

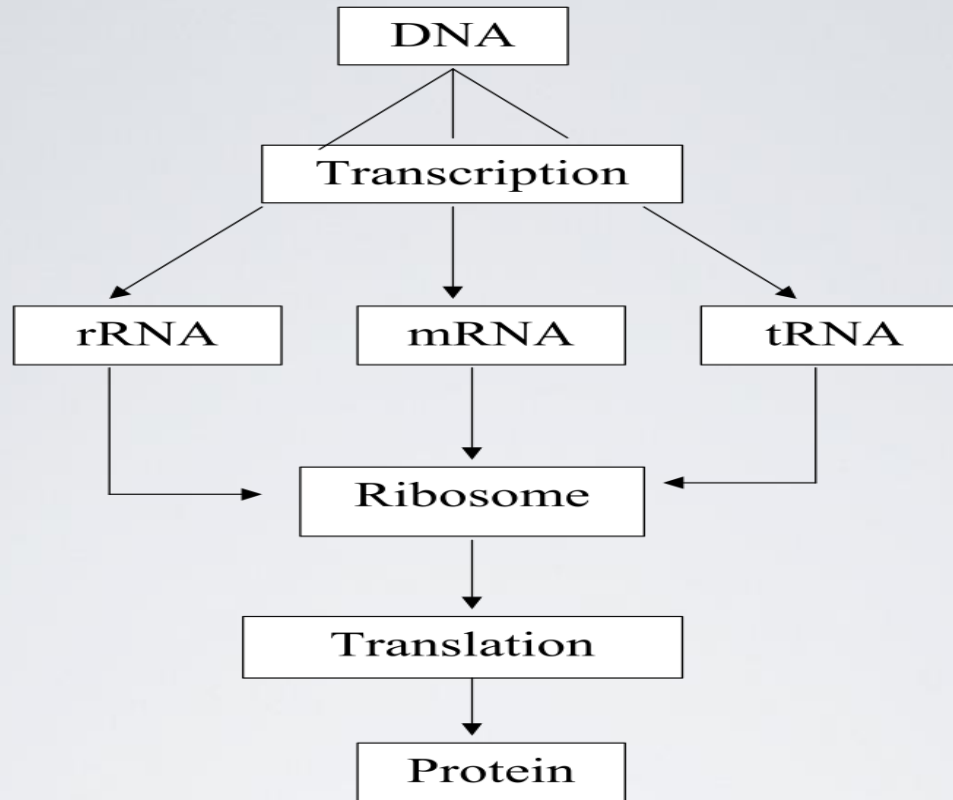


Umm AL Qura University

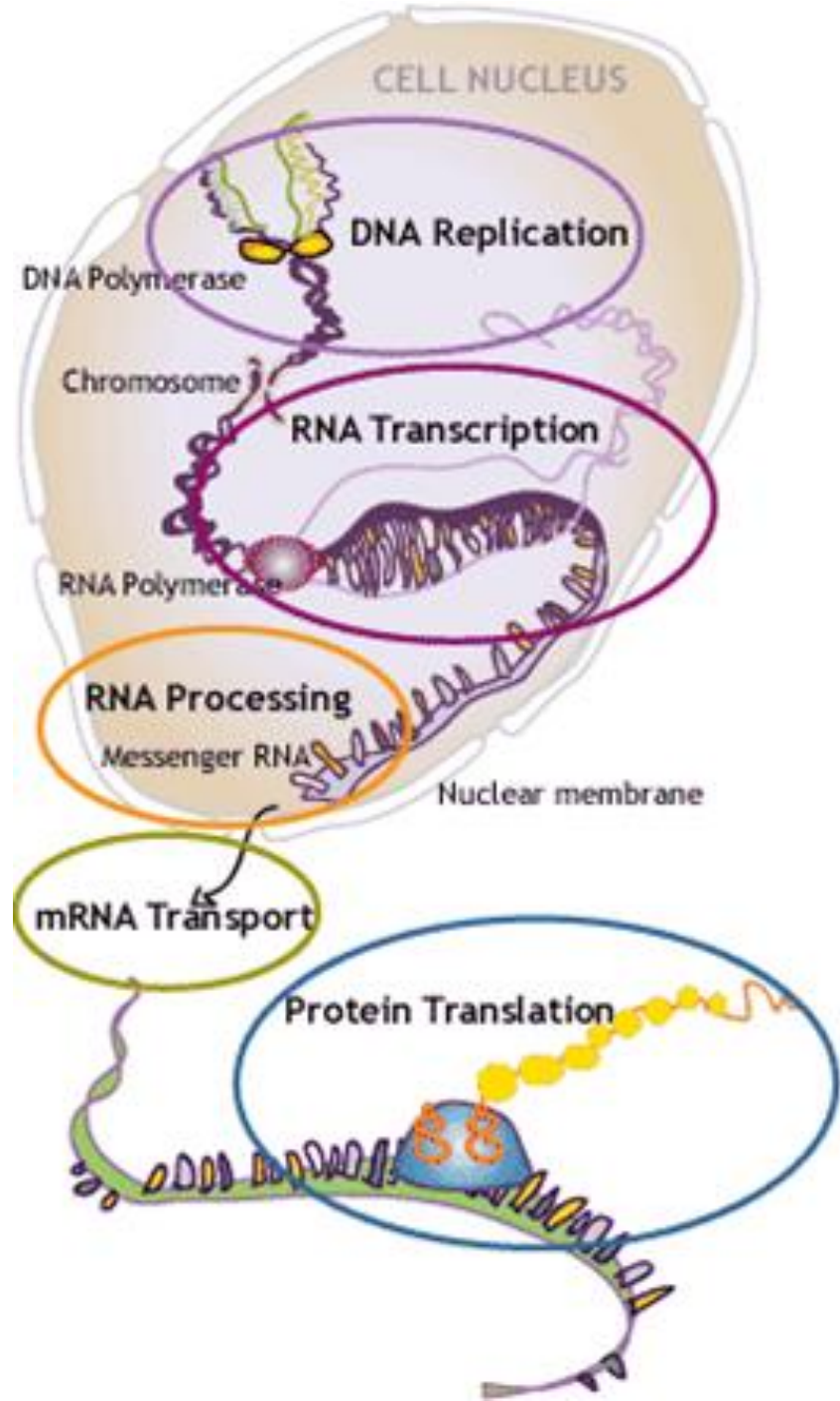
Translation

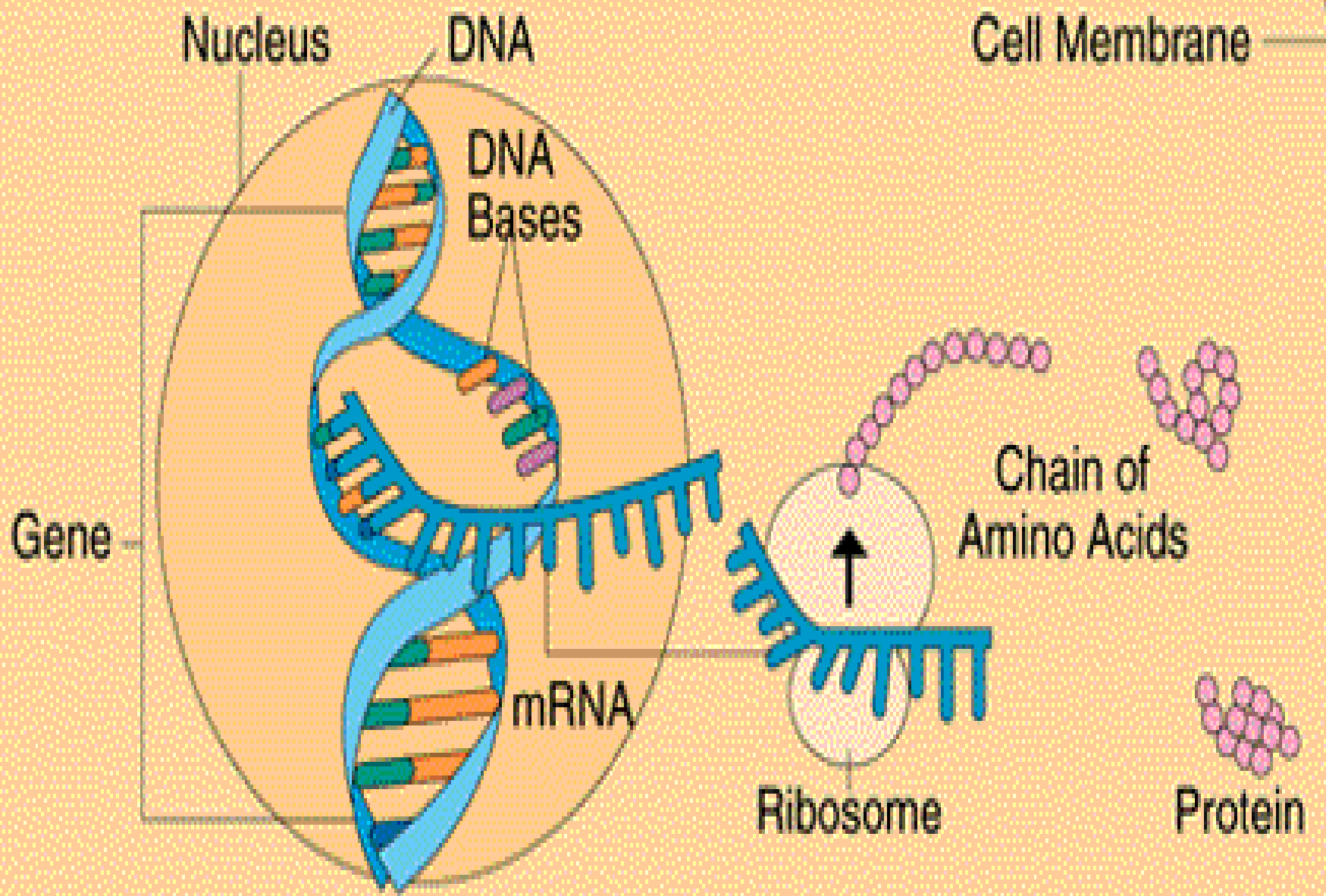
Dr Neda Bogari

The Central Dogma



- The process of the transfer of the genetic information
- From DNA to RNA to protein has been called the *central dogma*.
- Proteins can not be converted into RNA or DNA

