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**Semester: 4th Program: BS (MLT)**

**Instructor: Mr.Fazli Zahir Mian Subject: Molecular**

**Biology**

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**Question.1: 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.

**Question.2:** **Write note on the following.**

**Answer:**

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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**Answer:**

**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 preexisting 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.

1. **Proofreading**: initial base-pairing errors are usually corrected by DNA polymerase.

**THE END**