

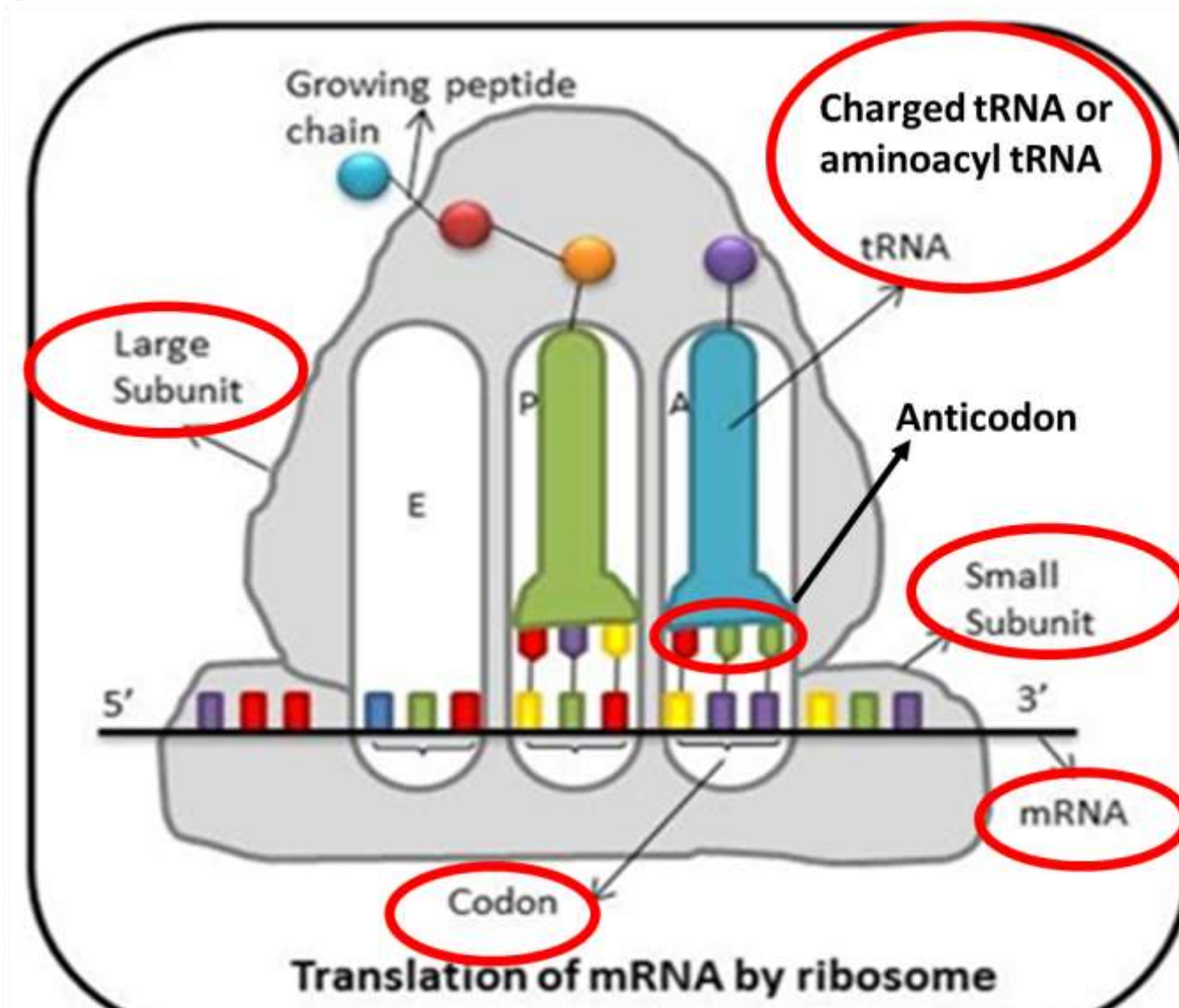
Unit III....Flow of information: from DNA to proteins

Contents (discussed) in the topic	Slide No.
1) What is central dogma	3
2) A cell model showing the flow of information from DNA to proteins	4
3) What is transcription and enzymes that carry out transcription?	5
4) Protein coding gene structure at DNA level and its components	7-8
5) Post-transcriptional processing of pre-mRNA to form functional mRNA for protein synthesis	9-11
6) Mature mRNA and genetic code table, how it is used.	12-14
7) What is translation	16
8) Components of translation process and Basic steps in translation process	17
9) Concept of codon-anticodon interaction and Wobble phenomenon during codon-anticodon interaction	18-19

Course code: SC301 (Biology)