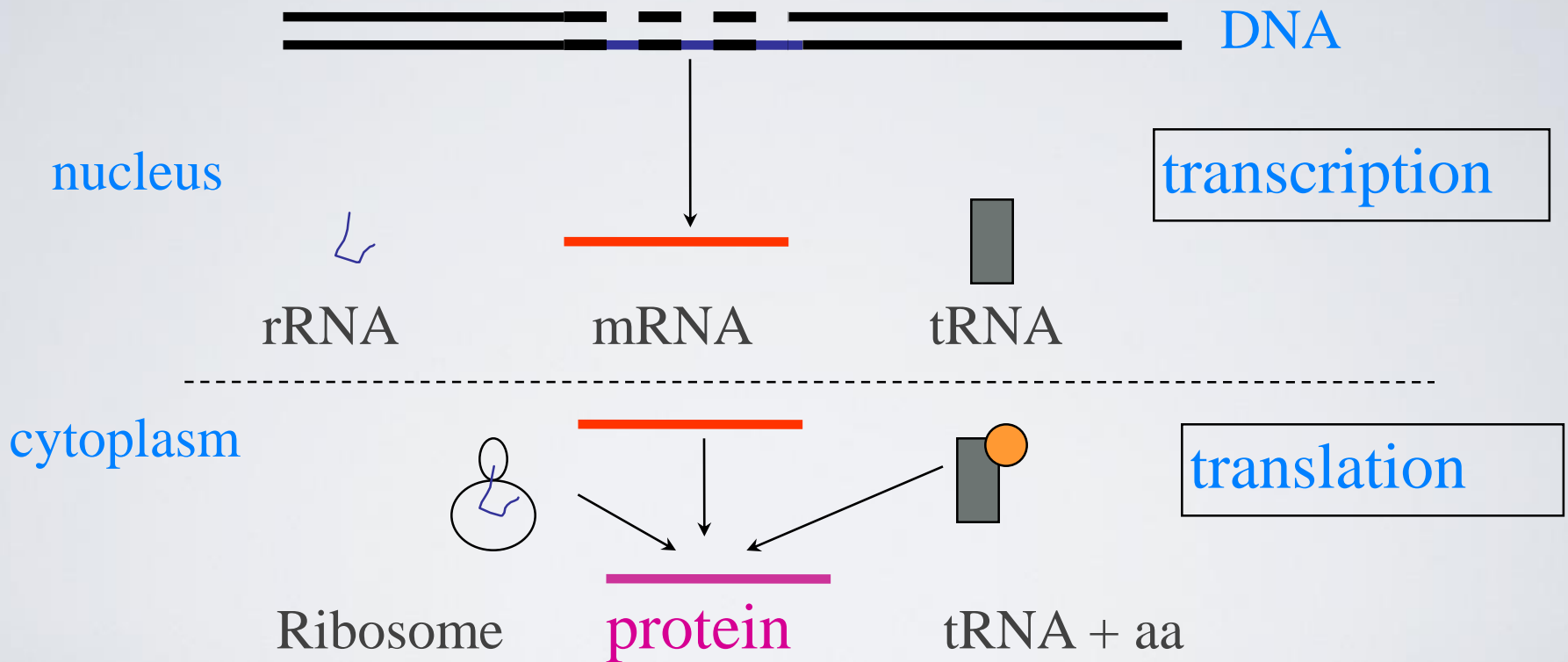




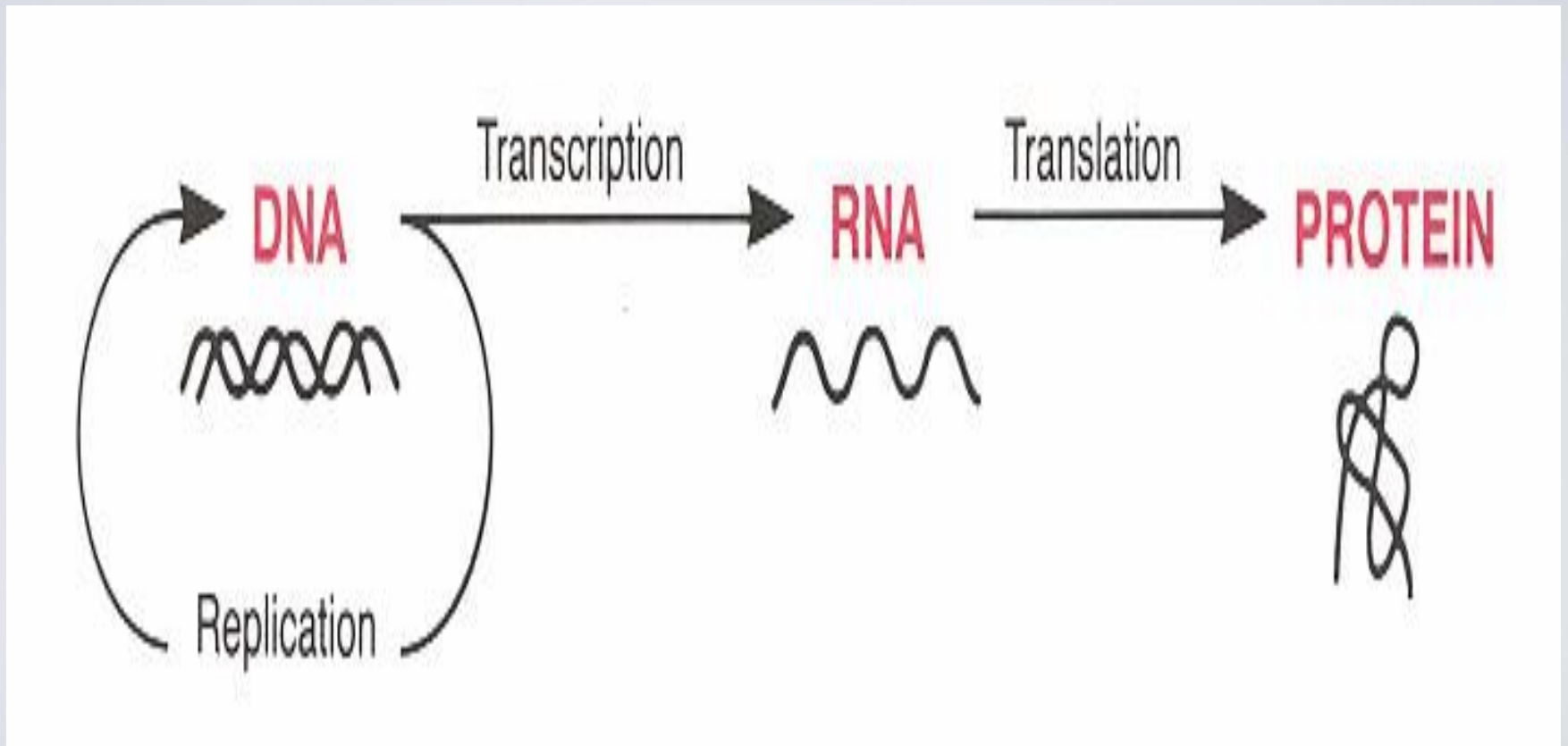
Central Dogma

- The concept that genetic information is only transmitted from **DNA** to **RNA** to **protein**.

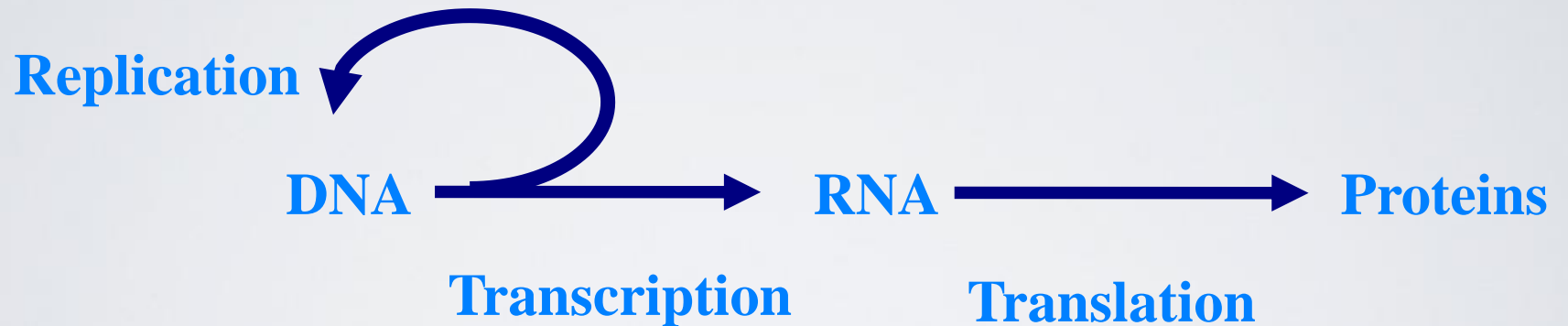
Central Dogma




The Central Dogma



The Central Dogma



Translation

- **Translation** is the transmission of the genetic information from **mRNA** to **protein**.
