



**ST. WILFRED'S P.G. COLLEGE**

*(Affiliated to the University of Rajasthan)*

# Unit wise Notes

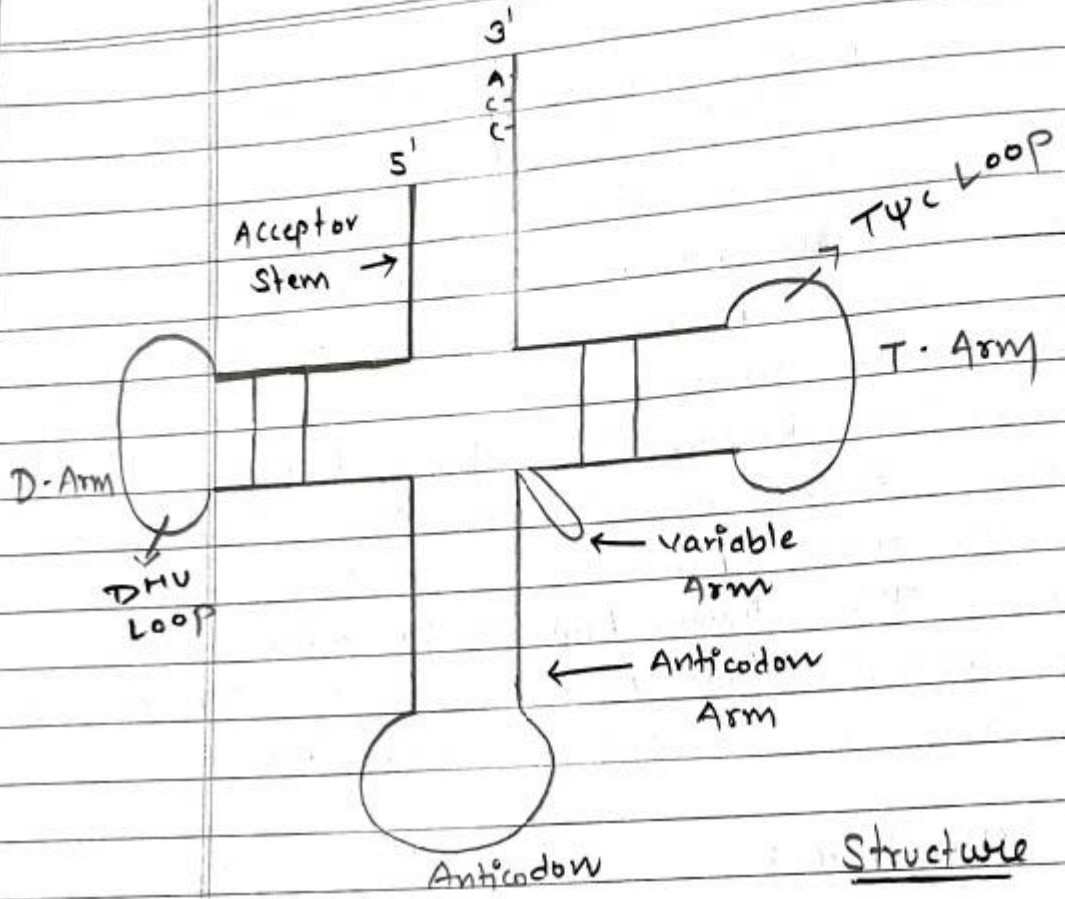
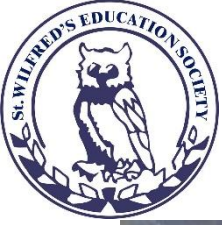
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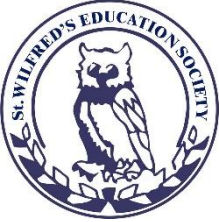
Structure of t-RNA

⇒ Clover leaf Structure of t-RNA : The Secondary folded structure of t-RNA has Three hairpin loops, which gives it an appearance of Three leafed clover.

• The main constituents of t-RNA are :

|| Acceptance Arm :

- it is formed by The base pairing of 7-9 A of 5' Terminal And 3' Terminal.
- The 5' Terminal has a phosphate group And



3' ends with a specific sequences of CCA or CCA Tail. The Amino Acid attaches to the 3' hydroxyl group of the acceptor arm.

- The aminoacylation of t-RNA or charging of t-RNA is the first step of the translation process.

- The enzyme aminoacyl t-RNA synthetase catalyses the reaction.

iii) DHU Loop :-

- D-Arm has a stem of 3-4 base pairs and it ends in a loop called D loop as it generally contains dihydrouridine, a modified nucleotide.

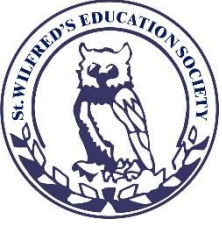
iv) Anticodon loop :-

- it has a 5 base pair long stem. It has an anticodon loop, which contains the complementary codon (3 Nt sequences) present on mRNA for the amino acid it carries.

