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BS MLT 4th semester

Molecular Biology

Mid-Term Assignment (Spring-2020) (BS-MLT 4th)

Course Title: Molecular Biology **Instructor: Mr. Fazli Zahir Mian**

Q1: Fill in the Blanks.

Answer

1. **James Watson & Francis crick**
2. **1962**
3. **Nucleic acid**
4. **Gene**
5. **Replication forks**
6. **Topoisomerase**
7. **Genetic code**
8. **Charging**
9. **Single strand binding proteins**

Q2: Write short notes on the following

1) Common tools of molecular biology

Following are the common tools of molecular biology

Nucleic acid fractionation

Polymerase chain reaction

Investigations, 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 acids

Nucleic acids were first insulated by Friedrich Miescher (1869) from pus cells.

They were named nuclein.

Hertwig (1884) anticipated nuclein to be the carter of genetic traits.

Because of their acidic nature they were named nucleinic acids then nucleic acids (Altmann, 1899).

Nucleic acids stock, convey, and help express hereditary information

The aminoalkanoic acid sequence of a polypeptide is programmed by a unit of inheritance called a gene

Genes are made from DNA, a macromolecule made from monomers called nucleotides

There are two types of nucleic acids

– Deoxyribonucleic acid (DNA)

– Ribonucleic acid (RNA)

3) Chargaff's rule

• Adenine must pair with Thymine

• Guanine must pair with Cytosine

• Their quantities in a particular DNA molecule will be approximately the same.

4) Wobble hypothesis

Crick (1996) proposed the 'wobble hypothesis' to elucidate the degeneracy of the ordering. Except for tryptophan and methionine, quite one codons direct the synthesis of 1 aminoalkanoic acid. There are 61codons that fusion amino acids, therefore, there must be 61 tRNAs each having different anticodons. But the total number of tRNAs is less than 61.

This may be explained that the anticodons of some tRNA read more than one codon. • Additionally identity of the third codon seems to be unimportant. For example CGU, CGC, CGA and CGG all code for arginine. It appears that CG specifies arginine and therefore the third letter isn't important

5) Names of main steps in Translation and Transcription

Translation is the final product of gene expression is a polypeptide chain of amino acids whose sequence was prescribed by the genetic code.

Steps in Translation

Initiation the 2 subunits of the ribosome close and therefore the start codon on the mRNA within the ribosome is aligned to line the reading frame

Elongation accused tRNAs attach and peptide bonds form between the amino acids

Termination could be a nucleotide triplet within messenger RNA that signs a termination of translation into proteins.

Transcription DNA-Directed RNA Synthesis

• Transcription has three phases:

Initiation: RNA polymerase recognizes and binds to a promoter sequence on DNA

Elongation: RNA polymerase elongates the nascent RNA molecule during a 5'-to-3' direction, antiparallel to the template DNA

Nucleotides are promote by complementary base pairing with the pattern strand

Termination: Special DNA sequences and protein assistants terminate transcription.

The transcription is released from the DNA.

This Primary Transcription is called the "pre- mRNA"

The pre-mRNA is managed to generate the mature mRNA

Q3: Explain the process of DNA Replication.

DNA a replication is means to produce new molecules that have the same base sequence

1 Origins of replication

Replication Forks: many 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:

Helicase: unwinding and separation

(Breaking H- Bonds) of the parental double helix.

Single-Strand Binding Proteins: proteins which confer and help preserve the separated strands apart.

Topoisomerase: enzyme which relieves stress on the DNA molecule by allowing free rotation around one strand.

Priming:

1. RNA primers: Before new DNA strands can practice, there must be small pre-existing primers (RNA) contemporary 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: produced as an only polymer in the 5’ to 3’ direction.

3. Lagging Strand: also synthesized within the 5’ to 3’ direction, but discontinuously against overall direction of replication.

4. Okazaki Fragments: sequence of short segments on the covering strand.

5. DNA ligase: An involving enzyme that catalyzes the creation of a covalent bond from the 3’ to 5’ end of joining stands.

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