



**RAJARATA UNIVERSITY OF SRI LANKA
FACULTY OF APPLIED SCIENCES, MIHINTALE.**

**B.Sc. (General) Degree in Applied Sciences
Third year – Semester I Examination – Oct /Nov 2015**

BOT 3104 – MOLECULAR BIOLOGY

Time: One and half hours

Part A

Underline the correct answer.

1. Which is the energy rich molecule required for initiation of translation?
 - (a) ATP
 - (b) GTP
 - (c) CTP
 - (d) AMP
2. The incorrect match is,
 - (a) initiation codon: 5'-AUG-3', 5'-GUG-3', 5'-UUG-3'
 - (b) GTP: energy source for elongation phase of translation
 - (c) 16S rRNA: located in the large sub unit of the ribosome
 - (d) Shine-Dalgarno sequence: ribosome binding site of bacteria
3. Which hydrogen bonds have been found to stabilize a polypeptide's folded shape?
 - I. **Hydrogen bonds between side chain atoms**
 - II. **Hydrogen bonds between backbone atoms**
 - III. **Hydrogen bonds between backbone atoms and side chain atoms**
 - (a) statement I only
 - (b) statement II only
 - (c) statement I and III only
 - (d) all of the above

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4. Which of the following statements about RNA splicing is **NOT** correct?
 - (a) Some introns can splice themselves out
 - (b) Splicing is required for some tRNAs
 - (c) The final step of splicing is formation of a phosphodiester linkage
 - (d) Introns often have a specific function after they are removed

5. What does the term 'protein domain' refer to?
 - (a) A region in the cell where a protein can be found
 - (b) A segment of a protein that can fold independently into its own compact 3D structure
 - (c) The functional activity of a protein
 - (d) The region in a protein that determines how it folds into a 3D structure

6. Tetracycline prevents protein synthesis by,
 - (a) preventing release of EF-G-GDP from the ribosome
 - (b) inhibiting peptidyl transferase
 - (c) inhibiting binding of aminoacyl tRNA to ribosome
 - (d) preventing translocation of A-site tRNA to P-site

7. Why are α helices and β sheets common folding patterns in polypeptides?
 - (a) The unique amino acid sequences that generate these folding patterns are common in polypeptides
 - (b) Molecular chaperones tend to fold polypeptides in these common folding patterns
 - (c) Amino acid side chains are not involved in forming the hydrogen bonds, allowing many different sequences to adopt these folding patterns
 - (d) All of the above

8. What is the eventual fate of an intron sequence after its excision from mRNA?
 - (a) It forms a foldback RNA around the lariat structure
 - (b) It combines with a protein complex to form small nuclear ribonucleoproteins (snRNPs)
 - (c) It is converted to linear RNA and is subsequently degraded by ribonucleases
 - (d) It is transported to the cytoplasm with the aid of the spliceosome

9. When the ribosome reaches a stop codon on the mRNA, no corresponding tRNA enters the A site. If the translation reaction were to be experimentally stopped at this point, which of the following would you be able to isolate?
 - (a) An assembled ribosome with a polypeptide attached to the tRNA in the P site
 - (b) Separated ribosomal subunits, a polypeptide and free tRNA
 - (c) An assembled ribosome with a separated polypeptide
 - (d) Separated ribosomal subunits with a polypeptide attached to the tRNA in the P site

10. In a particular bacterium, a mutation causes lower virulence. This mutation is in the middle of the gene that codes for the toxin which the bacterium produces. The normal and mutated mRNAs made from this sequence are both normal size, but the mutated protein is shorter in sequence length and less damaging to human cells. A student hypothesised following probable causes for the mutation.

- I. Deletion of 2 bases causing a frame shift**
- II. Single base change resulting in one amino acid change**
- III. Single base change causing a premature stop codon**
- IV. The mRNA has several large introns**
- V. The mutation affected a splice site, leading to alternative splicing and removing an exon**

From the above statements what type of mutation/s would be the likely cause of the mutated protein?

- (a) I and II only
 - (b) III and V only
 - (c) I, II and IV only
 - (d) All of the above
11. Which of the following is correct in terms of bond energy?
- (a) Covalent > Hydrogen > Ionic > van der Waals forces
 - (b) Covalent > Ionic > van der Waals forces > Hydrogen
 - (c) Ionic > Covalent > Hydrogen > van der Waals forces
 - (d) Covalent > Ionic > hydrogen > van der Waals forces
12. Which of the following is incorrect?
- (a) Frederick Griffith : bacterial transformation
 - (b) Oswald T. Avery and colleagues: proved that the active genetic material is DNA
 - (c) Ernest Haeckel : Demonstrated cell free DNA synthesis
 - (d) Matthew Meselson and Franklin Stahl : Model for DNA replication
13. Function of gyrase is to;
- (a) synthesize the RNA primer
 - (b) introduce negative supercoiling
 - (c) sealing nicks
 - (d) filling the gaps
14. Which of the following does not contribute to prokaryotic DNA replication?
- (a) Dna B
 - (b) Dna A
 - (c) DNA polymerase III
 - (d) DNA polymerase δ

15. Which of the following has both high fidelity and high processivity?
- (a) DNA polymerase α
 - (b) DNA polymerase β
 - (c) DNA polymerase δ
 - (d) All of the above
16. Which of the following is correct?
- (a) Eukaryotic DNA replication involves a single replicon
 - (b) DNA polymerase III is faster than its eukaryotic counterpart
 - (c) End replication problem is found in circular DNA
 - (d) Telomerase is the only method by which end replication problem is rectified
17. Which of the following is not a constituent of the prokaryotic promoter?
- (a) Pribnow box
 - (b) -35 sequence
 - (c) CAAT box
 - (d) Distance between -10 and -35
18. Which of the following is correct?
- (a) Sense mRNA is synthesized using the antisense DNA strand
 - (b) Sense mRNA is identical (except U instead of T) to template DNA strand
 - (c) Sense mRNA is complementary to sense DNA strand
 - (d) Anti sense mRNA is identical to coding DNA strand
19. Prokaryotic transcription ;
- (a) is not spatially separated from translation
 - (b) is carried out by a single RNA Polymerase
 - (c) involves σ factor based recognition of promoters
 - (d) consists of all of the above
20. Which of the following is not a post transcriptional modification in eukaryotes?
- (a) Methylation of cytosines
 - (b) Poly adenylation
 - (c) Cap formation
 - (d) Splicing

(30 marks)

Part B (I) –**Answer all questions.****1) a. Briefly state the role of snRNPs in RNA splicing.**

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b. Given that out of the 64 codons of mRNA, 61 codify amino acids that form polypeptide chains, list the functions of the three remaining.

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2) a. Briefly explain the need for DNA repair

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b. List common forms of DNA damage

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(30 marks)

Part B (II)

Answer one (1) question only.

Use labelled diagrams where appropriate

- 1)
 - a. Describe the structure of the prokaryotic RNA polymerase, clearly indicating the importance of each sub unit.
 - b. Even though there are plenty of rNTPs in the vicinity, explain why is that they never get incorporated into the growing DNA strands during DNA synthesis.
 - c. Illustrate the mechanism of rho dependent transcription termination.

- 2)
 - a. Depict the striking aspects of the adaptor molecule between the codons and amino acids in facilitating the translation, with reference to its secondary structure.
 - b. "The dissimilarity of prokaryotic and eukaryotic mRNA and ribosomes, results in distinctly different means of accomplishing the initiation of translation".
Would you abide with this statement? Explain your views of this assertion.

(40 marks)