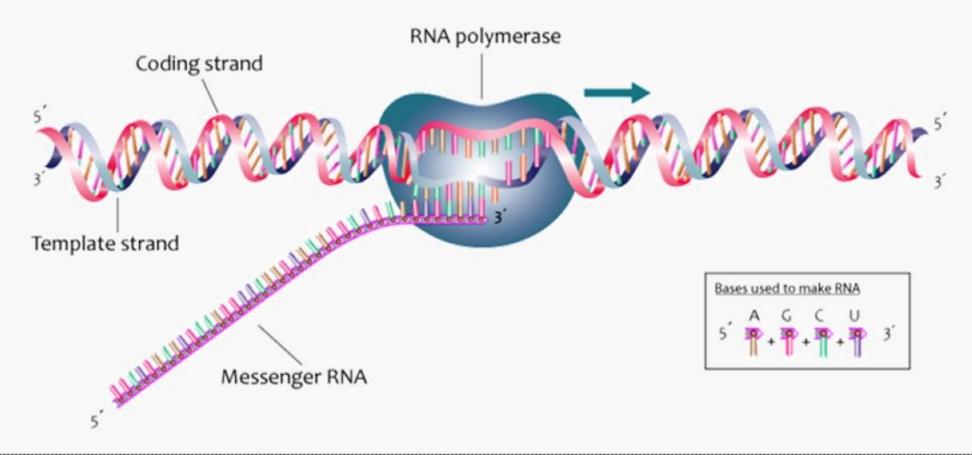
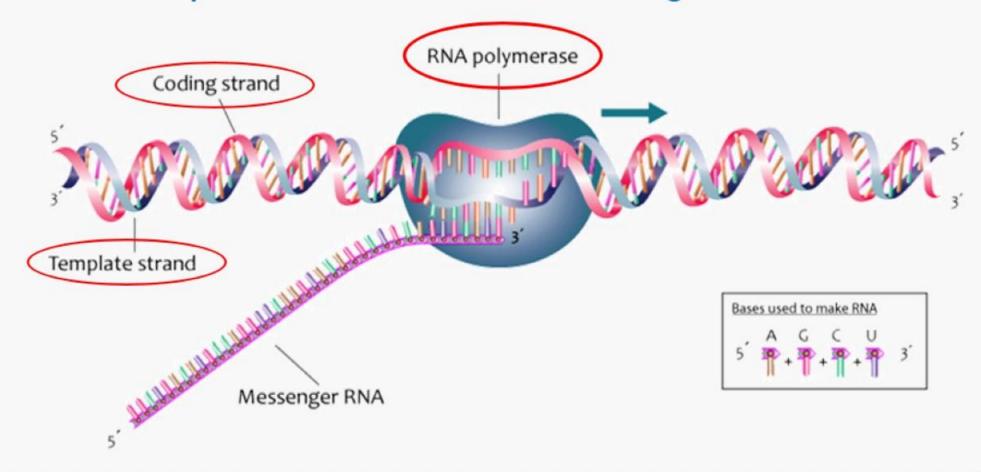


- It is the process of copying genetic information from one strand of the DNA into RNA.
- Here, adenine forms base pair with uracil instead of thymine.



- The DNA- dependent RNA polymerase catalyzes polymerization only in 5'→3' direction.
- 3' \rightarrow 5' acts as template strand and 5' \rightarrow 3' acts as coding strand.



- Both strands are not copied during transcription, because
 - The code for proteins is different in both strands. This complicates the translation.
 - If 2 RNA molecules are produced simultaneously, this would be complimentary to each other. It forms a double stranded RNA and prevents translation.

Template strand: RNA is built from this.



3'-ATGCATGCATGCATGCATGC-5'

5'-TACGTACGTACGTACGTACG-3'

Transcription

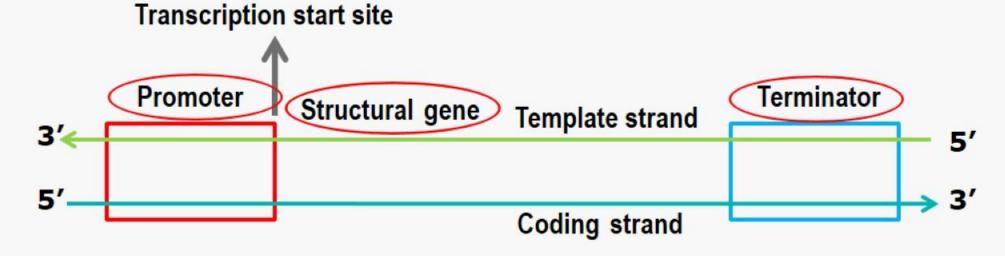
Coding strand: This is copied to RNA.