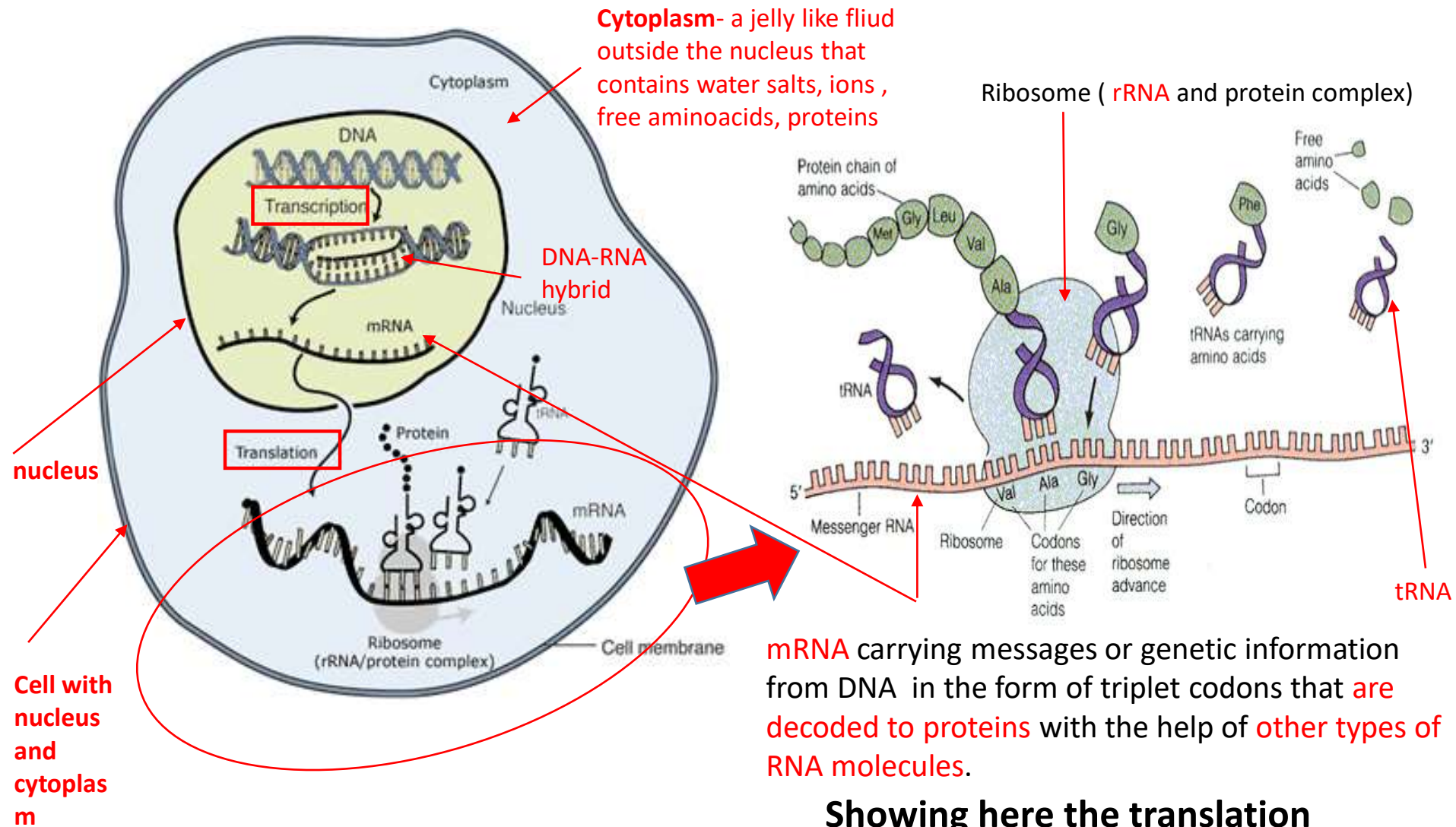
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As a whole rRNAs, tRNA and mRNA in protein synthesis process.....Translation



Using this figure, our main focus will be to study about mRNA features (exons-introns), post-transcriptional processing, genetic code and how they are read, Codon- anticodon interaction and wobbling

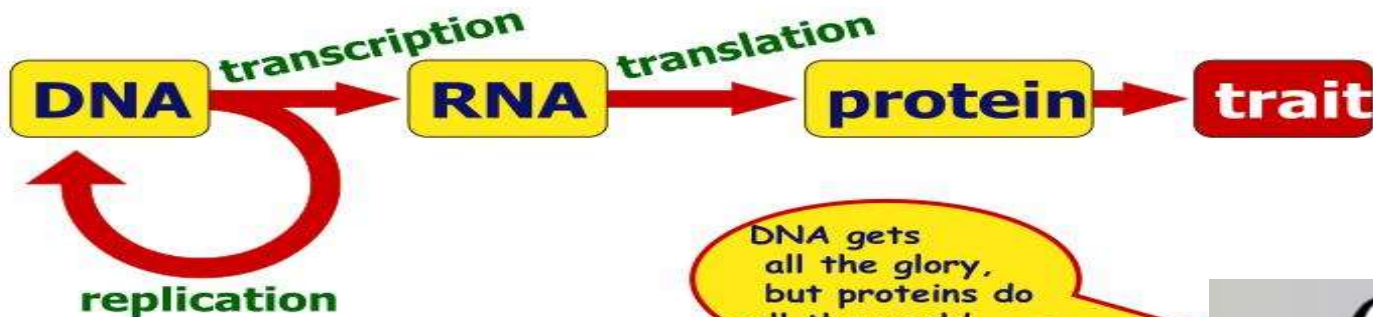
Overview of cell model showing flow of information



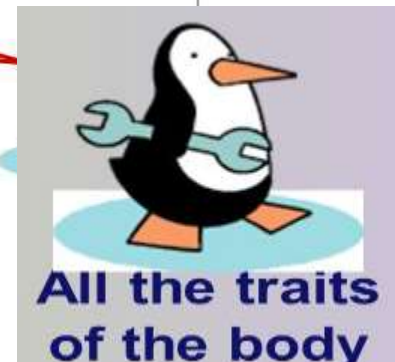
Flow of information: from DNA to proteins

The “Central Dogma”

