Library

INDIAN INSTITUTE OF TECHNOLOGY KHARAGPUR
Mid-Spring Semester 2017-18

Date of Examination: 27/02/2018 _____ Session (FN/AN): FN ____Duration: 2 hrs Full Marks: 60
Subject No.: BS20001_____ Subject: Science of Living System
Department/Center/School: School of Bioscience
Specific charts, graph paper, log book etc., required: None
Special Instructions (if any): None

Write down the (ONE) correct answer in your answer script. Each question carries one mark only. [20 marks]

1. _____ is an operational nucleic acid, whereas _____ is strictly an informational nucleic acid.

2. In Griffith's experiment, it was shown that _____ from smooth strain bacteria caused rough strain bacteria to be transformed.

3. Tetracycline inhibits
(A) cell wall synthesis (B) DNA synthesis
(C) RNA synthesis (D) protein synthesis

4. In *lac* operon, if you remove the *lac* operator (the repressor binding site), what will be the effect on the metabolic state of the bacteria?
(A) Lactose metabolizing enzymes will be produced irrespective of the presence or absence of lactose
(B) Glucose metabolism will be blocked
(C) Lactose will never be metabolized because the enzymes will never be synthesized
(D) RNA Polymerase will not be able to bind the promoter

5. Anti-codon is present in
(A) tRNA (B) mRNA
(C) DNA (D) rRNA

6. Protein secondary structures are stabilized primarily by
(A) hydrogen bonds (B) van der Waal's forces
(C) electrostatic interactions (D) amino acid sidechains

7. If you run 35 cycles of PCR, by what factor does the target sequence theoretically increase?

8. State TRUE or FALSE for the following statements:
(A) 5' end of nascent eukaryotic mRNA acquires a poly-A tail
(B) Splicing removes introns from eukaryotic transcripts

9. Metal ions such as Na^+, K^+ and Mg^{2+} interact with the following of DNA
(A) Nitrogenous base (B) Phosphate group (C) Sugar group (D) All of the above

10. Which of the following polymerases DOES NOT require a template sequence?
(A) DNA polymerase (B) RNA polymerase
(C) Taq polymerase (D) Poly-A polymerase

11. In order to conclude a forensic investigation using DNA sample, a forensic lab must have _____ and _____ facilities.

P.T.O.

12. Arrange the following in the increasing order of protein structure hierarchy:

a: α-helix b: amino acid sequence c: quaternary structure d: folded structure

(A) a, d, c, b (B) a, d, b, c (C) b, a, d, c (D) b, a, c, d

13. The rate of protein synthesis in prokaryote is limited by the rate of mRNA synthesis. If mRNA synthesis occurs at the rate of 51 nucleotides/sec, then the rate of protein synthesis occurs at:

(A) 12 amino acids/sec (B) 17 amino acids/sec
(C) 25 amino acids/sec (D) 50 amino acids/sec

14. If the genetic code is constructed following a new rule where pairs of nucleotides are used as codons, instead of triplets. How many different amino acids would such a code specify?

(A) 8 (B) 16 (C) 32 (D) 64

15. _____ is the only genetically encoded amino acid without a stereo isomer.

16. How many turns will be there in an 18 amino acid long α-helix?

17. Which of the following is an example of tertiary structure in a protein?

(A) A multimeric (multi-subunit) protein (B) An α-helix
(C) A β-pleated sheet (D) A globular domain

18. RNA required for protein synthesis is:

(A) mRNA (B) rRNA (C) tRNA (D) all of these

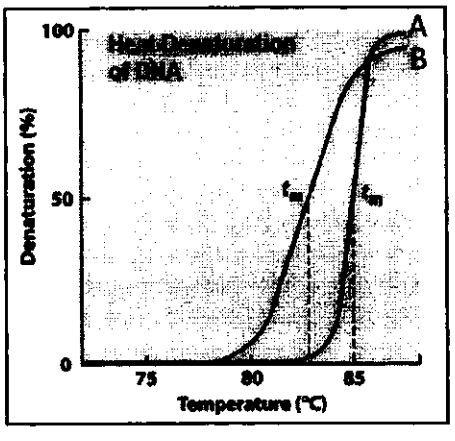
19. When both Cα atoms are on the same side of a peptide bond, it is called a _____ isomer.

20. Theoretically, a vast number of different proteins can be assembled from 20 different amino acids. How many polypeptide chains are possible that are 10 amino acids long?

(A) 20 X 10 (B) 20^{10} (C) 10^{20} (D) 20^{10} X 10^{20}

Answer the following questions briefly: **[40 marks]**

2. (a) The diagram on the right represents heat denaturation curves of nucleic acids. State the difference between sample A and B (both are double stranded DNA samples) in terms of their base composition and explain your answer. **[2]**