5'-UACGUACGUACGUACGUACG-3'

mRNA

TRANSCRIPTION UNIT

- It is the segment of DNA between the sites of initiation and termination of transcription.
- It consists of 3 regions:
 - A promoter: Binding site for RNA polymerase. Located towards 5'-end (upstream).
 - > Structural gene: Region b/w promoter & terminator where transcription takes place.
 - A terminator: The site where transcription stops. Located towards 3'-end (downstream).

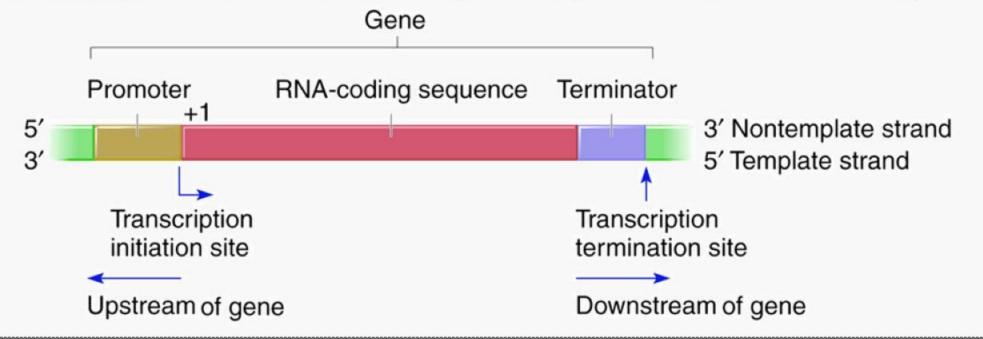


SCHEMATIC STRUCTURE OF A TRANSCRIPTION UNIT

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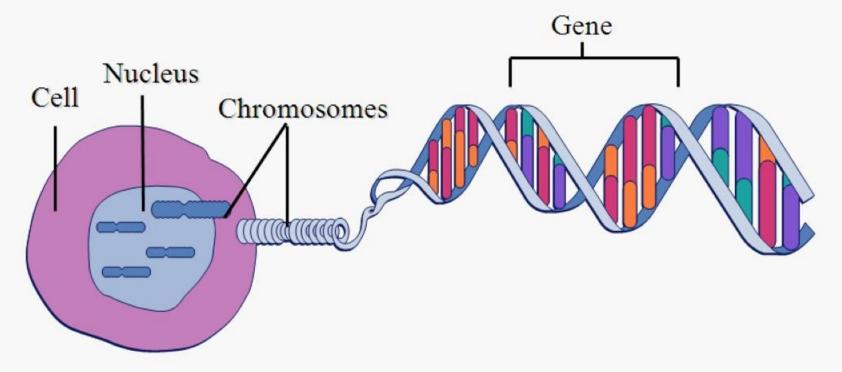
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TRANSCRIPTION TRANSCRIPTION UNIT & GENE

- Gene is a functional unit of inheritance. It is the DNA sequence coding for an RNA (mRNA, rRNA or tRNA).
- Cistron is a segment of DNA coding for a polypeptide during protein synthesis. It is the largest element of a gene.



TRANSCRIPTION TRANSCRIPTION UNIT & GENE

Structural gene in a transcription unit is 2 types:

- Monocistronic structural genes (split genes):
 - It is seen in eukaryotes.
 - Here, coding sequences (exons or expressed sequences) are interrupted by introns (intervening sequences).
 - Exons appear in processed mRNA. Introns do not appear in processed mRNA.
- Polycistronic structural genes:
 - It is seen in prokaryotes. Here, there are no split genes.