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



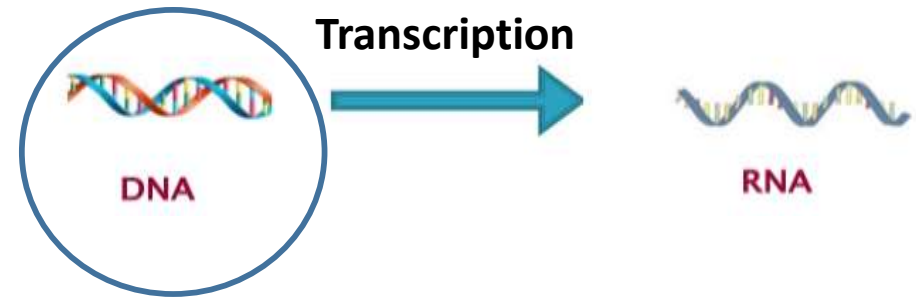
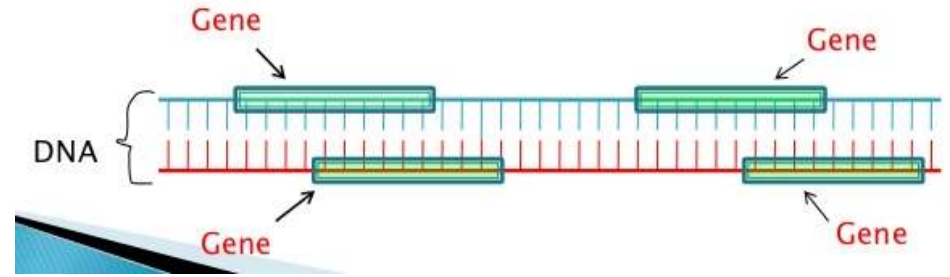
DNA gets
all the glory,
but proteins do
all the work!



TRANSCRIPTION (mRNA, rRNA and tRNA)

Transcription is the cellular process in which RNA (mRNA, rRNA, tRNA) is synthesized using DNA as a template known as transcription.

1. Transcription of protein-coding genes, and may present on any strand of DNA.
2. Transcription of rRNA genes and tRNA genes which do not code for proteins.



three enzymes in Transcription process

1. RNA Polymerase II- This is an enzyme that involves transcription of **mRNA**

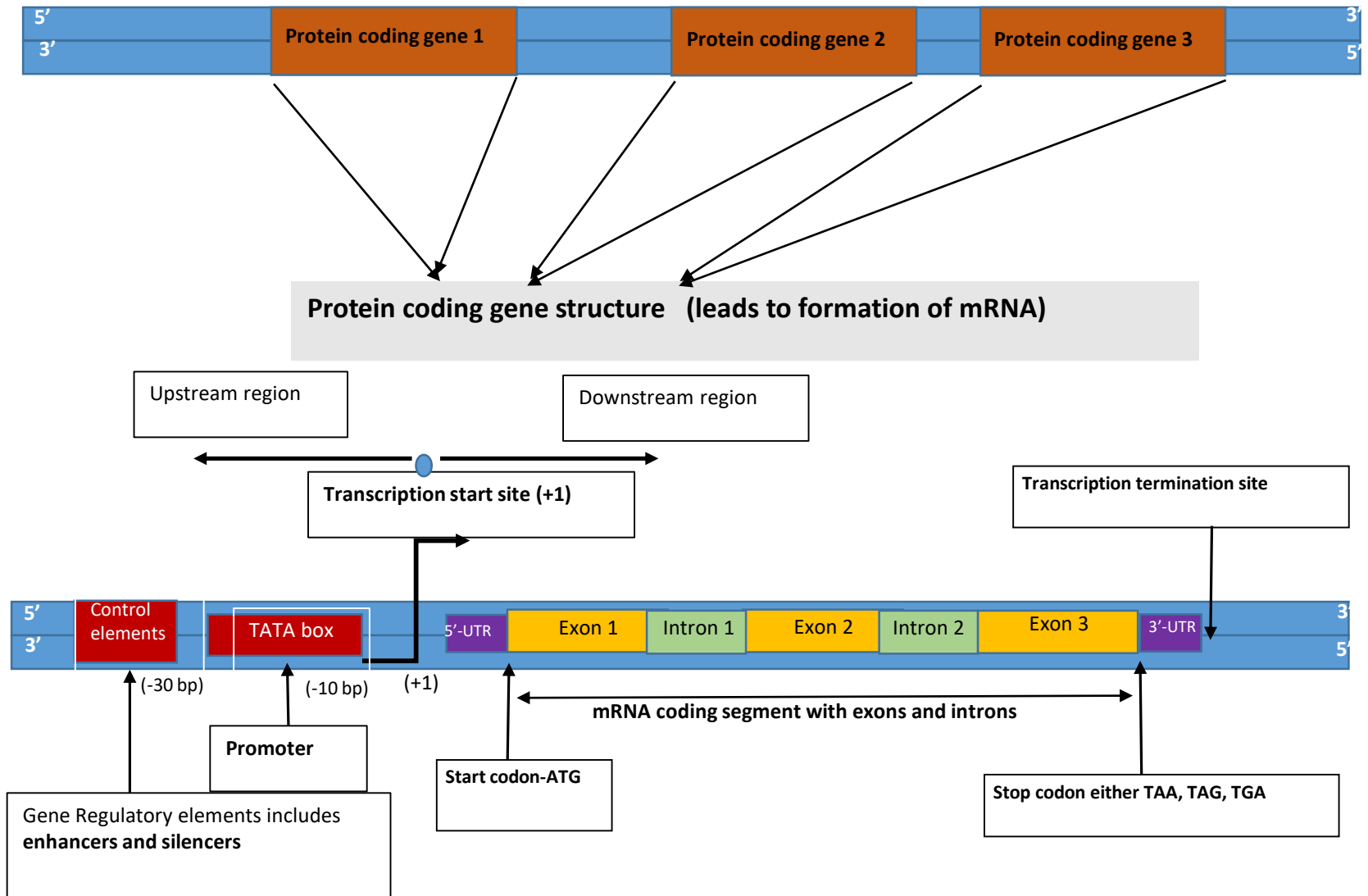
2. RNA Polymerase III- This is an enzyme that involves transcription of **tRNA and 5s rRNA**

3. RNA Polymerase I- This enzyme involves transcription of **28s rRNA, 18s rRNA and 5.8s rRNA**.

mRNA is a transcript of protein coding genes.

