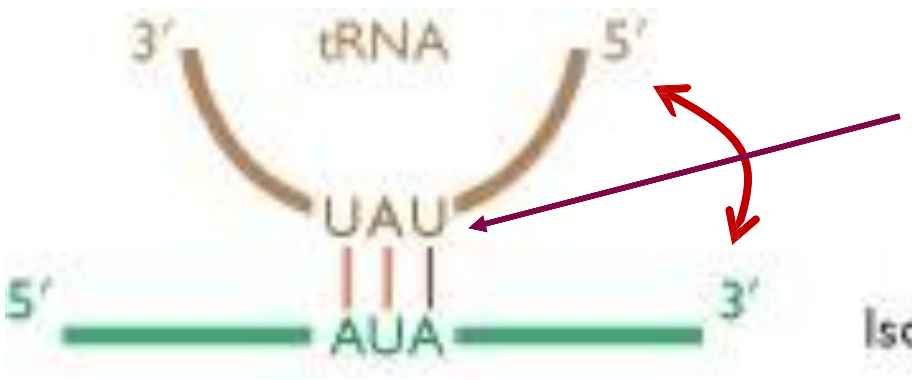
**open-reading frame:** A stretch of nucleotide sequence that encodes a polypeptide excluding the stop codons.

# ❑ Codon vs. anticodon

- tRNAs contain a three-nucleotide sequence known as "anticodon" that pairs in an anti-parallel manner with the "codon" of mRNA molecules.

(an anticodon is the part that recognizes the genetic codon)





We read tRNA anticodon from here (5' to 3')