- mRNA is transported from the **nucleus**  **cytoplasm** where it attached with the **ribosomes** which are the site of **protein synthesis**.

Types of RNA

📖 There are three main type of RNA

📄 messenger RNA (**mRNA**)

📄 Ribosomal RNA(**rRNA**)

📄 Transfer RNA (**tRNA**)

📄 Other types of RNA

Translation

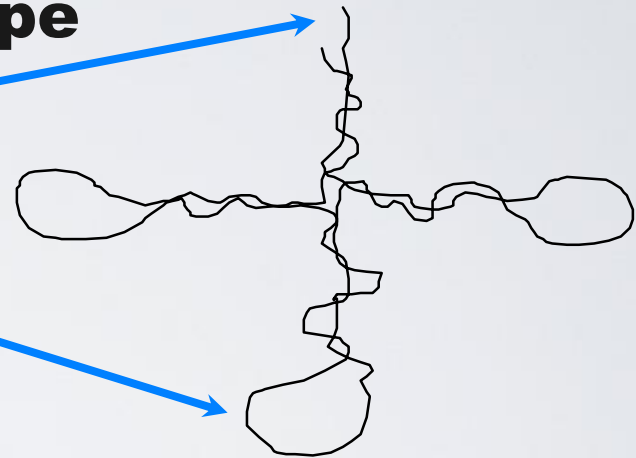
- The components needed for translation are mRNA, tRNA, ribosome, GTP, initiation factors, elongation factors, and release factors.