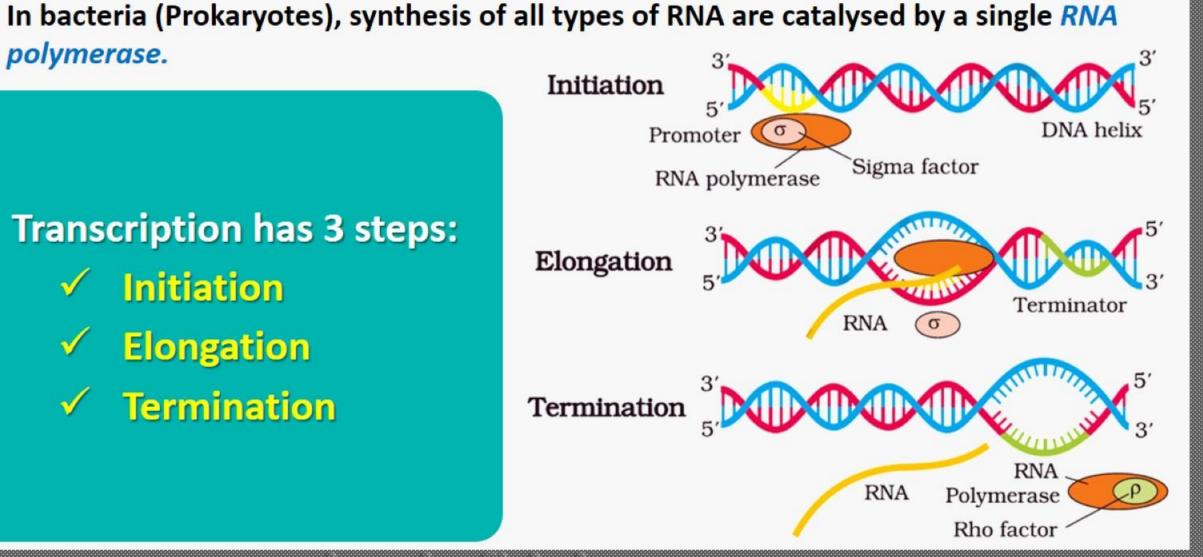


Monocistronic structural gene

Polycistronic structural gene

Transcription has 3 steps:

- Initiation
- **Elongation**
- **Termination**

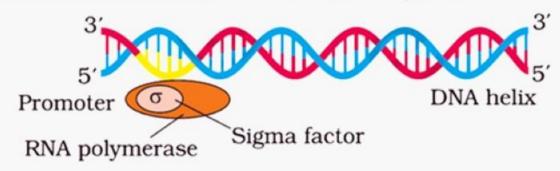


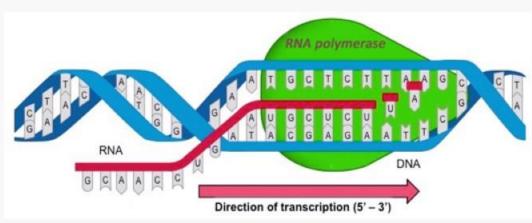
TRANSCRIPTION IN PROKARYOTES

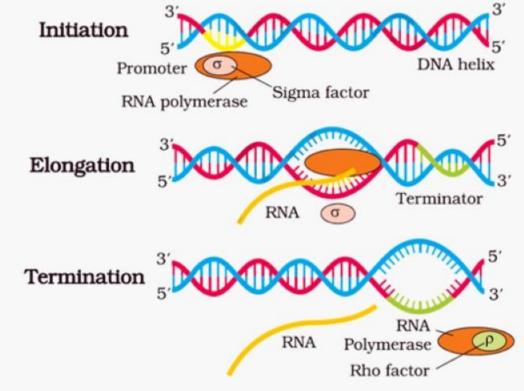
Initiation

- Here, RNA polymerase enzyme binds at the promoter site of DNA.
- This causes the local unwinding of the DNA double helix.

 An initiation factor (σ factor) present in RNA polymerase initiates the RNA synthesis.





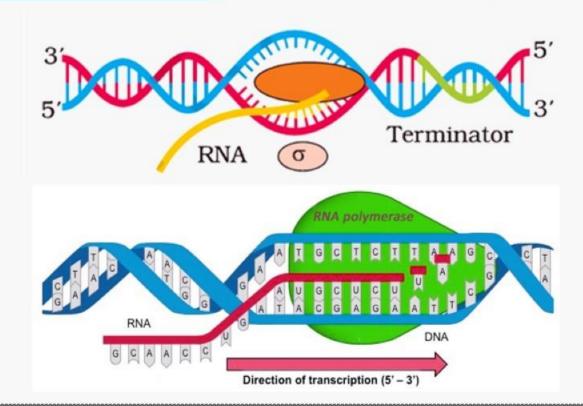


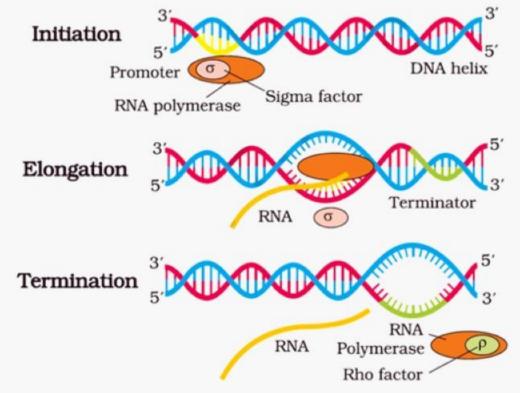
TRANSCRIPTION IN PROKARYOTES

Elongation

RNA chain is synthesized in 5'-3' direction.