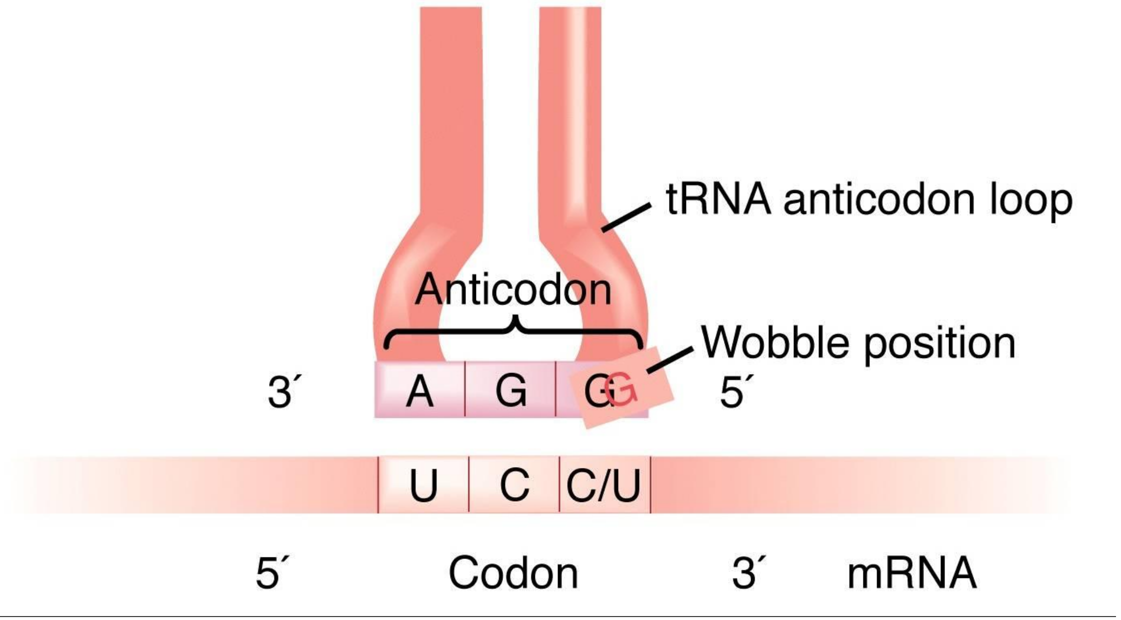
Be careful regarding this

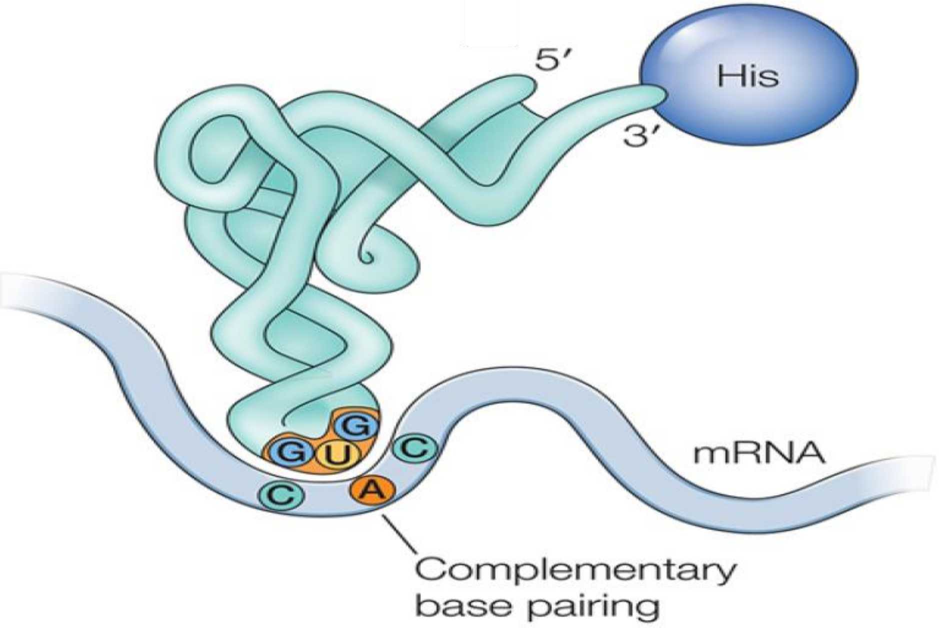
# ❑ Fidelity of translation (Translation's accuracy)

Accurate translation requires two steps:

First: accurate association of amino acid to tRNA

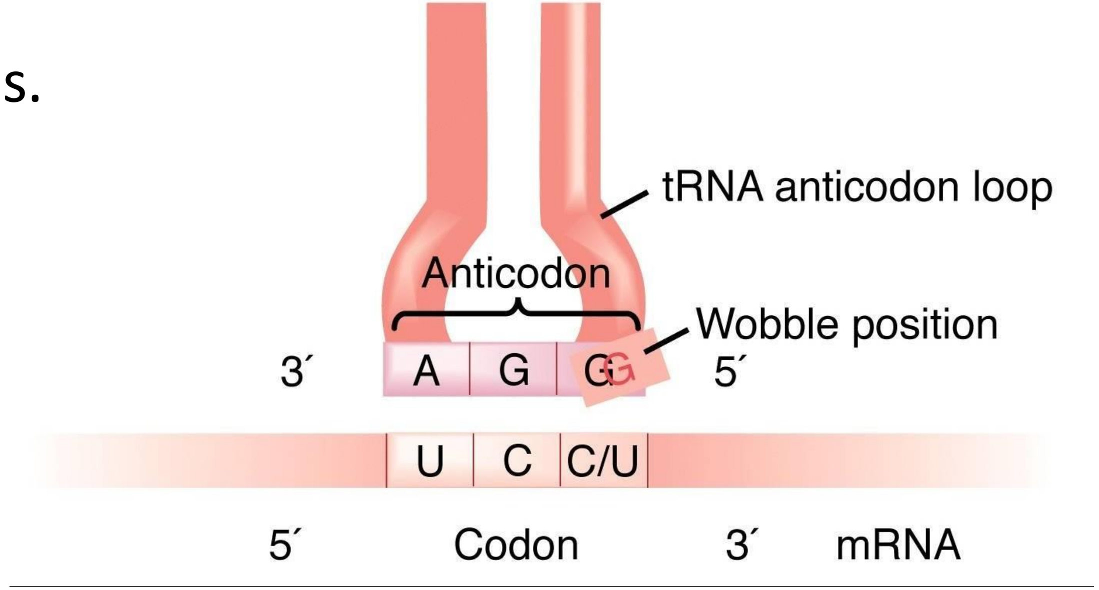
Second: a correct match between the tRNA 's anticodon and the mRNA's codon