Transfer RNA

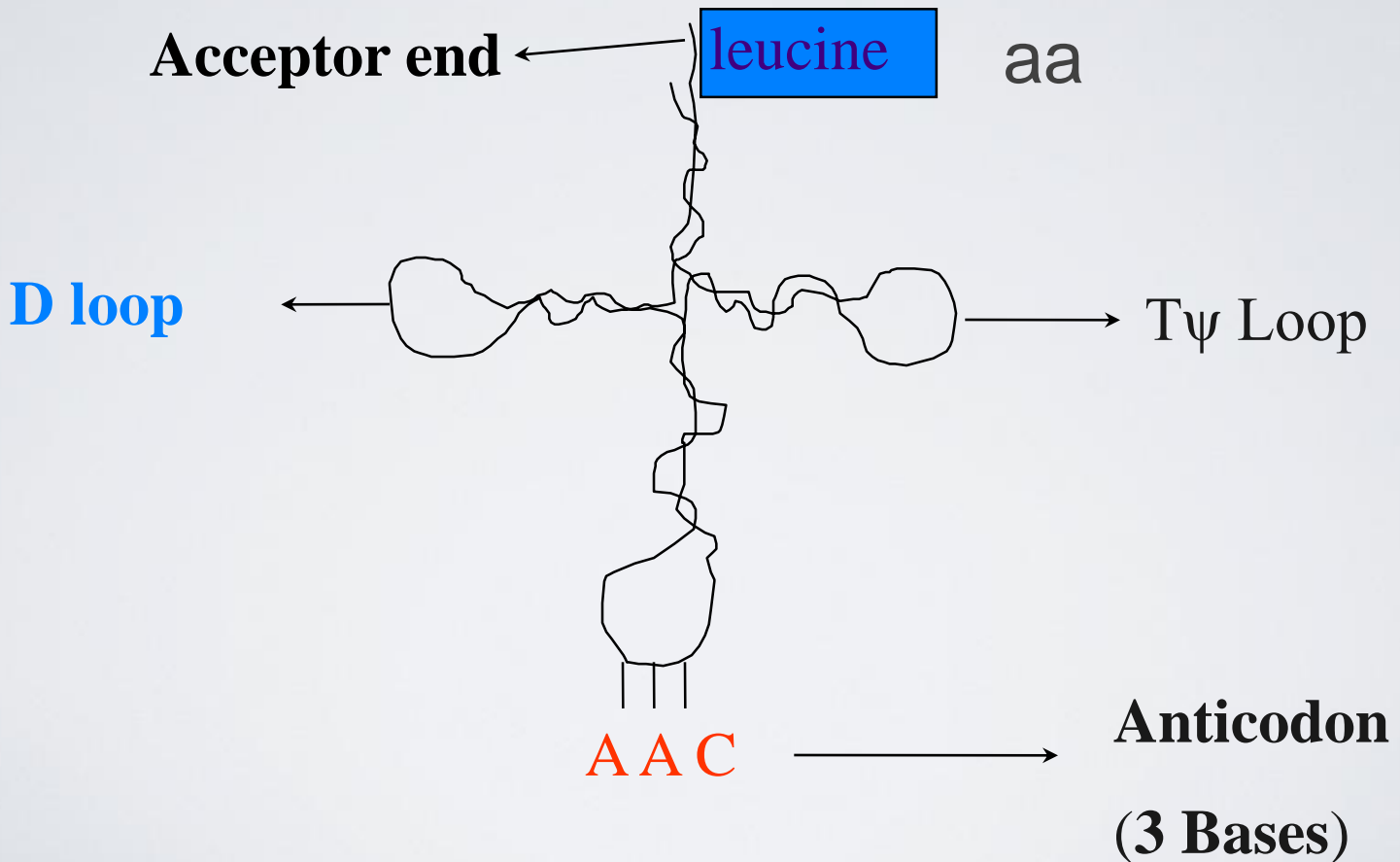
- In the **ribosomes** the mRNA forms the template for producing the specific sequence of **amino acids** of a particular **polypeptide**.
- In the cytoplasm there is **another form of RNA called transfer RNA** or tRNA.

t RNA

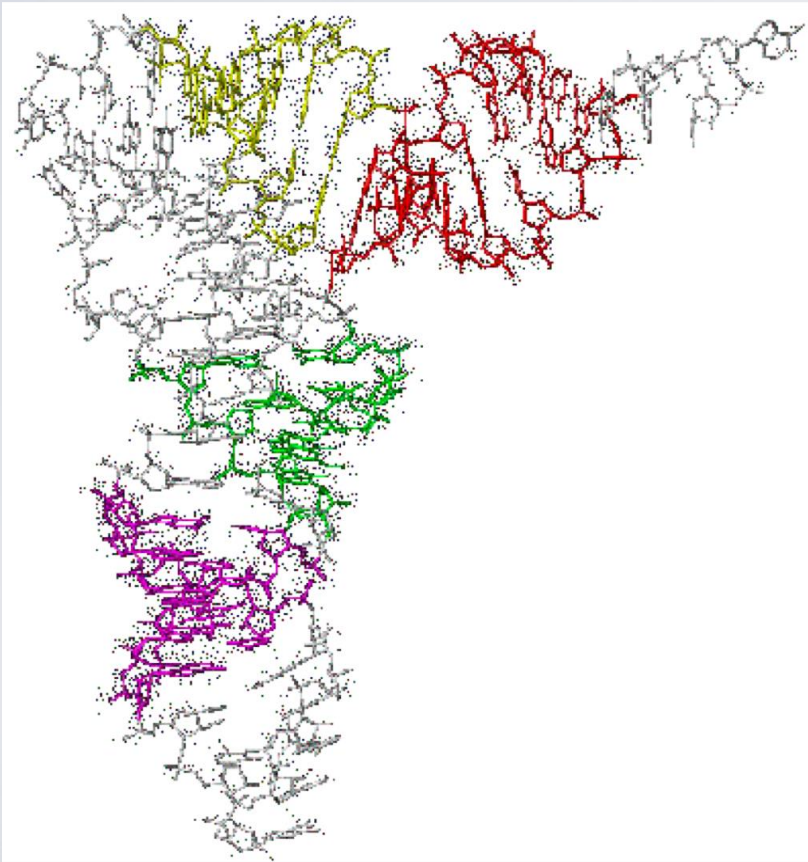
- **Small molecule**, 73 –93 nucleotides, **lower MW than** rRNA
- Single stranded: **clover leaf shape**
 - binds **aa** at one end
 - binds **mRNA** at the other end
- Different **tRNAs**
- Function - **adaptors to correctly order aa (amino Acid) on mRNA for protein synthesis.**