 In this process, activated ribonucleoside triphosphates (ATP, GTP, UTP & CTP) are added. This is complementary to the base sequence in the DNA template.

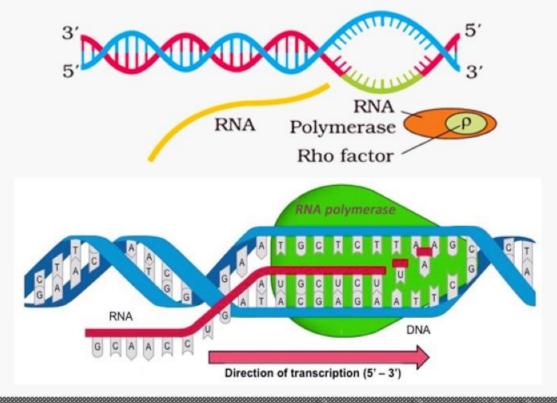


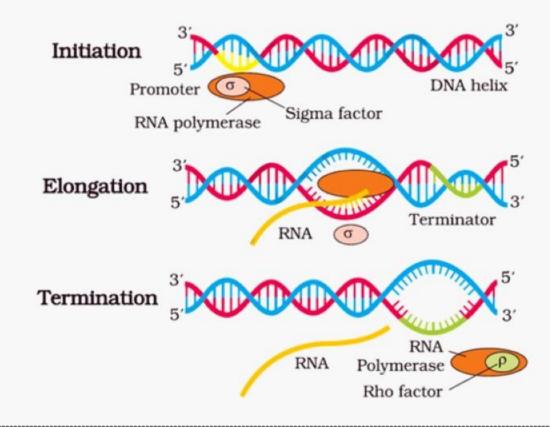


TRANSCRIPTION IN PROKARYOTES

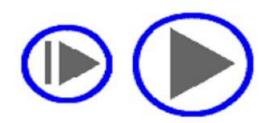
Termination

 A termination factor (ρ factor) binds to the RNA polymerase and terminates the transcription.





TRANSCRIPTION IN PROKARYOTES



Transcription

Promoter

Coding strand

Terminator



Template strand

RNA polymerase

mRNA

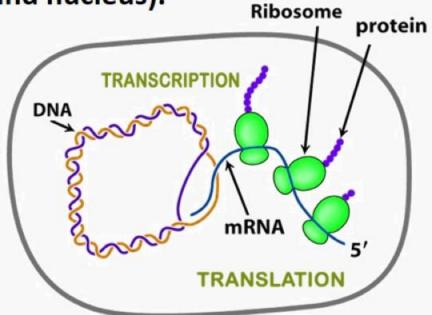
TRANSCRIPTION IN PROKARYOTES

In bacteria, transcription and translation can be coupled (translation begins before mRNA is fully transcribed) because

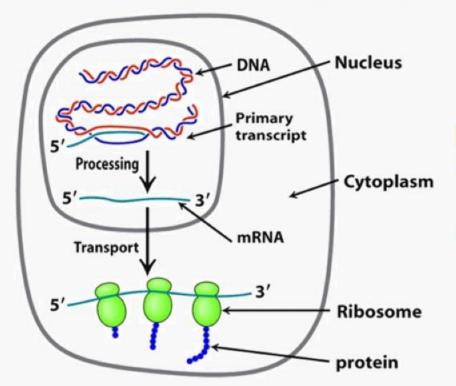
mRNA requires no processing to become active.

Transcription & translation take place in same compartment (no separation of cytosol

and nucleus).



Bacterial cell (Prokaryote)



Eukaryotic cell. No coupling of transcription and translation

TRANSCRIPTION IN EUKARYOTES

In eukaryotes, there are 2 additional complexities:

- 1. There are 3 RNA polymerases.
- The primary transcripts (hnRNA) contain exons and introns and are non-functional. Hence introns must be removed.

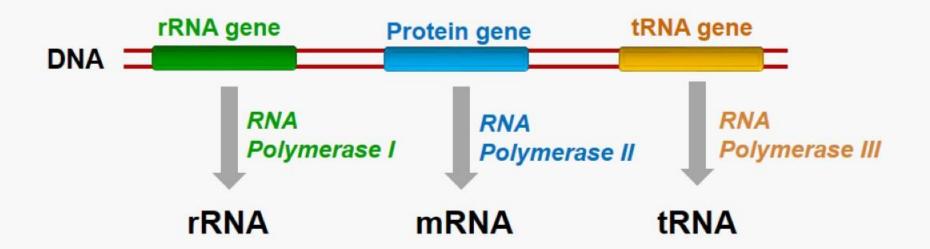


Primary transcripts (hnRNA)