How protein coding genes are arranged in DNA ?

Protein coding gene structure at DNA level



BASIC COMPONENTS OF PROTEIN CODING GENE

1. Promoter
2. ORFs-Open reading frames
3. Exons
4. Introns
5. 5'Untranslated region (5'UTR)-**leader sequence**
6. 3'-Untranslated region (3'UTR)-**trailer sequence**
7. Control Elements

1) Promoter (TATA box): The promoter region controls when and in what tissue a gene is expressed. RNA polymerases recognizes the specific nucleotide sequences of promoter region for binding and initiating transcription process.

2) Open Reading Frames (ORFS). An ORF is a continuous stretch of codons that begins with a start codon (usually AUG) and ends at a stop codon (usually UAA, UAG or UGA).

3) Exons: An exon is a coding region of a gene that contains the information required to encode a protein.

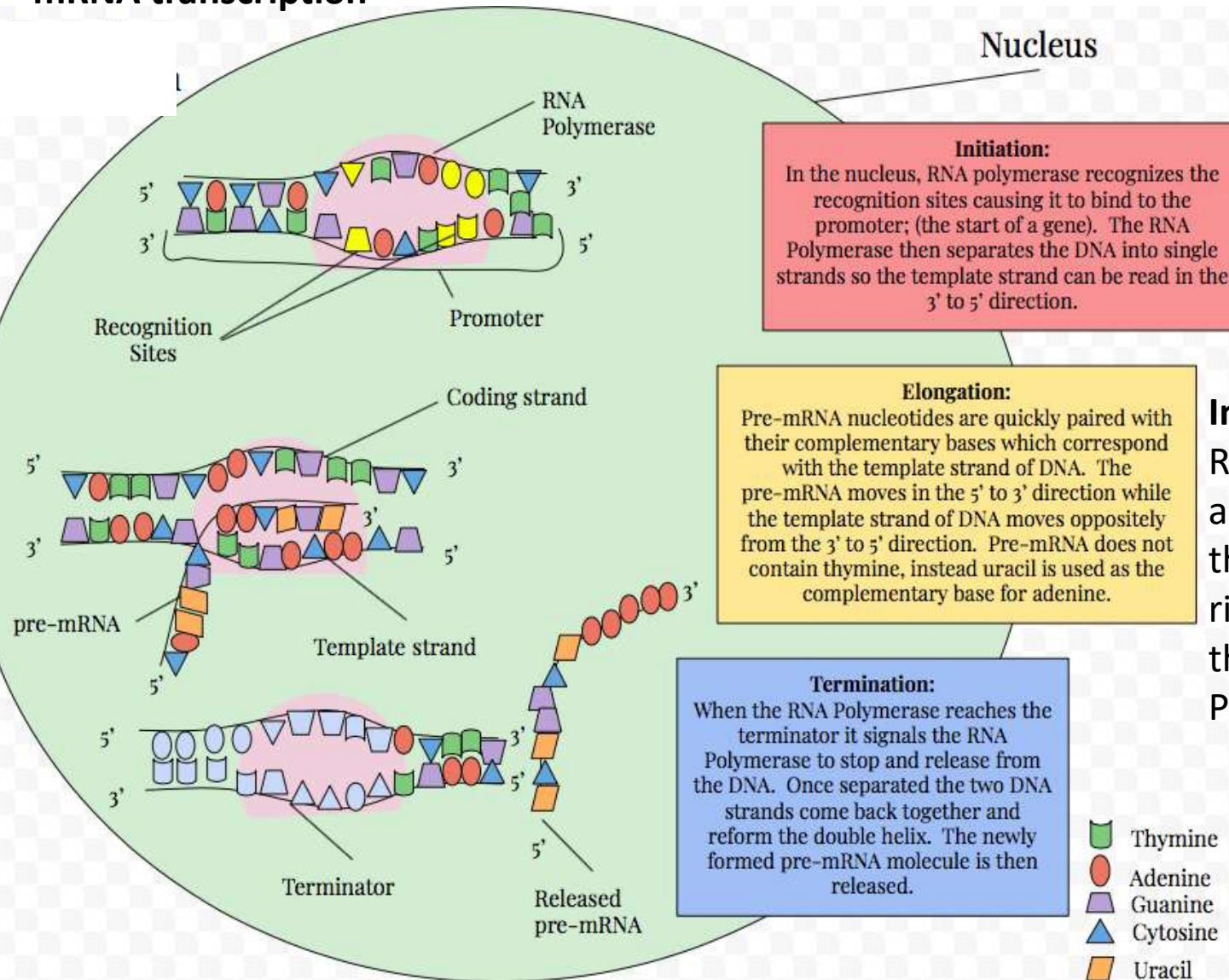
4) Introns: Introns are noncoding sections of an RNA transcript, or the DNA encoding it, that are spliced out before the RNA molecule is translated into a protein. Introns sequences do not code for amino acids

5) 5'- UTR is [upstream](#) from the coding sequence. Within the 5' UTR is a sequence that is recognized by the ribosome which allows the ribosome to bind and initiate translation.

