



CSIR-UGC-NET/JRF LIFE SCIENCES

TEST : MOLECULAR BIOLOGY

Time : 45 Minutes

Date : 13-05-2018

M.M. : 36

INSTRUCTION:

1. There are Two Parts. **Part-B** contains 6 objective type questions, each question carry 2 marks and **Part-C** contains 6 objective type questions, each question carry 4 marks.
2. There is negative marking, @ 25% will be deducted for each wrong answer.
3. Attempt all the questions, use of calculator is not allowed.

PART-B

1. Histone deacetylase (HDAC) catalyses the removal of acetyl group from N-terminal of histones. Which amino acid of histone is involved in this process?
 - (a) Lysine
 - (b) Arginine
 - (c) Asparagine
 - (d) Histidine
2. Attenuation is a mechanism involved in the regulation of tryptophan operon in *E. coli*. When tryptophan levels are high in the cell, region 2 of the *trpL* is blocked from pairing with region (c) This allows the pairing of region 3 and 4 leading to the formation a rho-independent termination. What would be the structure of the *trpL* region in *E. coli* cells where protein synthesis has been inhibited?
 - (a) Region 2 pairs with region 3 allowing transcription of the structural genes.
 - (b) Region 1 and 2 will pair, allowing 3 and 4 to pair leading to attenuation.
 - (c) There is no pairing in the *trpL* region and transcription of structural gene occurs.
 - (d) Region 2 and 3 will pair leading to attenuation.
3. In context to lac operon, if two bacterial strains P1, and P2 with the genotypes $O^+I^+Z^-$ and $O^+I^-Z^+$ respectively, were used to produce mero-diploid daughter strain D, which one of the following statements correctly predicts the expression of Z gene (β -galactosidase activity) in all the three strains? (O^+ , I^+ and Z^+ denote the wild type allele of the respective genes).
 - (a) P1 - No expression; P2 - constitutive expression; D - Inducible expression.
 - (b) P1 - No expression; P2 - constitutive expression; D - constitutive expression.
 - (c) P1 - No expression; P2 - Inducible expression; D - Inducible expression.
 - (d) P1 - Inducible expression; P2 - constitutive expression; D - Inducible expression.
4. Which of the following is responsible for the first step of the proof-reading during protein synthesis in *E. coli*?
 - (a) Initiation factor IF-2
 - (b) Elongation factor EF-Tu
 - (c) Aminoacyl tRNA synthetase
 - (d) Small subunit (30 S) of ribosome



5. In prokaryotes IF2 binds to
 (a) Initiator tRNA and GTP (b) Aminoacyl tRNA and ATP
 (c) Ribosome and mRNA (d) mRNA and 30 S subunit of ribosome
6. The U2 snRNA basepairs with
 (a) a sequence spanning the exon intron splicing site
 (b) the 3' splice site of the intron
 (c) a sequence spanning the intron exon splicing site
 (d) the branched sequence in the intron

PART-C

7. Match the terms in Group I with their associated functions in Group II.
- | Group I | Group II |
|------------------------------|--|
| P. Shine-Dalgarno sequences | 1. Aminoacylation of tRNA |
| Q. Leucine zipper | 2. Gene silencing |
| R. Aminoacyl tRNA synthetase | 3. Ribosome binding and facilitation of translation initiation |
| S. RNA interference (RNAi) | 4. Transcription factors |
| (a) P-3, Q-4, R-1, S-2 | (b) P-4, Q-3, R-2, S-1 |
| (c) P-2, Q-3, R-1, S-4 | (d) P-3, Q-2, R-4, S-1 |
8. Which one of the following statements about eukaryotic translation is NOT true ? In eukaryotic translation.
 (a) ribosome binding site on mRNA is called Kozak consensus sequences.
 (b) initiator tRNA is $tRNA_i^{f-met}$
 (c) initiator amino acid is methionine
 (d) translocation factor is eEF2
9. Aminoacyl-tRNA synthetases are very specific for aminoacylation of tRNAs with the correct cognate amino acids. However, there is a possibility of a mismatch between the tRNA and its cognate amino acid. This error is corrected by the inherent proof-reading activity of the aminoacyl-tRNA, synthetase. In case of two very similar amino acids, namely valine and isoleucine, isoleucyl-tRNA synthetase employs the following possible approaches for an error free aminoacylation
- It removes an incorrect amino acid by hydrolyzing the aminoacyl-AMP linkage following first reaction step.
 - It is activated for proof-reading activity, leading to breakage of the bond between the wrong amino acid and tRNA.
 - It has an intrinsic ability to recognize the structural difference between amino acids leading to abortive elimination of the non-cognate amino acid.
 - It gets sequestered in the second step with the wrong amino acid, and that freezes the aminoacylation process.
- Which of the following combinations is correct?
 (a) A and B (b) A and D (c) B and D (d) C and D
10. In recent years, genome-wide transcription study using high throughput sequence analysis has revealed some novel results that include:
 (i) presence of RNA polymerase in both intra- and intergenic regions of the genome
 (ii) existence of non-coding RNAs generated from mRNA coding genes.