- These unpaired bases of anticodon loop pair with the mRNA codon.

- Each codon is identified by a specific t-RNA.



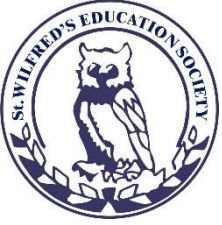


iv) T $\Psi$ C Loop :  
• The T-Arm consist of A stem of 4-5 bp and a loop containing pseudouridine modified uridine.

v) variable Loop :  
• it is present between the T $\Psi$ C loop and anticodon loop.  
• its size varies from 3-21 bases.  
• it helps in the recognition of the tRNA molecule.

→ tRNA function :->

- t-RNA plays an important role in protein synthesis.
- it acts as an adaptor molecule for linking amino acids to its specific codon present in mRNA.
- Aminoacylation of tRNA is the 1<sup>st</sup> step in protein synthesis.
- t-RNA is specific to each amino acid and carries them during the translation process in the ribosomal subunits.
- The t-RNA transfers the amino acids to the growing polypeptide chain in the ribosome.



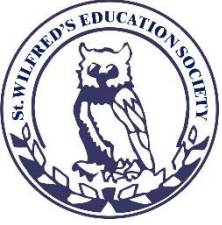
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which has 3 binding sites for tRNA, namely A, P and E which correspond to Aminoacyl, peptidyl and Exit respectively.

• This decoding of codons of mRNA by specific tRNAs continue until the entire seq. for a polypeptides chain is translated.



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## DNA And RNA Polymerases :

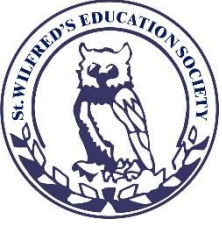
- polymerases are enzymes that catalyze the synthesis of polymers of nucleotides or nucleic acids.
- DNA polymerases are required during the process of DNA replication and DNA repair to assemble a new DNA strand.  
RNA polymerases are involved in the production of RNA molecules during the process of transcription.



## Similarities of DNA And RNA polymerases

1. Requires a DNA template strand and free nucleotides as substrates.
2. Catalyze the addition of nucleotides to the 3' end of a growing chain of nucleic acids. Such that growth of the chain is in the 5' to 3' direction.
3. Read the template strand of DNA in the 3' to 5' direction and bring in the correct nucleotides by complementary base pairing with the template.





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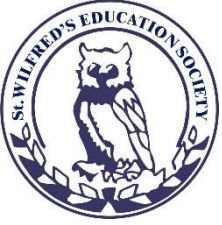
catalyze formation of phosphodiester bonds between adjacent nucleotides in the chain with the release of pyrophosphate.

in eukaryotic cells DNA and mRNA are produced in the nucleus.

### Differences of DNA and RNA polymerases :-

DNA polymerases require the 4 kinds deoxyribose triphosphate (dATP, dCTP, dGTP and dTTP) as substrate while RNA polymerases require the 4 ribose triphosphates (ATP, CTP, GTP, UTP) as substrates.

Initiation of synthesis of new DNA strands by DNA pol. occurs at specific DNA sequences called origin of replication and requires a small preexisting strand of nucleotides complementary to the template as a primer; while synthesis of RNA molecules by RNA pol. requires a region in the DNA called the promoter to determine the start and direction of RNA transcription but does not require a primer.



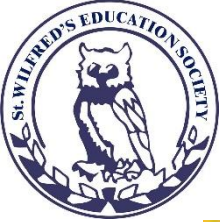
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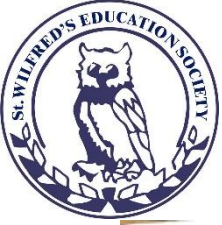
The main Replicative DNA poly. activities That minimize base-pairing while RNA pol. do not have the of proofreading Activity, And Rates are highest during Transcri





## r-RNA Processing:

- The r-RNA are structural molecules that have roles in protein synthesis; however these RNAs are not themselves translated.
- In eukaryotes, pre-r-RNA are transcribed, processed and assembled into ribosomes in the nucleus.
- The 4 r-RNA in eukaryotes are first transcribed as two long precursor molecules.
- One contains just the pre-r-RNA that will be processed into the 5S r-RNA; the other spans the 18S, 5.8S and 18S r-RNAs.
- Enzymes then cleave the precursors into subunits corresponding to each r-RNA.
- In bacteria, there are only 3 r-RNAs and all are transcribed in one long precursor molecule that is cleaved into the one long individual r-RNAs.
- Some of the bases of pre-r-RNAs are methylated for added stability.