6) 3'- UTR is found immediately following the translation stop codon. The 3' UTR plays a critical role in translation termination as well as post transcriptional modification.

Transcription process has three phases

mRNA transcription



Three phases in transcription

1. Initiation
2. Elongation
3. Termination

In elongation phase, Ribonucleotides are added to 3'-OH of the previous ribonucleotide by the activity of RNA Polymerase II.

Posttranscriptional processing of mRNA

1. Eukaryotic mRNA after transcription undergoes processing. This processing is called **posttranscriptional processing** before they can be translated. The unprocessed mRNA is called *pre-mRNA*.

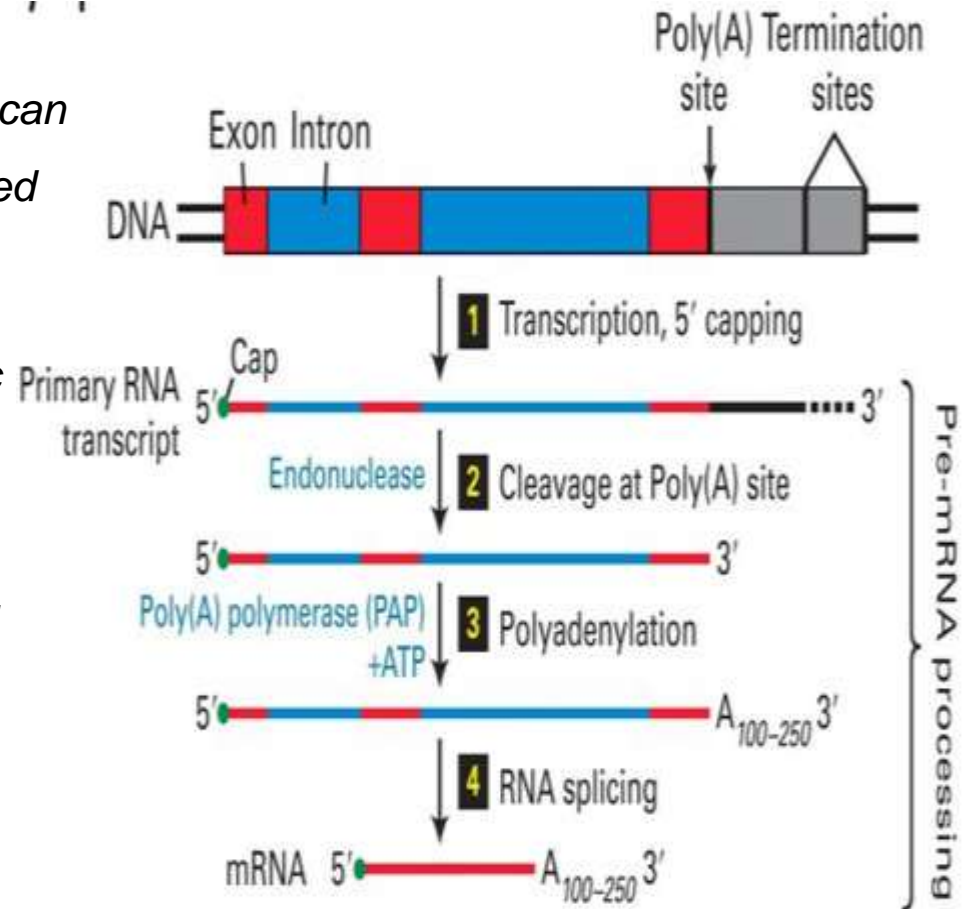
2. Three basic steps involved in eukaryotic mRNA processing:

a) **5' capping**

b) **Polyadenylation** – addition of poly A-tail

c) **mRNA splicing** -Joining of exons by removing introns. This is called **mRNA splicing**.

