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Q1: Fill in the Blanks.

- 1): **James Watson** and **Francis crick** discovered the double helical structure of the DNA molecule.
 - 2): Watson and crick were awarded Noble prize in **1962**.
 - 3): **Nucleic Acids** store, transmit, and help express hereditary information.
 - 4): The amino acid sequence of a polypeptide is programmed by a unit of inheritance called a **Gene**.
 - 5): Hundreds of Y shape regions of replicating DNA molecule where new stands are growing called **Replication Forks**.
 - 6): **Topoisomerase** are enzyme which relieves stress on the DNA molecule by allowing free rotation around a single strand.
 - 7): **Genetic code** is a dictionary that corresponds with sequence of nucleotides and sequence of amino acids.
 - 8): **Anti-codon** is the process of covalently attaching an amino acid to the tRNA .
 - 9): **Single-strand Binding proteins** are proteins which attach and help keep the separated strands apart.
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Q2: Write note on the following.

Ans:

- 1): **Common tools of molecular biology:**

- Nucleic acid fractionation
- Polymerase chain reaction
- Probes, Hybridization Vector, Molecular cloning Nucleic acid enzymes
Microarray
- DNA sequencing
- Electrophoretic separation of nucleic acid Detection of genes:
- DNA: Southern blotting; inSitu hybridization; FISH Technique
- *RNA: Northern blotting
- *Protein: Western blotting, immunohistochemistry

2): Nucleic Acid:

- Nucleic acids were first isolated by Friedrich Miescher (1869) from pus cells.
- They were named nucleon.
- Hertwig (1884) proposed nucleon to be the carrier of hereditary traits.
- Because of their acidic nature they were named nucleonic acids and then nucleic acids (Altmann, 1899).
- Nucleic acids store, transmit, and help express hereditary information
- The amino acid sequence of a polypeptide is programmed by a unit of inheritance called a gene
- Genes are made of DNA, a nucleic acid made of monomers called nucleotides.

3): Chargaff's rule:

- Adenine must pair with Thymine
- Guanine must pair with Cytosine
- Their amounts in a given DNA molecule will be about the same.

4): Wobble hypothesis:

- Crick postulated the 'wobble hypothesis' to account for the degeneracy of genetic code. According this hypothesis, the first two bases of a codon pair according to the normal base pairing rules with the last two base of the anticodon. Base-pairing at the third position of a codon is wobble.

5): Names of main steps in translation and transcription:

- 1): Initiation
 - 2): Elongation
 - 3): Termination
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Q3: Explain the process of DNA replication?

Ans:

DNA replication:

Origins of replication:

1. **Replication Forks:** hundreds of Y-shaped regions of replicating DNA molecules where new strands are growing.
2. **Replication Bubbles:** Hundreds of replicating bubbles (Eukaryotes). Single replication fork (bacteria).

Strand Separation:

1. **Helicase:** unwinding and separation (breaking H- Bonds) of the parental double helix.
2. **Single-Strand Binding Proteins:** proteins which attach and help keep the separated strands apart.
3. **Topoisomerase:** enzyme which relieves stress on the DNA molecule by allowing free rotation around a single strand.

Priming:

1. **RNA primers:** Before new DNA strands can form, there must be small pre-existing primers (RNA) present to start the addition of new nucleotides (DNA polymerase).
2. **Primase:** Enzyme that polymerizes (synthesizes) the RNA Primer.

Synthesis of the new DNA Strands:

1. **DNA polymerase:** with a RNA primer in place, DNA polymerase (enzyme) catalyze the synthesis of a new DNA strand in the 5' to 3' direction.
2. **Leading Strand:** synthesized as a single polymer in the 5' to 3' direction.

3. **Lagging Strand:** also synthesized in the 5' to 3' direction, but discontinuously against overall direction of replication.
4. **Okazaki Fragments:** series of short segments on the lagging strand.
5. **DNA ligase:** a linking enzyme that catalyzes the formation of a covalent bond from the 3' to 5' end of joining stands.
Example: joining two Okazaki fragments together.
6. **Proofreading:** initial base-pairing errors are usually corrected by DNA polymerase.

THE END