TRANSCRIPTION IN EUKARYOTES

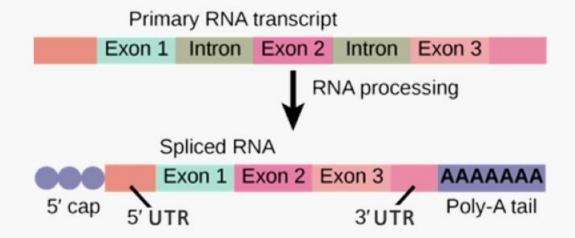
3 RNA polymerases in eukaryotes:

- RNA polymerase I: Transcribes rRNAs (28S, 18S & 5.8S).
- RNA polymerase II: Transcribes the heterogeneous nuclear RNA (hnRNA). It is the precursor of mRNA.
- RNA polymerase III: Transcribes tRNA, 5S rRNA and snRNAs (small nuclear RNAs).



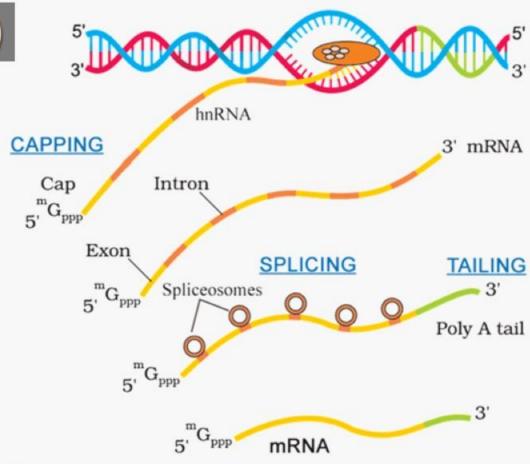
TRANSCRIPTION IN EUKARYOTES

Processing of primary transcripts (hnRNA)

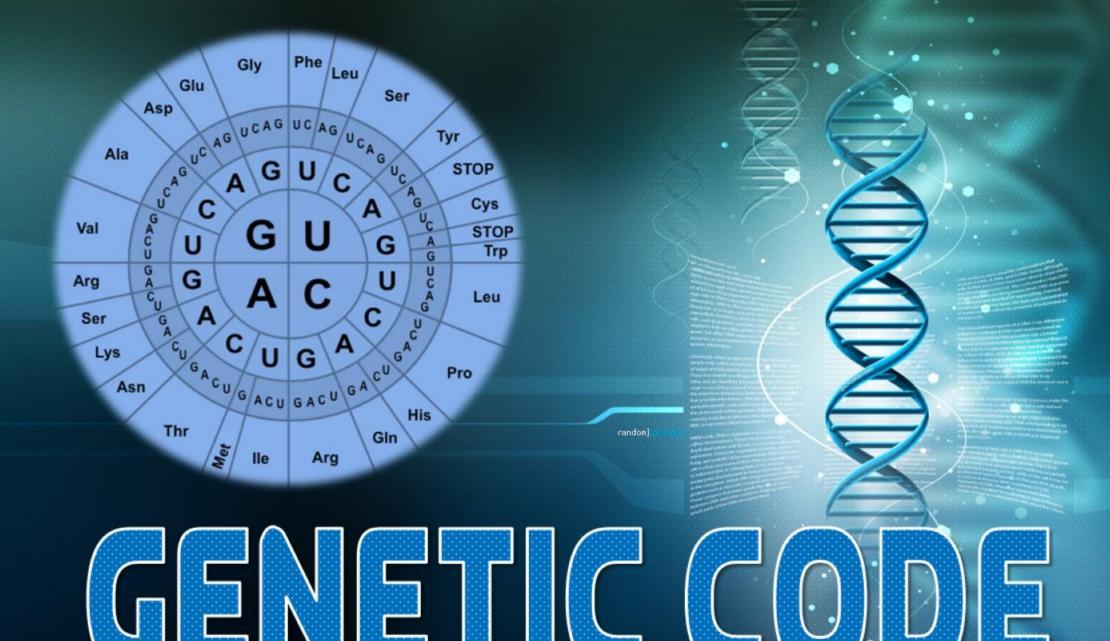


- Splicing: From hnRNA, introns are removed (by spliceosome) and exons are spliced together.
- Capping: Here, a nucleotide methyl guanosine triphosphate (cap) is added to 5' end of hnRNA.

3. Tailing (Polyadenylation): Here, adenylate residues (200-300) are added at 3'-end.



Now, it is the fully processed hnRNA, called mRNA.