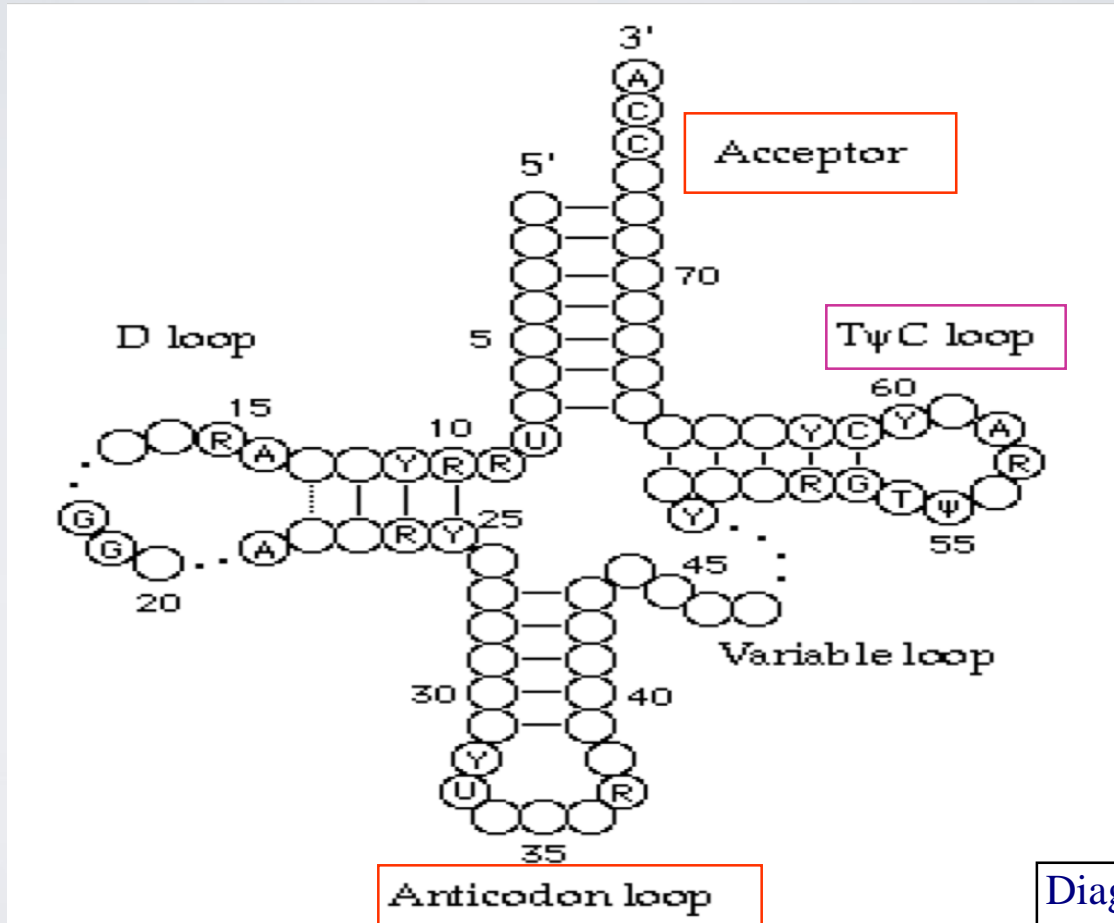
Charged tRNA



t RNA

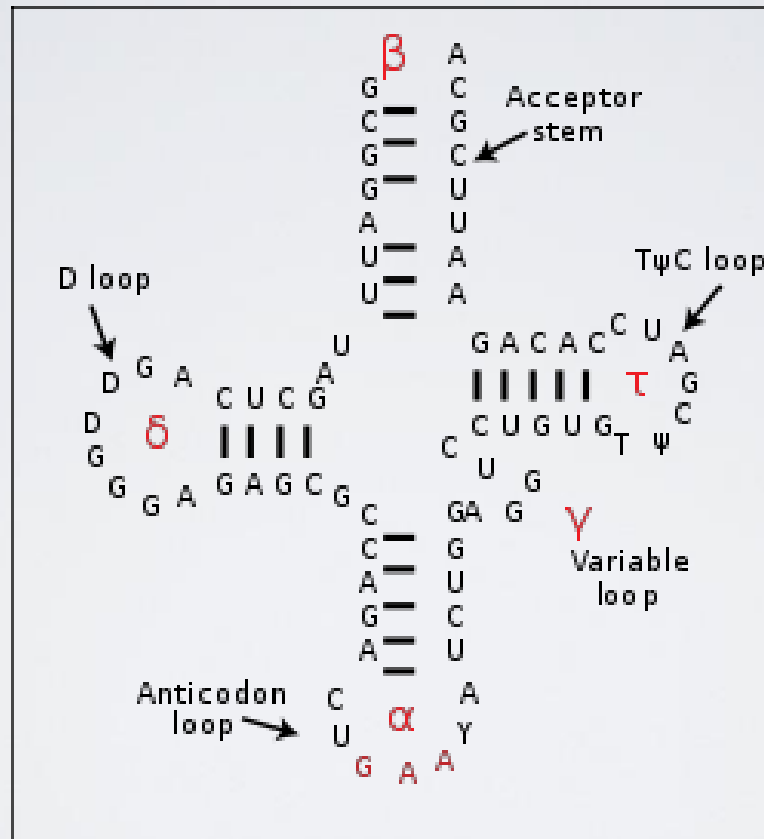


t RNA

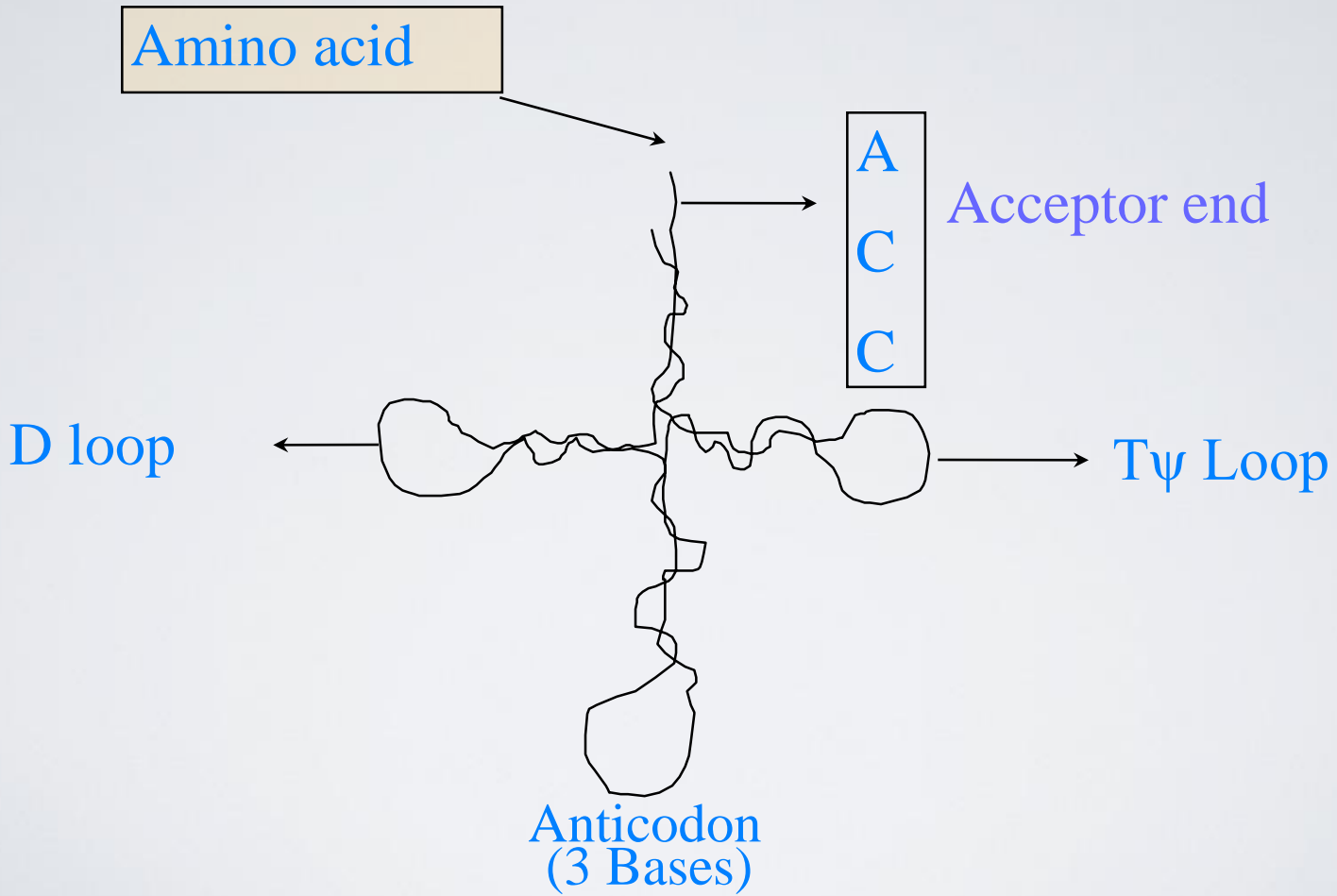


Diag.H Brezski

t RNA

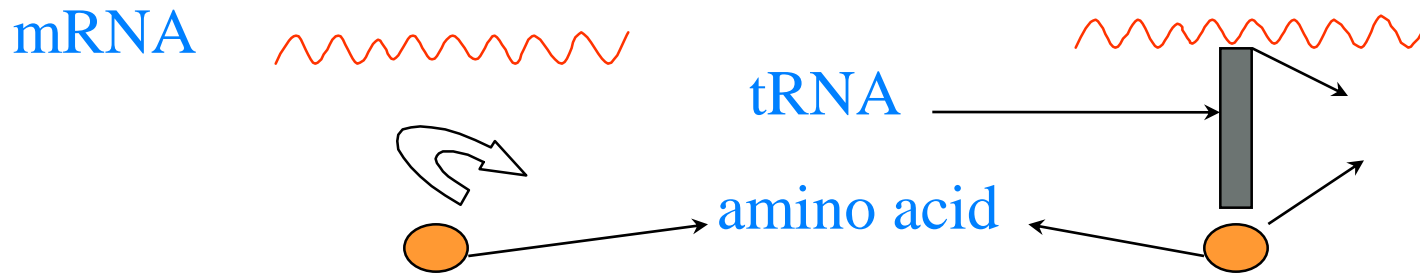


t RNA



Anticodons

Sites which base pair with mRNA

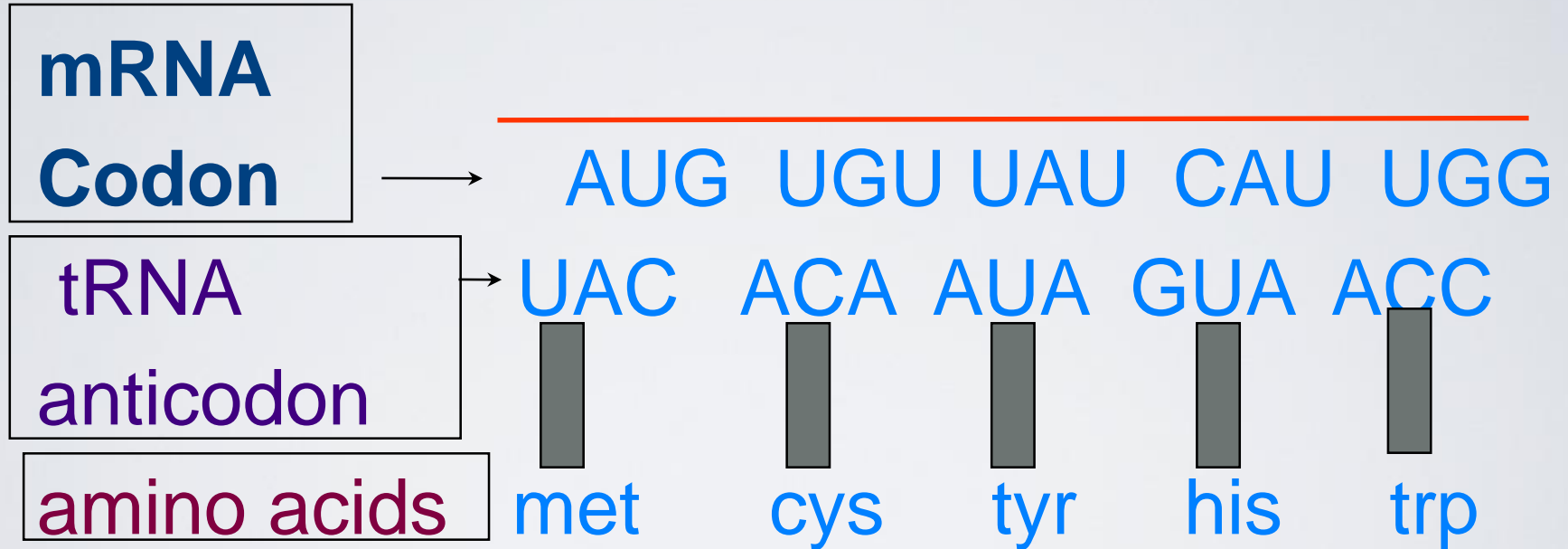


1.No reaction

2.Binding