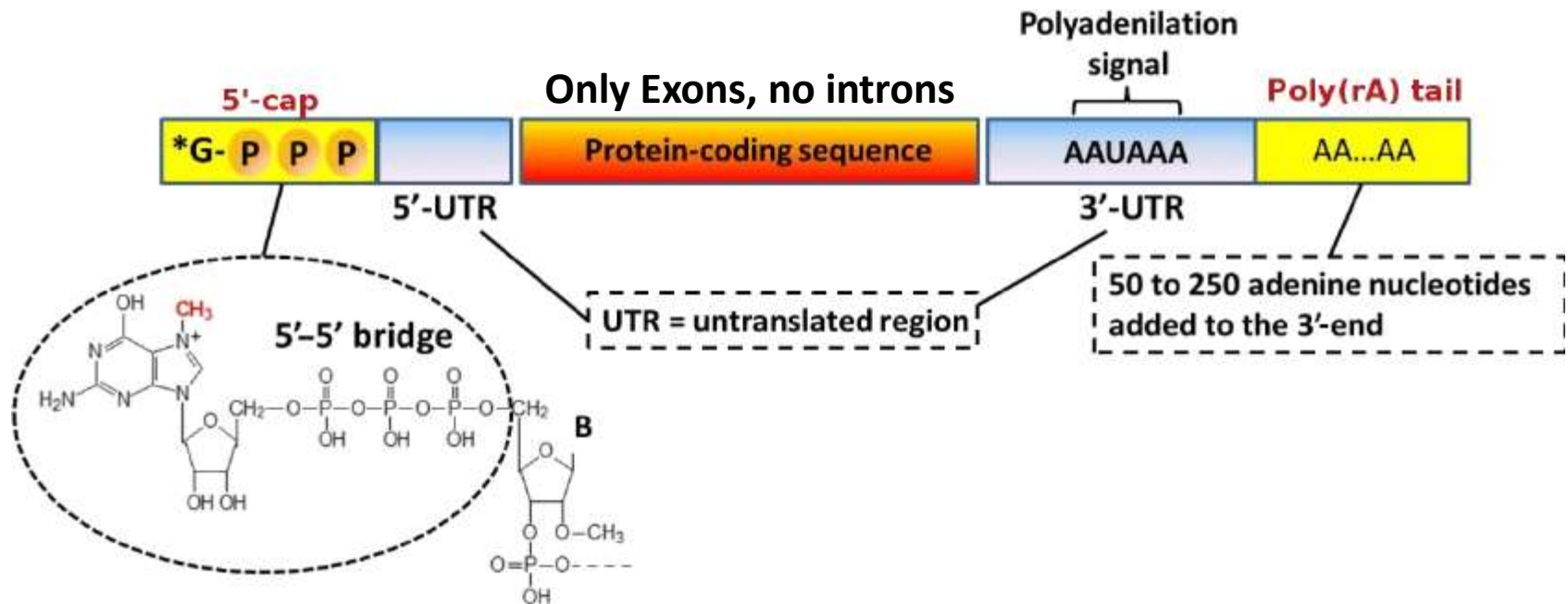
3) **Pre-mRNA processing takes place in the nucleus**. Mature mRNA is then transported into the cytoplasm for protein synthesis.



Pre-mRNA undergoes Posttranscriptional processing to form mature mRNA

Three posttranscriptional processing of pre-mRNA	What is it ?	Enzyme that carries out the process	What is its significance?
1) 5'-capping	Addition of 7-methylguanylate at the 5'-end of pre-mRNA . The 5'-5' triphosphate linkage is formed between the 7-methylguanylate and the first ribonucleotide of pre-mRNA	Guanylyl -7-methyl transferase	Protects the mRNA from degradation by nucleases. In addition, initiation factors involved in protein synthesis recognize the cap to help initiate translation by ribosomes
2) Polyadenylation	Addition of a poly(A) tail to a messenger RNA. The poly(A) tail consists of multiple adenosine monophosphates ; in other words, it is a stretch of RNA that has only adenine bases.	Poly-A-Polymerase	The poly (A) tail protects the mRNA from degradation, aids in the export of the mature mRNA to the cytoplasm, and is involved in binding proteins involved in initiating translation.
3) RNA splicing	Introns are removed, and exons are joined	Spliceosomes	It increases the efficiency of protein synthesis by keeping only the coding regions and removing non-coding regions

Mature mRNA is formed after posttranscriptional processing

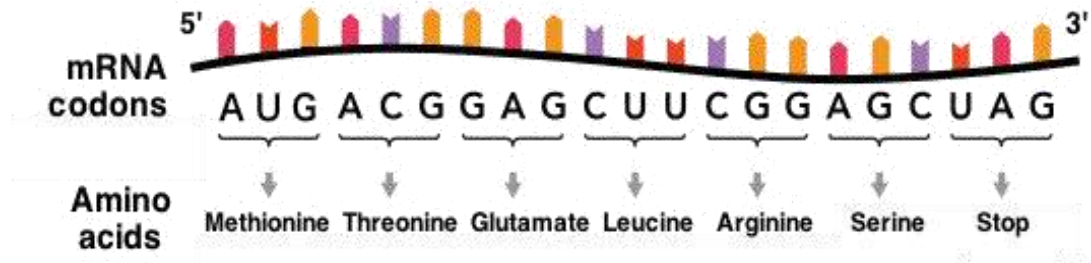


Start codon in mRNA-**AUG**

Stop codon in mRNA-**UAA, UAG, and UGA**

mRNA carries Genetic code from DNA

Only exons; codons which will code for amino acids



Genetic code table

		Second Letter					
		U	C	A	G		
At the 5'end 1st letter	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 Leu CUC CUA CUG	CCU CCC Pro CCA CCG	CAU His CAC CAA Gln CAG	CGU Arg CGC CGA CGG	U	C
	A	AUU Ile AUC AUA AUG Met	ACU Thr ACC ACA ACG	AAU Asn AAC AAA Lys AAG	AGU Ser AGC AGA Arg AGG	U	C
	G	GUU Val GUC GUA GUG	GCU Ala GCC GCA GCG	GAU Asp GAC GAA Glu GAG	GGU Gly GGC GGA GGG	U	C
						A	G
						At the 3'end 3rd letter	

mRNA carries **Genetic code** from DNA and during translation of these codes to amino acid messages, it has to follow some rules, discussed below

1. **Genetic code**- It is the set of rules by which information encoded in the genetic material is translated into proteins by living cells. The genetic code is the set of triplet nucleotides and so also known as triplet codon
2. The Nobel prize winner (1968) –Nirenberg and Khorai described the **following features of genetic code**.