- It is the sequence of nucleotides (nitrogen bases) in mRNA that contains information for protein synthesis (translation).
- The sequence of 3 bases determining a single amino acid is called codon.

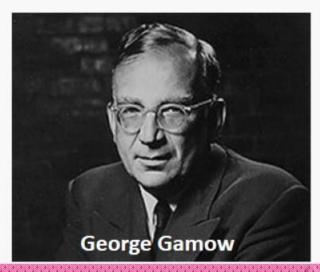
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Codons: 1 2 3 4 5 6 7 8 9

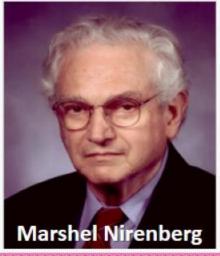
5'-AUGUACGUACGUACGUACGUUAA-3' mRNA

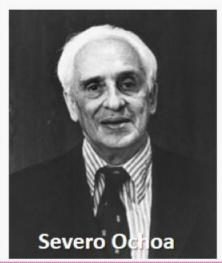
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- George Gamow suggested that for coding 20 amino acids, the code should be made up
 of 3 nucleotides. Thus, there are 64 codons (4³= 4 x 4 x 4).
- Har Gobind Khorana developed the chemical method in synthesizing RNA molecules with defined combinations of bases (homopolymers & copolymers).
- Marshall Nirenberg developed cell-free system for protein synthesis.
- Severo Ochoa enzyme (polynucleotide phosphorylase) is used to polymerize RNA with defined sequences in a template independent manner.





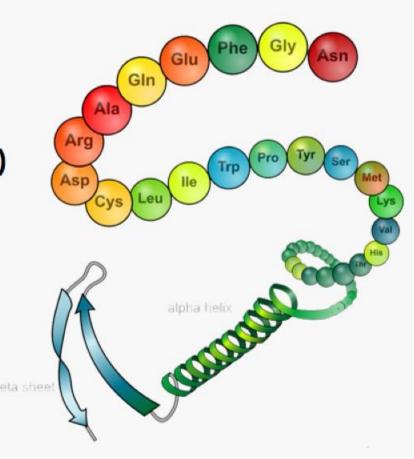




20 types of amino acids involved in translation

- Alanine (ala)
- 2. Arginine (arg)
- 3. Asparagine (asn)
- 4. Aspartic acid (asp)
- 5. Cystein (cys)
- 6. Glutamine (gln)
- Glutamic acid (glu)
- Glycine (gly)
- Histidine (his)
- 10. Isoleucine (iso)

- 11. Leucine (leu)
- 12. Lysine (lys)
- 13. Methionine (met)
- Phenyl alanine (phe)
- 15. Proline (pro)
- 16. Serine (ser)
- 17. Threonine (thr)
- 18. Tryptophan (trp)
- 19. Tyrosine (tyr)
- 20. Valine (val)



CODONS FOR VARIOUS AMINO ACIDS

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THE GENETIC CODE DICTIONARY

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

lagint contained on the count

- Codon is triplet (three-letter code).
- 61 codons code for amino acids. 3 codons (UAA, UAG & UGA) do not code for any amino acids. They act as stop codons (Termination codons or non-sense codons).
- AUG has dual functions. It codes for Methionine and acts as initiator codon. In eukaryotes, methionine is the first amino acid and formyl methionine in prokaryotes.
- An amino acid is coded by many codons (except AUG for methionine & UGG for tryptophan). Such codons are called degenerate codons.



SALIENT FEATURES OF GENETIC CODE

- No punctuations b/w adjacent codons (comma less code). The codon is read in mRNA in a contiguous fashion.
- Genetic code is universal. E.g. From bacteria to human UUU codes for Phenylalanine.
 Some exceptions are found in mitochondrial codons, and in some protozoans.
- Genetic code is non-overlapping.
- Genetic code is unambiguous & specific. i.e. one codon specifies only one amino acid.