- (iii) existence of sense and antisense transcripts generated from the promoter and untranslated region of many annotated genes.

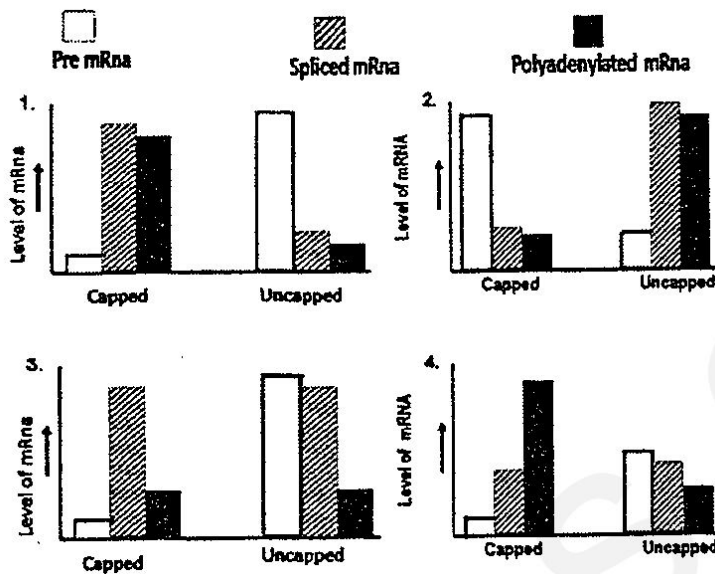
Possible interpretation of the above results are:

- RNA polymerase can loosely bind to any part of the genome but its affinity becomes strong only when it reaches the promoter.
- Binding of RNA polymerase to non-promoter regions of the genome leads to the generation of various non-coding regulatory RNAs.
- Non-coding RNAs are generated from mRNA coding genes due to aberrant transcription initiation and termination.
- Sense and antisense transcripts are generated from the promoter and untranslated regions of protein coding genes by a novel mechanism of bidirectional transcription.

Identify the correct combination of the above interpretations:

- (a) A and B (b) B and D (c) A and D (d) B and C

11. You are working with an *in vitro* eukaryotic transcription system, which produced both capped and uncapped mRNAs. You incubated these mRNAs with mammalian cell nuclear extract and then quantified the different products as shown below. Which of the following graphs correctly represents the expected result?



12. During elongation step of protein synthesis, translocation moves the mRNA and the peptidyl t-RNA by one codon through the ribosome. Translocation in *E. coli* involves GTP and EF-G. However, *in vitro* translocation can take place independent of GTP and EF-G. Based on these observations, the following hypotheses can be made:

- The molecular mechanism of translocation *in vitro* is completely different from that *in vivo*.
- Translocation activity is independent of GTP hydrolysis.
- Translocation activity is completely dependent on GTP and EF-G.
- Translocation activity is inherent in ribosomes, however, the rate of translocation *in vivo* is enhanced significantly in presence of GTP and EF-G.

Which one of the following combinations is correct?

- (a) only (D) (b) (A) and (C) (c) (A) and (B) (d) (C) and (D)





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[ANSWERS]

PART-B

1. (a) 2. (b) 3. (a) 4. (c) 5. (a) 6. (d)

PART-C

7. (a) 8. (b) 9. (d) 10. (c) 11. (a) 12. (a)



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