- tRNA is an adaptor molecule.
- No direct pairing between mRNA and amino acids

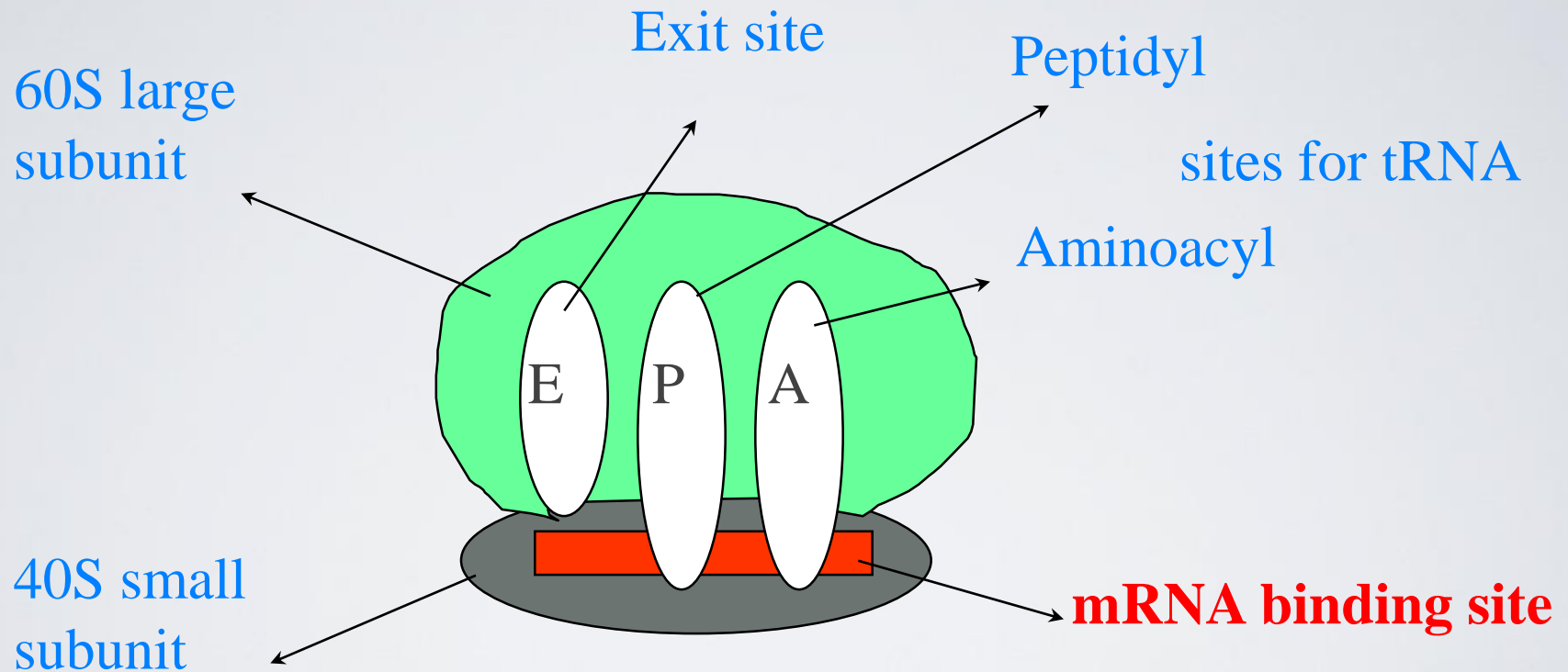
Base pairing



Function of Ribosomes

- **Translation of information** encoded in the mRNA
- **holds mRNA and tRNA together**
- Forms **peptide bond** between **amino acids**
- **Ensures** accuracy of **protein synthesis**