No base ("comma") b/w adjacent codons

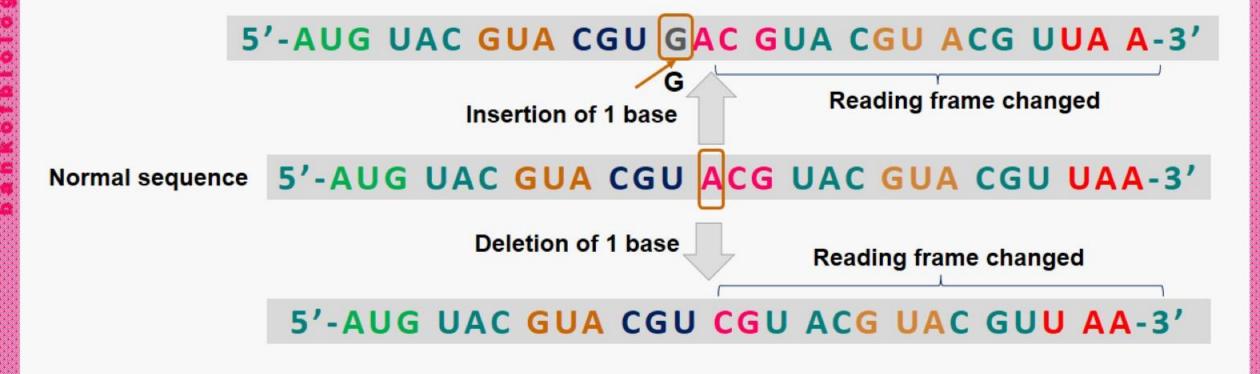


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Overlapping codons

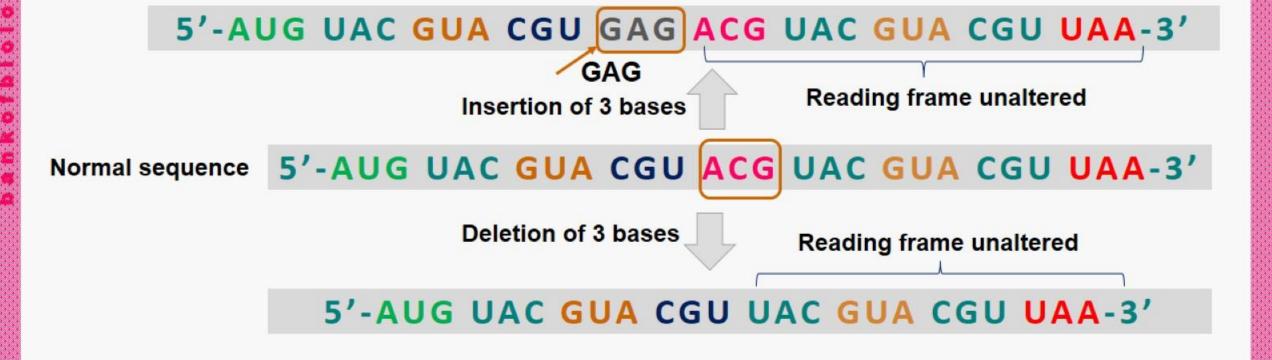
MUTATION AND GENETIC CODE

- Relationship between genes & DNA are best understood by mutation studies. Deletions
 & rearrangements in a DNA may cause loss or gain of a gene and so a function.
- Insertion or deletion of one or two bases changes the reading frame from the point of insertion or deletion. It is called frame-shift insertion or deletion mutations.

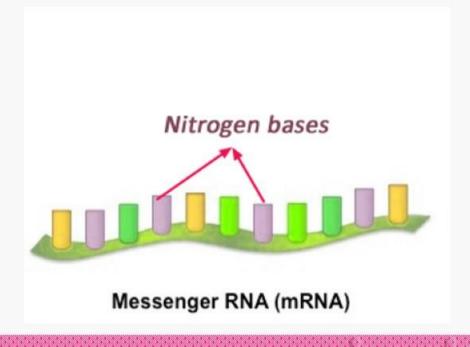


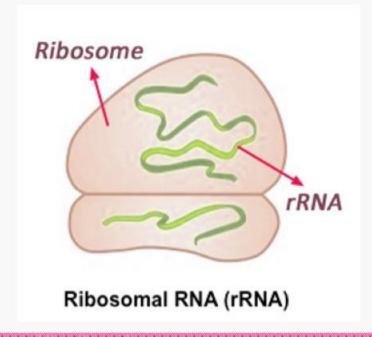
MUTATION AND GENETIC CODE

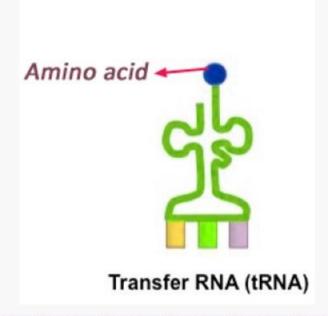
- Insertion/ deletion of three or its multiple bases insert or delete one or multiple codon.
 The reading frame remains unaltered from that point onwards. Hence one or multiple amino acids are inserted /deleted.
- It proves that codon is a triplet and is read contiguously.