# ❑ Wobble base pairing

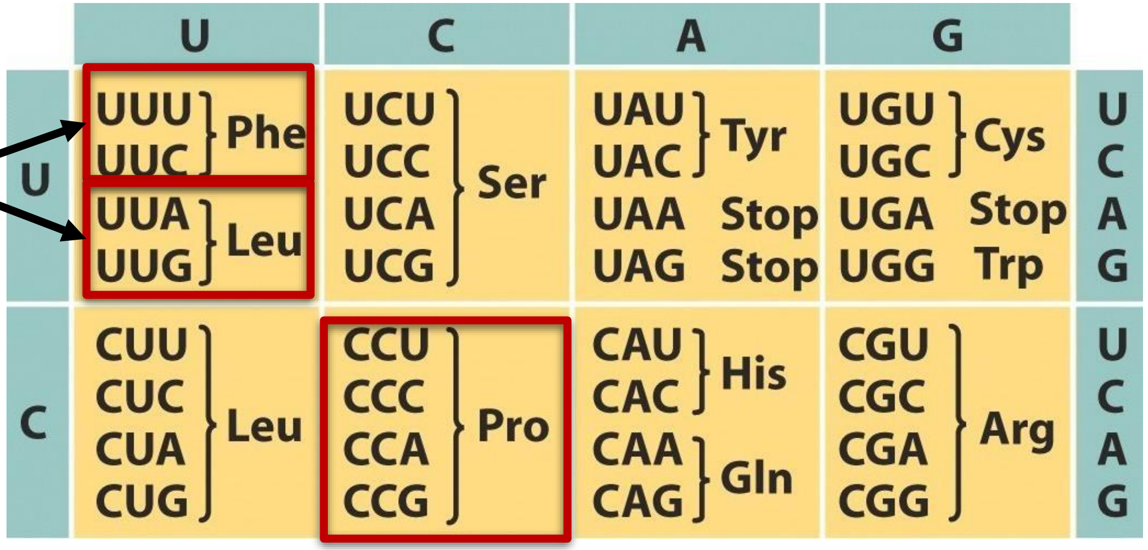
- There is flexible pairing at the third base of a codon to the anticodon allowing some tRNAs to bind to more than one codon.
- Even if a mutation happened in the third nucleotide of a codon, most probably the amino acid will be the same.
- It is called **wobble base pairing.**
- The bases that are common to several codons are usually the first and second bases, with more room for variation in the third base.
- The genetic codon is degenerate
- It acts as a buffer against deleterious mutations.



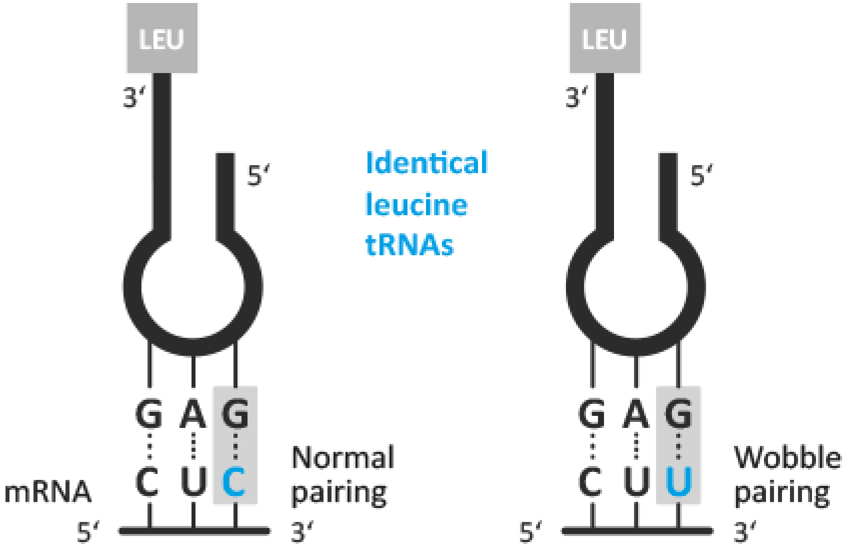
# ❑ Examples of wobble base pairing

- Relaxed base pairing results from the formation of G-U base pairs.