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- mature r-RNA make up 50-60% of each
- Some of a Ribosome's RNA molecules are structural, whereas others have catalytic or binding activity.
- The Eukaryotic Ribosome is composed of two subunits: a larger subunit (60S) and a smaller subunit (40S).
- The 60S subunit is composed of the 28S rRNA, 5.8S rRNA, and 50 proteins.
- The 40S subunit is composed of the 18S rRNA and 33 proteins.
- The bacterial Ribosome is composed of two subunits, with slightly different components.
- The bacterial large subunit is called the 50S subunit and is composed of the 23S rRNA, 5S rRNA, and 31 proteins. While the bacterial small subunit is called the 30S subunit and is composed of the 16S rRNA and 21 proteins.
- The two subunits join to constitute a functional Ribosome that is capable of creating proteins.





## Genetic code :

- genetic code Refers To The Relationship between The Sequence of Nitrogenous Bases (UAG) in mRNA and The Sequence of Amino Acids in a polypeptide chain.
- In other words, The Relationship between The 4 letters language of (Amino Acid) Nucleotides and 20 Letters Language of Amino Acids is known as Genetic code.
- DNA (or RNA) Carries all The genetic information And it is expressed in The form of proteins.
- proteins are made of 20 different Amino Acids.
- The information About The number And Sequence of These Amino Acids forming protein is present in DNA and during Transcription is passed over to m-RNA. The form in which it is Transferred was not understood for long.
- Sugar (pentose) And phosphate of DNA could not perform This job of passing on The genetic message to m-RNA because Sugar is only of one Type and Also The phosphate. This leaves only 4 Nucleotides to form The message for 20 Amino Acids But 4 Nucleotides are Too Few for Twenty Amino Acids.

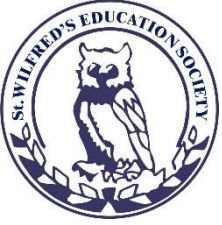




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- This difficult problem was solved with the discovery of a codon (hereditary unit of a gene) containing coded information for one Amino Acid consists of three Nucleotides (i.e. a Triplet codon). Thus for Twenty Amino Acids, 64 ( $4 \times 4 \times 4$  or  $4^3 = 64$ ) possible permutations are available.
- This break through resulted into 64 codons dictionary. - The genetic code.
- According to Bark (1970) The genetic code is a code for Amino Acids. Specifically it is concerned with as to what codons specify what Amino Acids.
- The genetic code is the outcome of experiments performed by M. Nirenberg, S. Ochoa, H. Khorana, F. Crick was awarded Nobel prize in 1961 for this outstanding work.
- The dictionary of genetic code employs the letters in RNA (U, C, A, G i.e. A = Adenine, U = Uracil, C = Cytosine, G = Guanine)
- The codon for the Amino Acids, which are the same in all known life forms, have been determined experimentally.



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More Than one codon can signal a particular amino Acid To be incorporated into a protein.

In addition, Some codon serves special functions:

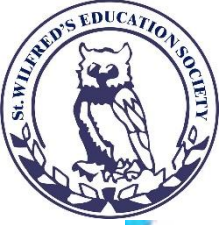
AUG is an initiator codon signaling for the start of synthesis of a peptide, and

for the incorporation of methionine into the growing chain of a peptide. other special-purpose codons are UAA (ochre), UAG (Amber), and UGA (Umber), all of which signal stop.

When the ribosomal synthesis site encounters one of these STOP codons, the peptide chain is released and assumes its secondary and tertiary structures.

Since UAA (ochre), UAG (Amber) and UGA (Umber) do not specify any amino acid they are also called nonsense codons.





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## Co-linearity :

DNA is a linear polynucleotide chain and a protein is linear polypeptide chain.

The Sequence of Amino Acids in a polypeptide chain corresponds to the Sequence of Nucleotide bases in the gene (DNA) that code for it.

Change in a specific codon in DNA produces a change of Amino Acid in the corresponding position in the polypeptide.

The gene and the polypeptide it codes for are said to be co-linear.

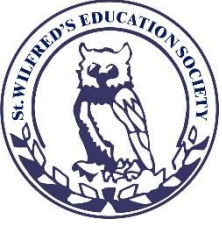
## Gene-polypeptide parity :

A specific gene transcribes a specific m-RNA that produces a specific polypeptide.

On this basis, a cell can have only as many types of polypeptides as it has types of genes.

However, this does not apply to certain viruses which have overlapping genes.





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CCUCAG  
└──┬──┬──┘

This is overlapping

CCU, CAG

No overlapping

4. The code is Comma Less :

- A comma less code means That no nucleotide or comma is present in between Two codon.
- Therefore, code is continuous and comma less and No letter is wasted between Two words or codon.

AUG                      CAG  
a<sup>1</sup>                              a<sup>2</sup>

5. The code is unambiguous :

- There is no ambiguity in The genetic code. A given codon always codes for a particular Amino Acid whenever it is present.

6. The code is universal :

- The genetic code has been found to be universal in all kinds of living organism. Prokaryotes And Eukaryotes.