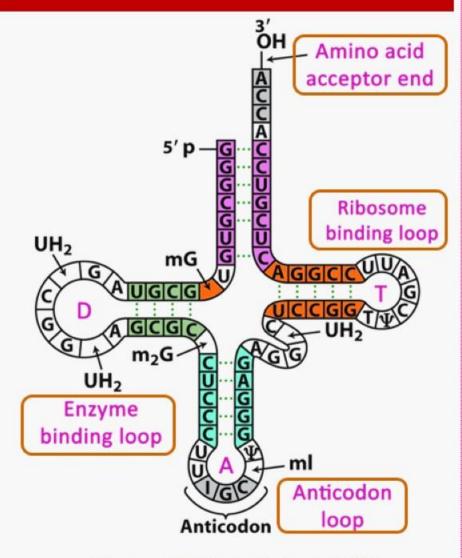
- mRNA (messenger RNA): Provide template for translation (protein synthesis).
- rRNA (ribosomal RNA): Structural & catalytic role during translation. E.g. 23S rRNA in bacteria acts as ribozyme.
- tRNA (transfer RNA or sRNA or soluble RNA): Brings amino acids for protein synthesis and reads the genetic code.







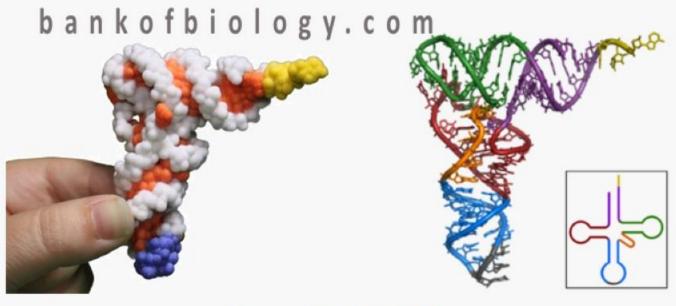
- Francis Crick postulated presence of an adapter molecule that can read the code and to link with amino acids.
- tRNA is called adapter molecule because it has
 - An Anticodon (NODOC) loop that has bases complementary to the codon.
 - An amino acid acceptor end to which amino acid binds.
 - Ribosome binding loop.
 - Enzyme binding loop.



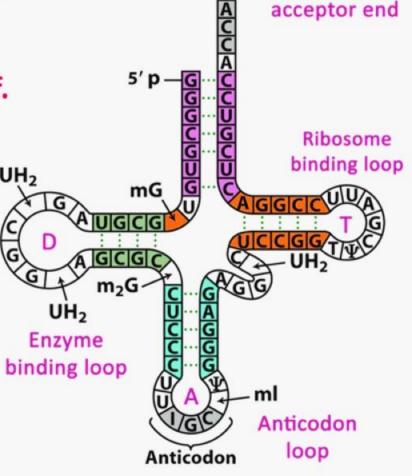
Clover leaf model of tRNA

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- For initiation, there is another tRNA called initiator tRNA.
- There are no tRNAs for stop codons.
- Secondary (2-D) structure of tRNA looks like a clover-leaf.
- 3-D structure looks like inverted 'L'.



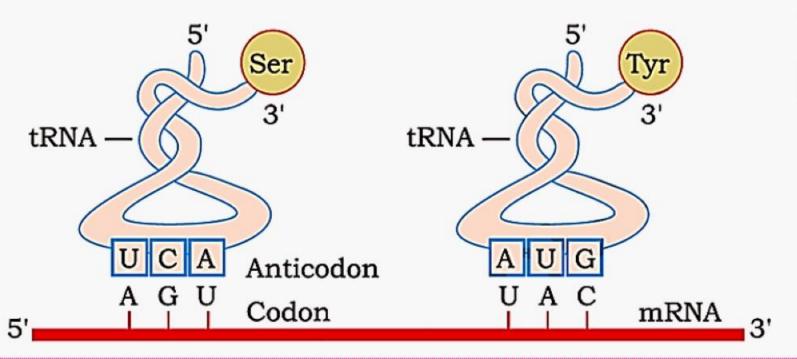
3D model of tRNA

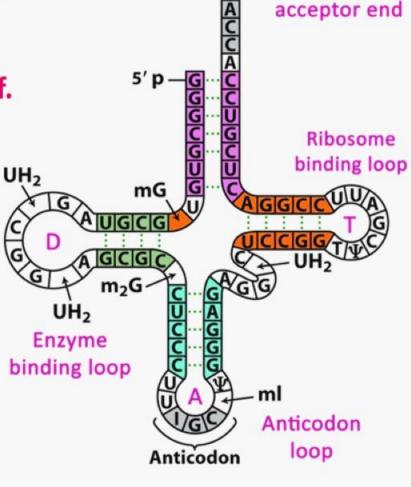


Clover leaf model of tRNA

Amino acid

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Clover leaf model of tRNA

Amino acid