Both are hydrophobic amino acids



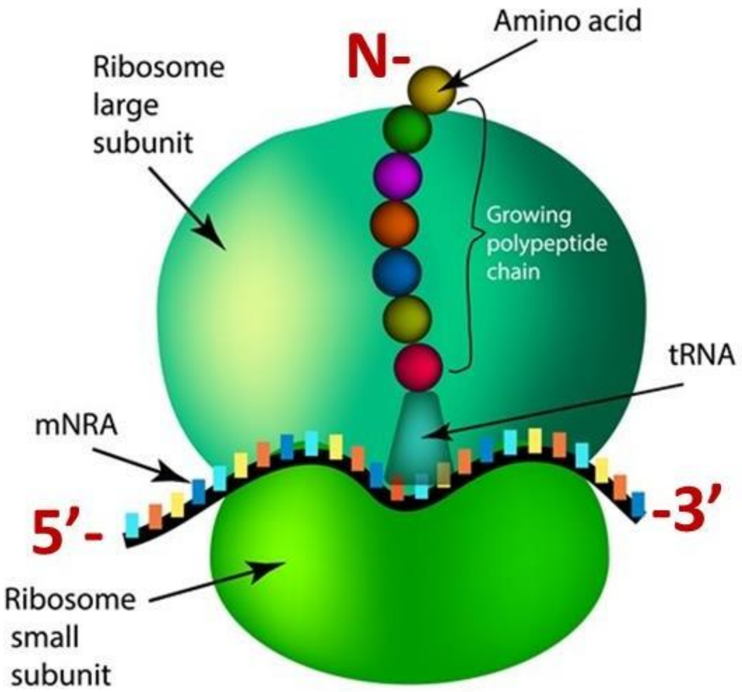
| | U | | C | | A | | G | | |
|---|---|---|---|---|---|---|---|---|---|
| U | UUU | Phe | UCU | Ser | UAU | Tyr | UGU | Cys | U |
| | UUC | | UCC | | UAC | | UGC | | C |
| | UUA | Leu | UCA | | UAA | Stop | UGA | Stop | A |
| | UUG | | UCG | | UAG | Stop | UGG | Trp | G |
| C | CUU | Leu | CCU | Pro | CAU | His | CGU | Arg | U |
| | CUC | | CCC | | CAC | | CGC | | C |
| | CUA | | CCA | | CAA | Gln | CGA | | A |
| | CUG | | CCG | | CAG | | CGG | | G |



If we have a mutation in the third nucleotide, the amino acid will change but most probably the type of amino acid will be the same (hydrophobic here) , so it gives some protection to the cell.

# ❑ Ribosomes

- Ribosomes are the sites of protein synthesis (they are composed of proteins and rRNAs)
- E. coli contains about 20,000 ribosomes (~25% of the dry weight of the cell).
- Rapidly growing mammalian cells contain about 10 million ribosomes.

