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Open Book Test – July 23rd, 2025

Time = 1hr

Marks : 25 M

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1. What is the complementary base pairing rule in DNA? Provide an example. (2M)

Ans: The complementary base pairing rule in DNA states that adenine (A) pairs with thymine (T), and cytosine (C) pairs with guanine (G).

Example: If one strand has the sequence A-T-G-C, the complementary strand will be T-A-C-G.

2. Suppose a mutation causes a substitution of one base in a DNA strand. Analyze how this could affect the resulting protein. (2M)

Ans: A base substitution mutation can change the codon in mRNA, which may result in a different amino acid in the protein. This can affect the protein's structure and function.

3. Given a short sequence of DNA, how would you determine the complementary strand? What structural rules must be followed? (2M)

Ans: To find the complementary strand, match each base with its pair: A with T, and C with G.

Rule: The strands must run in opposite directions (antiparallel) and follow base pairing rules.

4. What were the primary goals of the Human Genome Project, and how did its completion redefine our understanding of the human genome? (2M)

Ans: The main goals were to map all human genes and sequence the entire DNA.

Impact: It revealed that humans have fewer genes than expected and helped in identifying genes linked to diseases.

5. Critically assess the statement: “The Human Genome Project was a starting point, not a conclusion.” (2M)

Ans: The Human Genome Project (HGP) successfully mapped the entire human DNA sequence, but that was only the beginning. It gave scientists a reference to study how genes function, how they are regulated, and how they contribute to diseases. Much work was still needed to understand the complexity of gene interactions, making the HGP a foundation for future research.

6. When searching for a gene in NCBI Gene (e.g., BRCA1), what types of information are typically available on the gene's summary page? (2M)

Ans: The NCBI Gene summary page provides information such as the gene's full name, function, location on the chromosome, and associated diseases. It also includes gene sequences, expression patterns, and links to related research articles.

7. Discuss the role of the ribosome in translation. (2M)

Ans: The ribosome is the site of protein synthesis. It reads the mRNA sequence in codons and matches them with the correct tRNA carrying amino acids. It links amino acids together to form a polypeptide chain during translation.

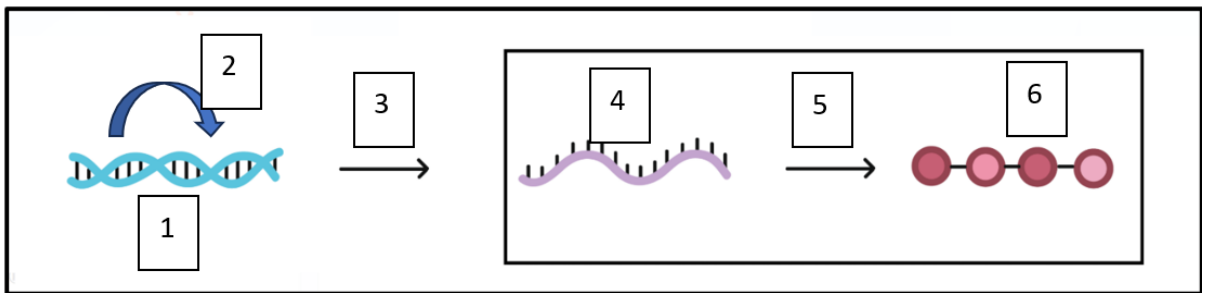
8. Compare mitosis and meiosis in terms of genetic variability, purpose, and end products. (2M)

Ans: Mitosis produces two identical cells for growth and repair, with no genetic variation. Meiosis produces four genetically different cells (gametes) for reproduction, increasing genetic diversity.

9. Given the command `fastq-dump --split-files --gzip SRR1234567`, analyze what this does and when it would be necessary. (2M)

Ans: This command downloads the sequencing data for SRR1234567 from the SRA database, splits paired-end reads into two separate files (one for each read direction), and compresses them using gzip. It's used when working with paired-end RNA or DNA sequencing data.

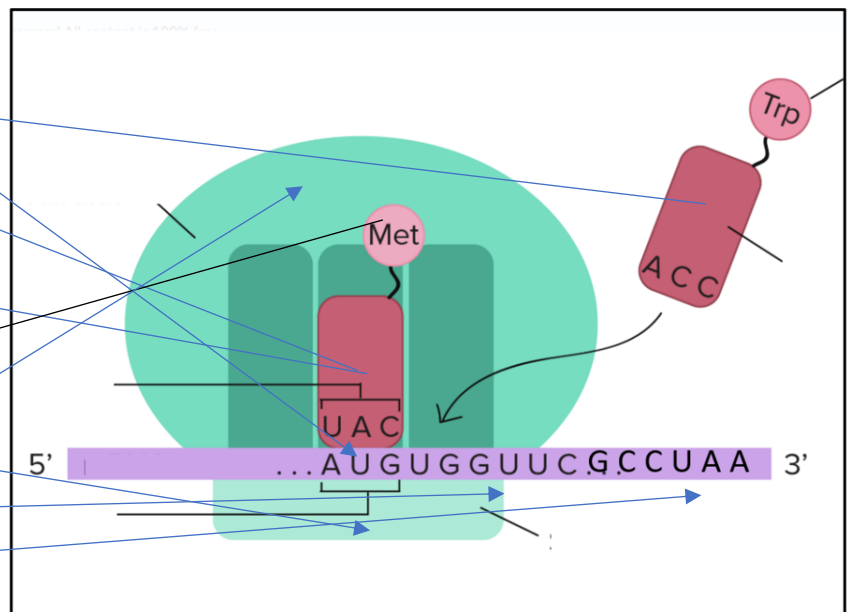
10. Fill in the steps of the Central dogma of Molecular Biology (2M)



1. DNA
2. Transcription
3. mRNA
4. Translation
5. Polypeptide
6. Protein

11. Match the following terms to the steps on the diagram (5M)

- a) Start codon
- b) Ribosomal A site
- c) Ribosomal P site
- d) Ribosomal E site
- e) tRNA anticodon
- f) Growing polypeptide chain
- g) Large ribosomal subunit
- h) Small ribosomal subunit
- i) mRNA strand
- j) Stop codon



- a) Start codon – **AUG**
- b) Ribosomal A site – **ACC**
- c) Ribosomal P site – **UAC**
- d) Ribosomal E site – **(empty left site)**
- e) tRNA anticodon – **UAC**
- f) Growing polypeptide chain – **Met**
- g) Large ribosomal subunit – **(top green part)**
- h) Small ribosomal subunit – **(bottom green part)**
- i) mRNA strand – **...AUGGUUUCGCCUAA...**
- j) Stop codon – **UAA**