- a) **Nonoverlapping**: one codon follow another
- b) **Triplet of nucleotides and polarity** : one codon with a 3' direction.
- c) **Unambiguous**: all 64 codons are defined (either an amino acid or a stop codon. One codon cannot specify more than one amino acid.
- d) **Commaless**: Code is read from start to end. No stoppir or jumping about (introns already removed).
- e) **Degeneracy**: more than one codon for one amino acids.
- f) **Universal**: All organisms use same genetic code (but some minor exceptions).
- g) **The genetic code AUG codes for Methionine** and is the start codon in all organisms.

Genetic Code- Table

		Second Letter											
		U		C		A		G					
1st letter	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							
1st letter	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							
1st letter	A	AUU Ile	ACU Thr	AAU Asn	AGU Ser	U							
		AUC	ACC	AAC	AGC	C							
		AUA	ACA	AAA Lys	AGA Arg	A							
		AUG Met	ACG	AAG	AGG	G							
1st letter	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							

Sample question

Q.1) Write the amino acid sequence of the following codons in mRNA.

5'-AUGCUCUUUGUGACCAAGAGGGAG-3'

Ans 1) Codons are read in triplet in 5'-3' direction. E.g. in the above sequence **AUG** at the 5'-end is **the first codon**. Immediate second codon is CUC. There should not be jumping in reading codon sequence (following the rules of genetic code).

Therefore, **from the genetic code table**, the amino acid sequence derived from the above mRNA sequence is :

NH₂-met-leu-phe-val-thr-lys-arg-glu-COO⁻

where NH₂ means amino terminal end and COO⁻ carboxyl terminal end

Q.2) How many codons will be required to form a hexapeptide sequence and how many bases will be required to form hexapeptide sequence?

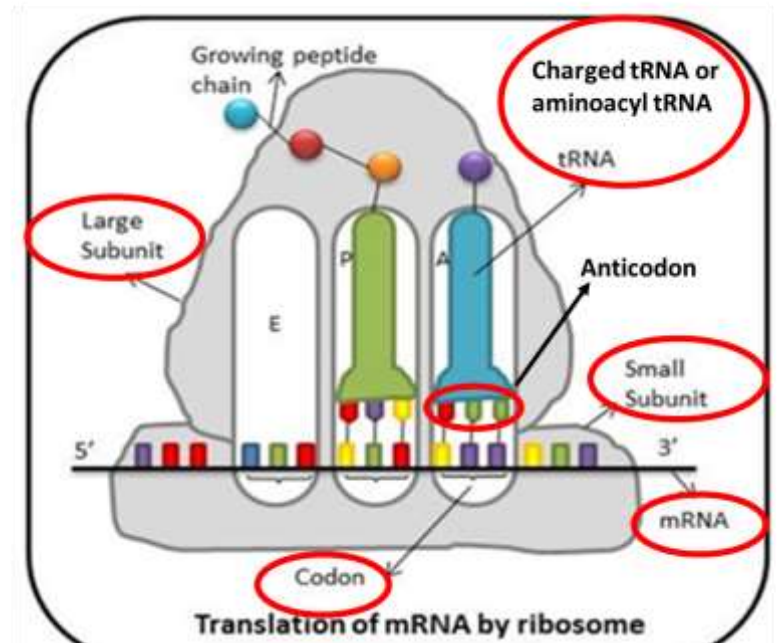
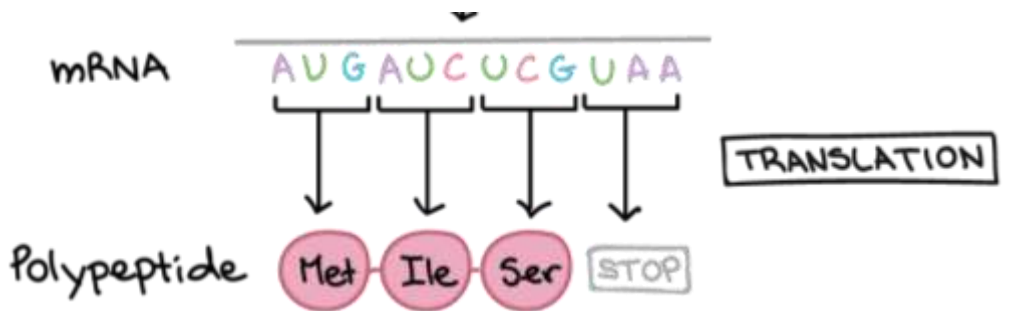
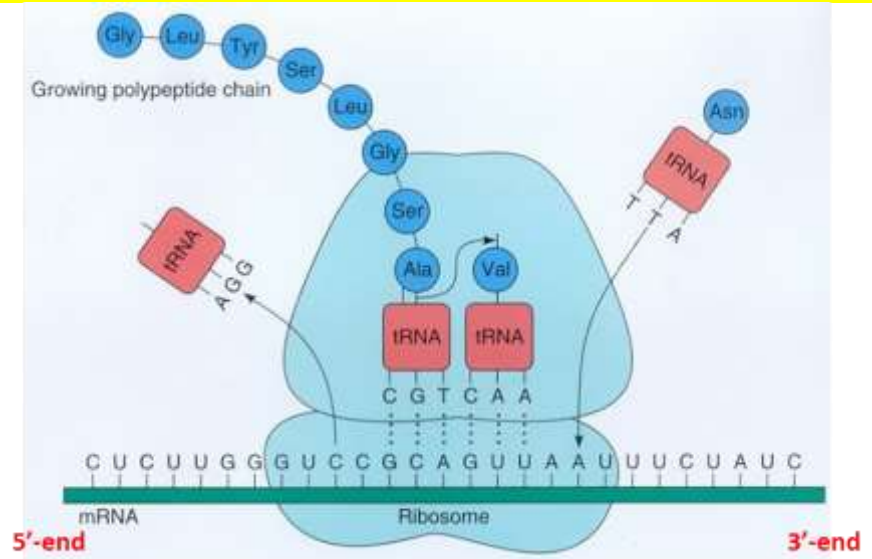
Ans.2) Hexapeptide means 6 amino acid. One codon for one amino acid.