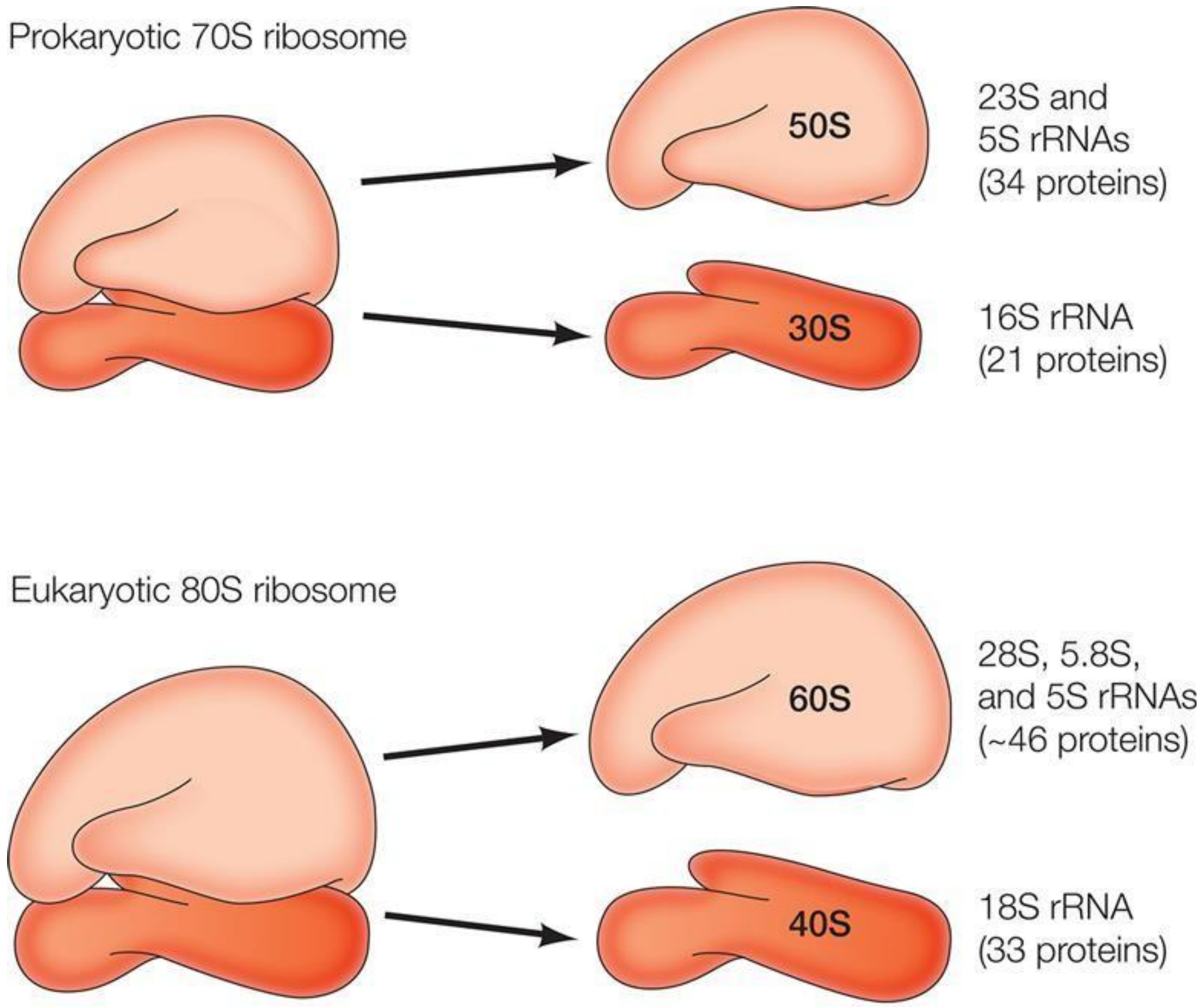


**The peptidyl transferase reaction of a peptide bond is catalyzed by the rRNA of the large ribosomal subunit.**

rRNA acts as an enzyme, while protein provide structural support.

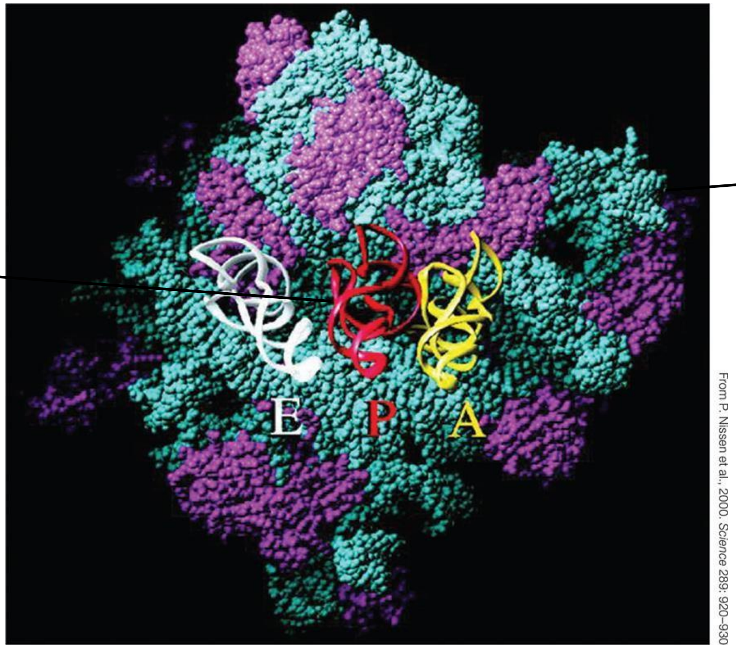
# ❑ Ribosome structure

- Prokaryotes and eukaryotes share a similar ribosome structure, consisting of large and small subunits.
- The weight and the composition of both ribosomes in prokaryotes and eukaryotes are almost the same.



# ❑ Functional and structural components of ribosomes

- Ribosomes facilitate specific coupling of tRNA anticodons with mRNA codons in protein synthesis.
- The RNA components are responsible for the catalytic function of the ribosome, and the protein components enhance the function of the rRNA molecules.