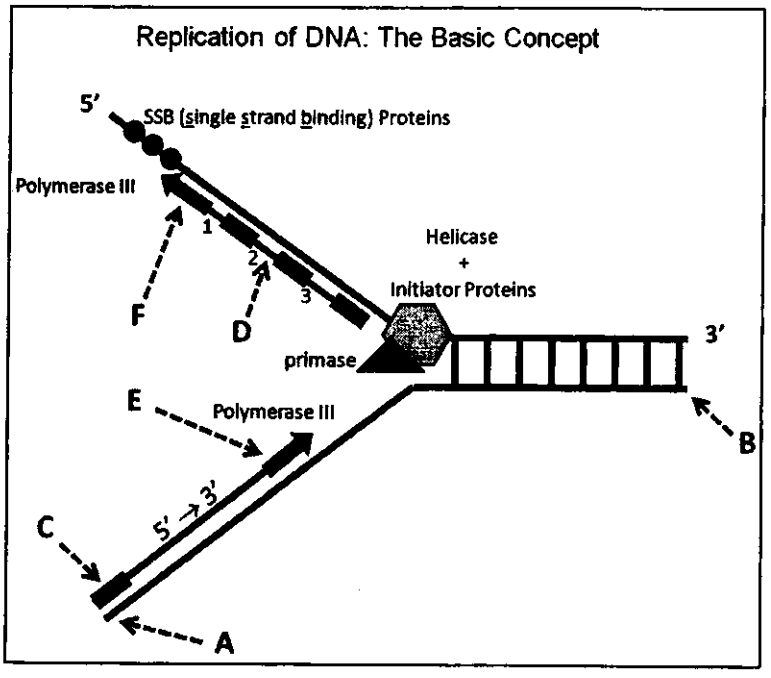


(b) Explain why RNA is unstable compared to DNA. **[1]**

P.T.O.

(c) The diagram on the right depicts the process of replication. Label each of these letters (i.e. **A** to **F**) from the following list (each option will be used only ONCE): **[3]**

(i) DNA primer
(ii) RNA primer
(iii) Leading strand
(iv) 5' end
(v) 3' end
(vi) Lagging strand
(vii) Polymerase I
(viii) Okazaki fragment
(ix) Ligase
(x) Topo-isomerase



(d) Suppose we assign numerical values to each nucleotide base as follows:
A: 0; T: 1; G: 2; C: 3

In that case, the DNA sequence 5'-TATA-3' will have a numerical value of 68 (in base 10).

Now, convert the following DNA sequence to their numerical value in base 10 (show calculation): **[2]**
5' TCCGAG 3'

3. (a) Why Polymerase Chain Reaction (PCR) requires thermo-stable DNA polymerase (for example Taq polymerase)? **[2]**

(b) During Sanger Sequencing method, the ratio of ddNTP : dNTP is kept at 1:100. Explain your answer. **[2]**

(c) Result from a Sanger sequencing experiment shows that the sense strand (coding strand) sequence is as following:
5' TGCAACCG 3'.
Sketch the gel pattern that would lead to this conclusion. **[2]**

(d) A compact disc (CD) stores about 4.8×10^9 bits of information in a 96 cm^2 area. This information is stored as a binary code - that is, every bit is either a 0 or a 1. **[2]**
(i) How many bits would it take to specify each nucleotide in a DNA sequence?
(ii) How many CDs would it take to store the information contained in the human genome (genome size: 3×10^9 nucleotides)?

4. (a) The following sequence represents coding strand (also known as sense strand) of a gene:
5'ATGACCGTTCGTAAAATAGCGATC 3'

(i) What will be the mRNA sequence if this gene is being transcribed? **[2]**
(ii) How many codons should be present in this mRNA? **[2]**
(iii) If the whole mRNA gets translated, how many amino acids and peptide bonds should be present in the translated product? **[2]**

P.T.O.

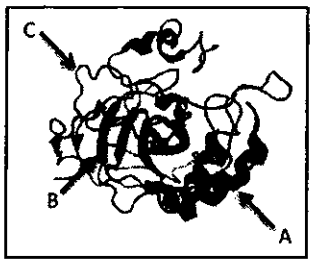
(b) Match the following: [2]

Ribosome	Termination of transcription
RNA hair-pin	Splicing
Intron	Recognition of codon
tRNA	Translation

5. (a) Draw the structure of a dipeptide. You can show their side chains as R1 and R2 and indicate the following: [2+1+1.5]

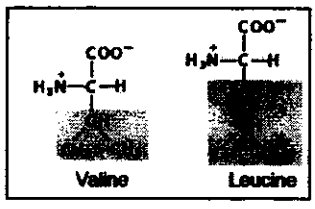
(i) peptide bond
(ii) phi, psi and omega angles

(b) The shape of hair is determined in part by the pattern of disulfide bonds in keratin, its major protein. How can curls be induced? [2]



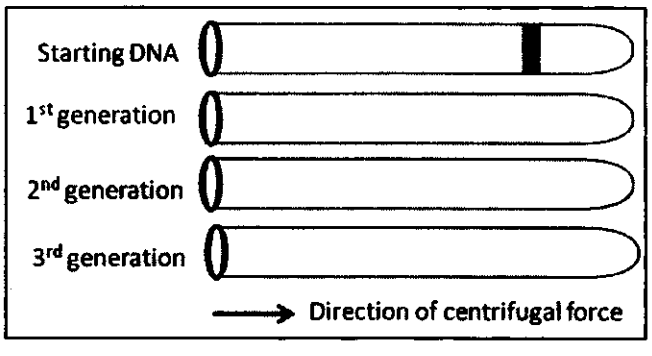
(c) Identify the secondary structural elements (A, B and C) from the protein structure on the left. [1.5]

6. (a) Would you expect to find a segment of a protein with Val-Leu-Leu-Val sequence at the core or at the surface of a globular protein? Justify your answer. Structures of these two amino acids are shown in the right. [3]



(b) Protein structure is determined by the protein's amino acid sequence. Should a protein in which the original order of all amino acids is reversed have the same structure as the original protein? [2]

(c) In order to understand the process of replication, bacterial cells were grown in the presence of heavy nitrogen (^{15}N-isotope) until all the DNA contained the heavy form of nitrogen (this is your starting DNA). These bacteria were then transferred to a medium that only contained the light form of nitrogen (^{14}N-isotope). At different time points, DNA was isolated from the bacteria and subjected to density gradient ultracentrifugation.



Indicate the location of the DNA band(s) after 1st generation, after 2nd generation and after 3rd generation using 3 test tubes as shown in the diagram. Location of DNA at the beginning of experiment is shown in the top most tube. [3]