In mRNA **6 codons** will code for 6 amino acids to form hexapeptide sequence and one stop codon.

One codon has 3 bases. Therefore , 6 codons will have, 3x6=18 bases total

Translationin cytoplasm

1. Translation is the process in which mRNA associates with ribosomes and directs synthesis of a protein by converting the sequence of nucleotides in mRNA into specific sequence of amino acids.
2. The mRNA is translated from its 5'-end to its 3'-end, producing a protein synthesized from its amino terminal end to its carboxyl terminal end.



What are the components required for translation process

Translation takes place in cell cytoplasm and the Components required for translation process are :

- a) **mRNA**- that carries codons
- b) **Intact ribosomes**- for performing catalytic activity in formation of peptide bond between amino acids brought by tRNA. It has three sites: aminoacyl-tRNA binding site (A-site), peptidyl site (P-site) and Exit site (E-site).
- c) **tRNA**- that carries amino acid to the site of protein synthesis
- d) **Energy in the form of ATP and GTP**
- e) **Free amino acids**

The basic steps involved in Translation process

- **1. Initiation:** ribosome (small and large ribosome) binds mRNA at **start codon -AUG** . Ribosome has catalytic activity to form peptide bonds between amino acids brought by tRNA at the site.
- **2. Elongation:** polypeptide chain elongates by successively adding amino acids
- **3. Termination:** When a stop codon is encountered in mRNA, polypeptide is released and ribosome dissociates.

What is Codon-anticodon interaction during translation process

Codon- present in mRNA

Anticodon- present in tRNA. The anticodon which is present in tRNA forms complementary base pair with the codon in mRNA. The codon that codes for a particular amino acid is carried by tRNA. **In tRNA, inosine (I) as base is also found.**

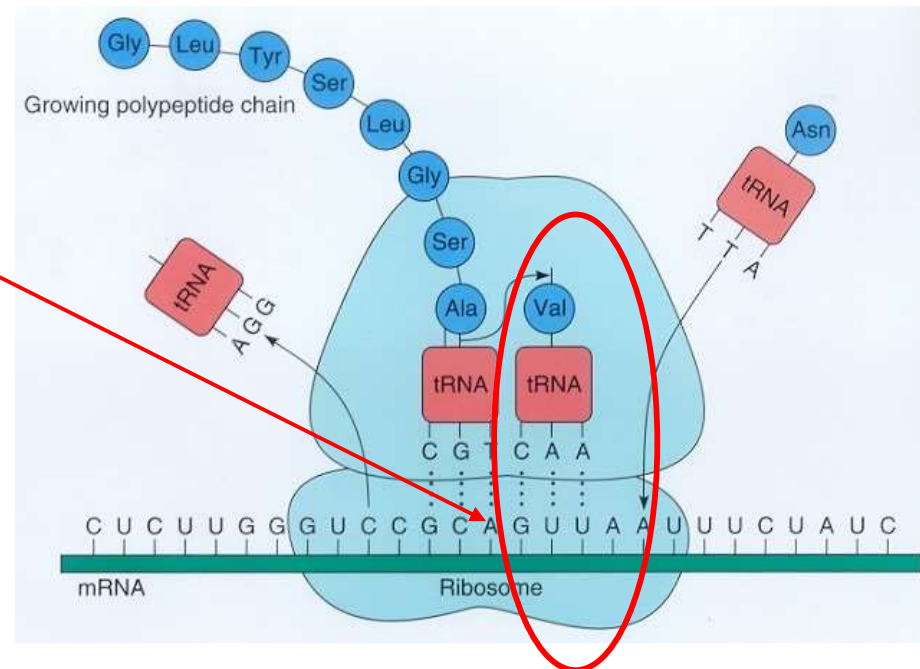
Codon-anticodon interaction shown in the figure:

Here, codon in mRNA is : **GUU** (valine amino acid);

Anticodon in tRNA is : **CAA**.

tRNA carries amino acid valine at its 5'end.

GUU and CAA forms complementary base pair.



Wobbling phenomenon of during codon-anticodon interactions

- Non standard base pairing is observed between the third base of the codon and first base of anticodon.
- The reduced specificity between the third base of the codon and the complementary nucleotide in anticodon is responsible for wobbling.

Example of wobbling phenomenon

- Proline has 4 codons(5'-3')
- CCU } 3'-GGI-5' (anticodon)
- CCC } 3'-GGC-5' (anticodon)
- CCA } 3'-GGU-5' (anticodon)
- CCG } 3'-GGU-5' (anticodon)
- The first three codons can be recognized by a single t RNA having Inosine at the first place.(IGG- 5'-3')

5'-CCU-3'- pair with anticodon GGI, GGA, GGG (3'-5')

5'-CCC-3'-pair with anticodon GGI, GGG (3'-5')

5'-CCA-3'-pair with anticodon GGU, GGI (3'-5')

t RNA (first base)	m RNA (Third base)	Base pairing
C	G	Traditional
A	U	Traditional
U	A	Traditional
U	G	Nontraditional
G	C	Traditional
G	U	Nontraditional
I	U	Nontraditional
I	C	Nontraditional
I	A	Nontraditional