Ribosome Structure



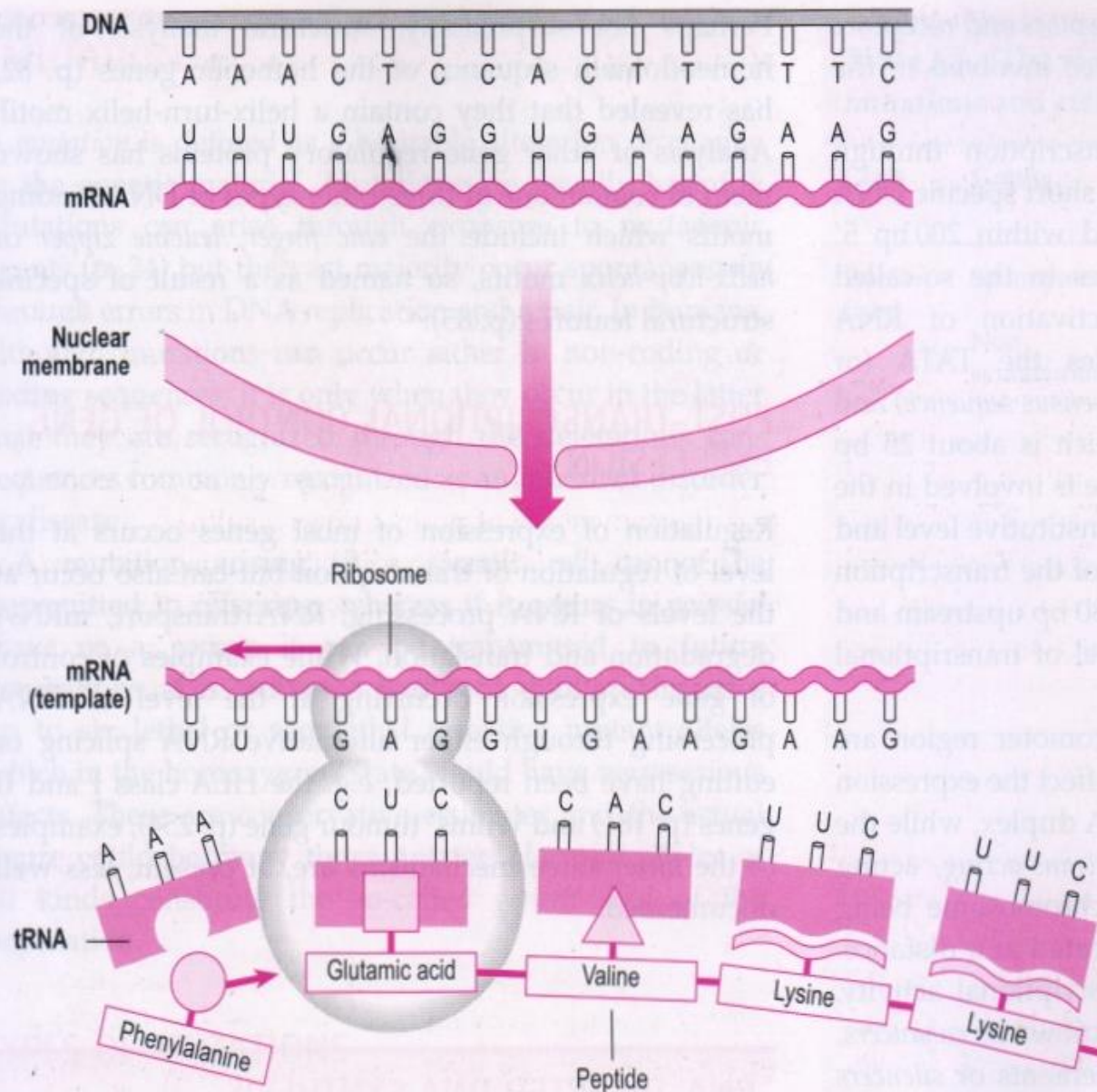


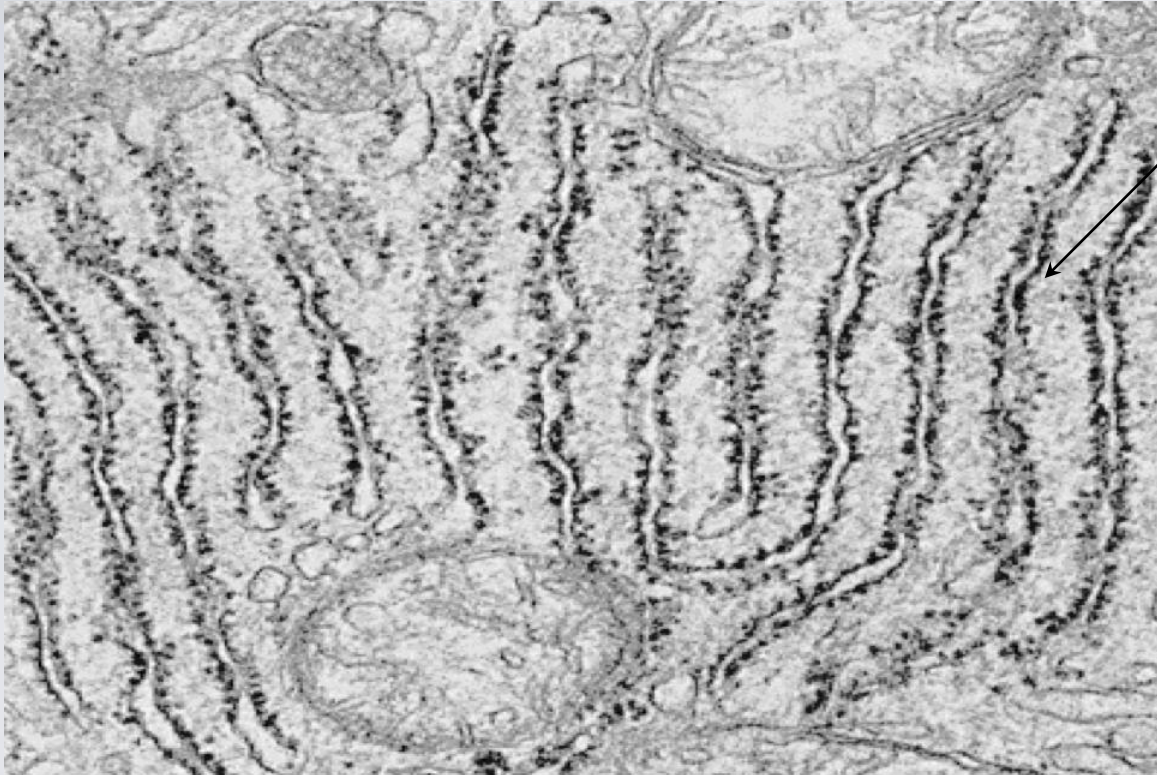
Fig. 2.8

Representation of the way in which genetic information is translated into protein.

rRNA

- **Large molecule, double and single helix**
- **Constituent of ribosomes in association with 55 different proteins**
- **Function : translation - correct spatial orientation of aa**

r RNA



ribosomes

The ribosome consists of two unequal subunits

- Small Subunits S
- Large Subunit L

- Electron micrograph of Endoplasmic Reticulum

- **r RNA**

- joins with various proteins to form ribosome, vital in translation

- **mRNA**

- sequence of bases which codes for the order of amino acids in polypeptide

Genetic Code

Groups of nucleic acid bases (codons)
which code for the 20 amino acids

CRACKING THE CODE


1. How many bases make up a codon?
2. Do codons overlap?
3. Are there gaps in the code?
4. What are the code words?

- DNA is composed of four different nitrogenous bases, then a single base cannot specify one amino acid.
- If two bases were to specify one amino acid, there would only be 4^2 or 16 possible combinations.
- If three bases specified one amino acid then there would be 4^3 or 64.
- This is more than enough to account for all the 20 known amino acids and is known as the genetic code.

Genetic Code

- Groups of nucleic acid bases which code for the 20 amino acids
 - Unit of information is **the codon** - a sequence of 3 bases on mRNA
 - 64 possible codons
 - each codon is assigned to one amino acid or a punctuation signal

Genetic Code cont.

- Triplet code
 - Codon: trinucleotide in mRNA codes for a specific amino acid or a stop-start signal
- no overlap
 - read sequentially in 5' - 3' direction
- 5' - AGUCAGUCAAGUCAGUCAGUC - 3'


The diagram shows the mRNA sequence 5' - AGUCAGUCAAGUCAGUCAGUC - 3'. Four brackets are drawn under the sequence, grouping the nucleotides into four non-overlapping triplets: AGU, CAG, UCA, and AAG. Below the sequence, a thick black arrow points to the right, labeled 'direction of reading'.

