Blue Print (As per PU Board)

Topic	1 mark questions	2 marks questions	3 marks questions	5 marks questions	Total Marks
Molecular Basis of Inheritance	1	3	1	3	25

One mark questions

1. **Why eukaryotic genes are called split genes?**

   Answer: They have both coding (exons) and non-coding (introns) sequences

2. **Structural genes in prokaryotes are called polycistronic give reason**

   Answer: Prokaryotic genes code for many proteins or Polypeptides during protein synthesis

3. **Define genetic code?**

   Answer: The sequence of three nucleotides in DNA or RNA, which codes for a particular amino acid during protein synthesis is called genetic code

Two marks questions

4. **What are 'S' and 'R' strains of streptococcus pneumonia?**

   Answer: Smooth walled collonies and rough walled colonies of streptococcus pneumonia on culture plate.

5. **What are monocistronic and polycistronic unit of m-RNA**

   Answer: (1) mRNA which produces only one type of protein is monocistrons (2) mRNA which produces many types of protein is polycistronic

6. **What is splicing and tailing?**

   Answer: Removal of introns and joining only eons is splicing.

   Adding adenylate residue at 3′ end is called tailing.

Three marks questions

7. **Explain the post transcriptional events in eukaryotes**

   Answer: (1) Cappins: An unusual nucleotide (methyl guanosine triphosphate) is added to 5′ end of hRNA

   (2) Tailing: Adenylated residues (200 - 300) are added at 3′ end of hnRNA

   (3) RNA splicing: The primary transcription has both exons and introns are removed and exons are joined by a process called splicing.

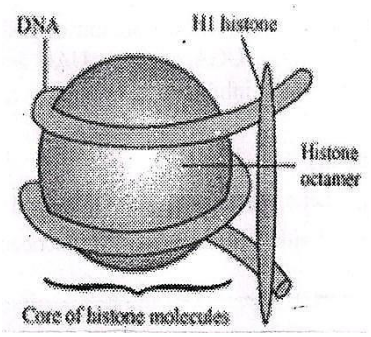
8. **List application of DNA finger techniques**

Answer: Application of DNA finger printing – is widely used in forensics since every DNA of every tissue from an individual has the same degree of polymorphism

- It forms the basis of paternity testing since a child inherits polymorphism from both its parents

9. **Explain the structure of Nucleosome.**

Answer: Nucleosome in a chromatin resembles beads presents on string. Beads on siting structural in chromatin are further packaged to form chromatin fibres, which further will and condense to form chromosomes during metaphase. Non – histone helps in packaging of chromatin at higher level

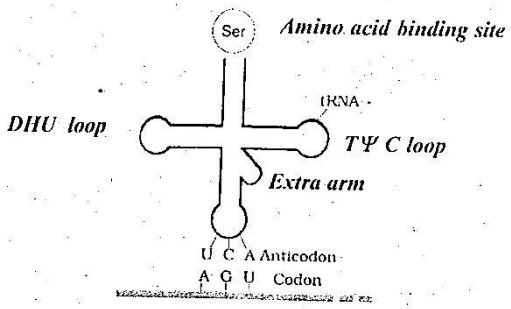


They have positively charged basic proteins called histone an octomer. and DNA that is negatively charged winds around the histone octomer (Positively charged) to form nucleosome.

Five marks questions

10. **With a neat labeled diagram. Explain –tRNA.**

Answer: structure of tRNA: It is found in the cytoplasm of the cell. It is called soluble RNA and is short. It is synthesized in the nucleus of a cell and constitutes about 15% to 20% of the total RNA According to R. Holly (1964) it has triclover leaf – like structure and for this invention he was awarded with noble prize. It consists of 3 loops (dihydroxy uridine nucleotide loop or DHU loop, pseudo uridine loop or TCG loop, and Anticodon loop) and 2 free arms one of the arms is a short arm. Which ends in 'G' and the long= arm ends in C–C–A. the activated amino acid gets attached to C–C–A end one of the loops, opposite the free arms, called acceptor anticodon recognises the codon of mRNA, as it is complementary to the latter, hence it also called recognition site. It helps in picking an amiono acid from cytoplasm and transforming them on the site of biosynthesis of protein.



Structure of t - RNA

11. **Explain the structure of waston and crick model of DNA**

Answer: In 1953 James waston and Francis crick based on X-ray diffraction data produced by Maurice Wilkins and Rosalind franklin, proposed a very simple but famous double Helix model for structure of DNA

(i) The backbone of DNA strand is composed of repeated units of sugar and phosphate molecules.

(ii) The pairing of nitrogenous bases are always between a specific purins and pyrimides that is between adenine and Thymine, Guanine and cytosine and vice versa. This type of base pairing is called complementary base pairing

(iii) Due to complementary base pairing the amount of purines and pyrmidies in DNA are equal the ratios between A and T, G and C are constant and equal to one

(iv) The bases in two strands are paired through hydrogen bond (H-bonds) forming base pairs (bp) there are 2 bonds between A and T and 3 bonds between G and C

(v) The two strands are coiled in right handed fashion

(vi) The pitch of the helix is 3.4 nm or 34 $A°$ and there are roughly 10 bp in each turn

(vii) Double stranded DNA molecule has a diameter of $20A°$ and distance between two successive base pairs is 0.34 nm $(3.4A°)$

(viii) The plane of one base pairs stacks over the other in double helix. This in addition to H – bonds confers stability of the helical structures. A = T and G ≡ C this is called chargaff's rule of base equivalence.

12. **Explain semi conservation replication of DNA**

Answer: The replication occurs during S-phase of Interphase during cell-cycle. The process of replication is proved qualitatively by J. Herbert Tayler and quantitatively by Meselson and stahl. Replication starts at specific region on the DNA called origin of replication. During replication the two strands of DNA unwind and separate due to breakage of H-bonds between them with the help of DNA unwinding enzyme helicase. The region in the ori site where replication begins appear like a 'Y' shaped configuration called replication fork RNA primer molecule which is complimentary to the DNA attaches to the old DNA strand (template) to provide by 3′ – OH ends for incoming nucleotides brought by DNA polymerase. DNA polymerase adds new nucleotides through base complementation since both the strands are antiparallel, DNA polymerase produces continuous stretches towards replication force (5′ – 3′ direction) called leading strand but due to opposite arrangements of nucleotides on the other strand discontinues steches of DNA fragments are formed called okazaki fragments, it is called the lagging strand. These fragments are later connected together by the enzyme DNA ligase.