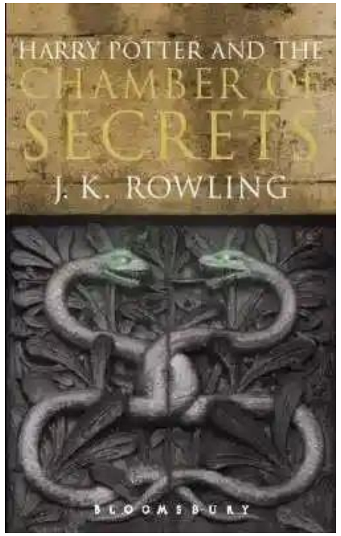


From P. Nissen et al., 2000. Science 289: 920–930

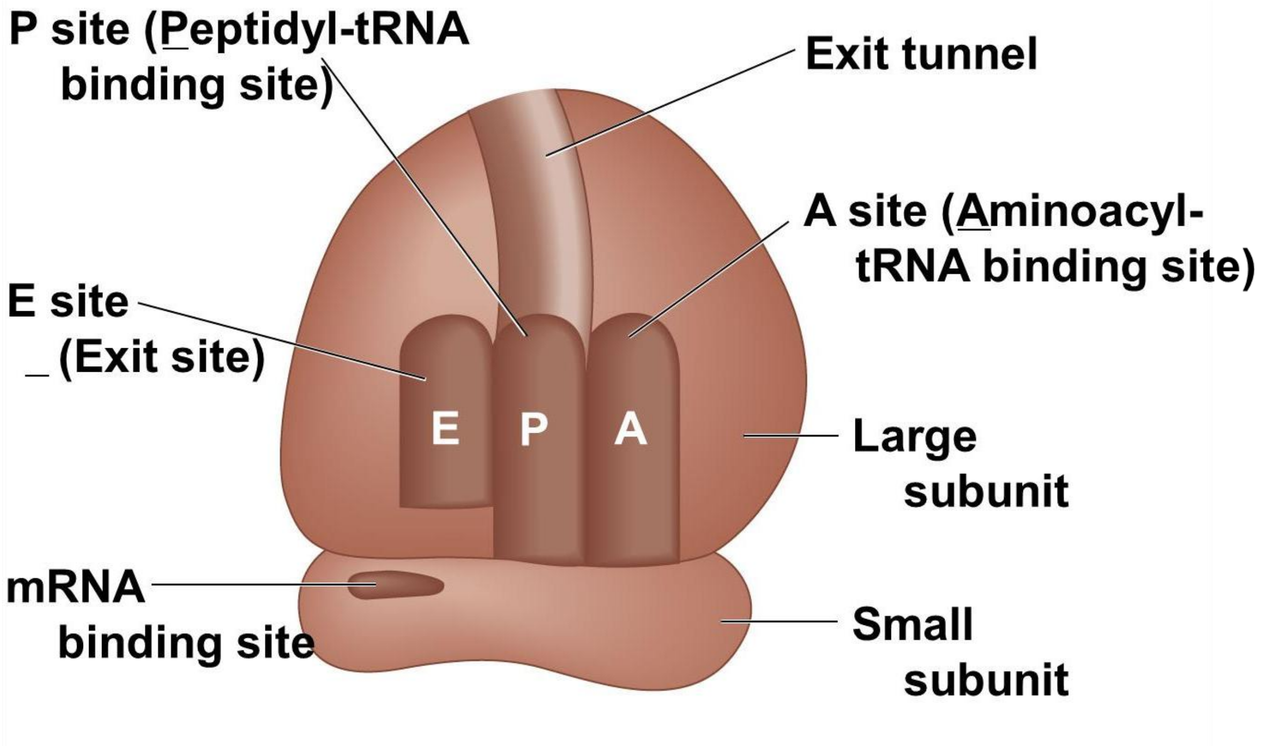
- ➢ rRNA (they are in the middle of the ribosome).
- ➢ Peptide synthesis take place around rRNA molecules.

- ➢ Proteins (they provide structural support and enhance the function of the rRNA molecules).

# ❑ The chambers of secret



- The large ribosomal subunit is composed of three chambers (E, P, & A chambers).



tRNA binding sites on a ribosome:

The **P site** holds the tRNA that carries the growing polypeptide chain

The **A site** holds the tRNA that carries the next amino acid to be added to the chain

The **E site** is the exit site, where discharged tRNAs leave the ribosome (when tRNA no longer carries an amino acid, it is referred to as discharged).

# رسالة من الفريق العلمي:

قال رسول الله ﷺ:

أَحَبُّ الكَلامِ إلى اللهِ أرْبَعٌ: سُبْحانَ اللهِ والْحَمْدُ لِلَّهِ ولا إلَهَ إلَّا اللَّهُ واللَّهُ أكْبَرُ، لا يَضُرُّكَ بأَيِّهِنَّ بَدَأْتَ

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