direction of reading

- Termination of translation of the mRNA is signaled by the presence of one of the three stop or termination codons.
- One codon just code for one amino acid
ex. ATG always just encodes methionine amino acid.
- CUU , CUC, CUA and CUG are different codons but code for the same amino acid , which is Leucine amino acid.
This phenomenon called *Degeneracy* of genetic code and usually these codons just differ in nucleotide #3 (number 3).
Same case for most amino acids not just for leucine.

Second Position

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

Triplet Codons:

- However, some amino acids are coded for more than one triplet
- Termination of translation of mRNA is signalled by the presence of one of the three STOP or termination

Post-translation modification

- Protein folding
- Peptide cleavage
- Chemical modification in ER lumen or the Golgi apparatus
- Intein splicing

VIRTUAL RIBOSOME

Translation table: Standard SGC0

▷Seq1

Reading frame: 1

```

M V L S A A D K G N V K A A W G K V G G H A A E Y G A E A L
5' ATGGTGTCTGTCTGCCGCCGACAAGGGCAATGTCAAGGCCGCCTGGGGCAAGGTTGGCGGCCACGCTGCAGAGTATGGCGCAGAGGCCCTG 90
>>>...))).....)))

E R M F L S F P T T K T Y F P H F D L S H G S A Q V K G H G
5' GAGAGGATGTTCCCTGAGCTTCCCCACCACCAAGACCTACTTCCCCCACTTCGACCTGAGCCACGGCTCCGCGCAGGTCAAGGGCCACGGC 180
.....>>>...))).....)))

A K V A A A L T K A V E H L D D L P G A L S E L S D L H A H
5' GCGAAGGTGGCCGCCGCGCTGACCAAAGCGGTGGAACACCTGGACGACCTGCCCGGTGCCCTGTCTGAACTGAGTGACCTGCACGCTCAC 270
.....))).....))).....))).....))).....))).....)))

K L R V D P V N F K L L S H S L L V T L A S H L P S D F T P
5' AAGCTGCGTGTGGACCCGGTCAACTTCAAGCTTCTGAGCCACTCCCTGCTGGTGACCCTGGCCTCCCACCTCCCAGTGATTTACACCCC 360
...))).....))).....))))).....))).....)))

A V H A S L D K F L A N V S T V L T S K Y R *
5' GCGGTCCACGCCTCCCTGGACAAGTCTTGGCCAACGTGAGCACCGTGCTGACCTCCAAATACCGTTAA 429
.....))).....))).....))))).....)***
```

Annotation key:

- ▷>>> : START codon (strict)
-))) : START codon (alternative)
- *** : STOP