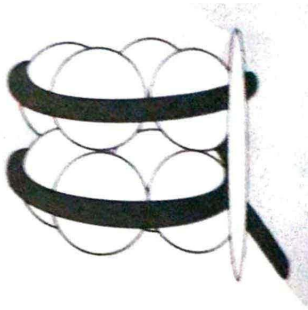
CHAPTER



5 Molecular Basis of Inheritance

5.1. The DNA

1. Match List-I with List-II:

List-I	List-II
(a) Histones	(i) Loosely packed chromatin
(b) Nucleosome	(ii) Densely packed chromatin
(c) Euchromatin	(iii) Positively charged basic proteins
(d) Heterochromatin	(iv) DNA wrapped around histone octamer

Choose the correct answer from the options given below:

	(a)	(b)	(c)	(d)
(A)	(iv)	(iii)	(ii)	(i)
(B)	(iii)	(i)	(iv)	(ii)
(C)	(ii)	(iii)	(iv)	(i)
(D)	(iii)	(iv)	(i)	(ii)

[Re-NEET 2024]

2. Given below are two statements:

Statement I: In prokaryotes, the positively charged DNA is held with some negatively charged proteins in a region called nucleoid.

Statement II: In eukaryotes, the negatively charged DNA is wrapped around the positively charged histone octamer to form nucleosome.

In the light of the above statements, choose the correct answer from the options given below:

(A) Statement I is correct but Statement II is false.
(B) Statement I is incorrect but Statement II is true.
(C) Both Statement I and Statement II are true.
(D) Both Statement I and Statement II are false.

[NEET 2023]

3. Read the following statements and choose the set of correct statements.

(I) Euchromatin is loosely packed chromatin.
(II) Heterochromatin is transcriptionally active.
(III) Histone octamer is wrapped by negatively charged DNA in nucleosome.
(IV) Histones are rich in lysine and arginine.
(V) A typical nucleosome contains 400 bp of DNA helix.

Choose the correct answer from the options given below.

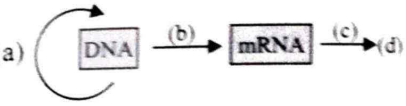
(A) (I), (III) and (IV) (B) (II) and (V)
(C) (I), (III) and (V) (D) (II), (IV) and (V)

[NEET 2022]

4. If the length of a DNA molecule is 1.1 metres, what will be the approximate number of base pairs?

(A) 6.6×10^9 bp (B) 3.3×10^6 bp
(B) 6.6×10^6 bp (D) 3.3×10^9 bp **[NEET 2022]**

5. Complete the flow chart on central dogma.



(A) (a)-Replication; (b)-Transcription; (c)-Transduction; (d)-Protein
(B) (a)-Translation; (b)-Replication; (c)-Transcription; (b)-Transduction
(C) (a)-Replication; (b)-Transcription; (c)-Translation; (d)-Protein
(D) (a)-Transduction; (b)-Translation; (c)-Replication; (d)-Protein **[NEET 2021]**

6. If Adenine makes 30% of the DNA molecule, what will be the percentage of Thymine, Guanine and Cytosine in it?

(A) T : 20 ; G : 30 ; C : 20
(B) T : 20 ; G : 20 ; C : 30
(C) T : 30 ; G : 20 ; C : 20
(D) T : 20 ; G : 25 ; C : 25 **[NEET 2021]**

7. Which one of the following statement about histones is wrong?

(A) The pH of histones is slightly acidic.
(B) Histones are rich in amino acids lysine and arginine.
(C) Histones are organized to form a unit of 8 molecules.
(D) Histones carry positive charge in the side chain.

[NEET 2021]

8. *E. coli* has only 4.6×10^6 base pairs and completes the process of replication within 18 minutes, then the average rate of polymerisation is approximately:

(A) 2000 bp/s (B) 3000 bp/s
(C) 4000 bp/s (D) 1000 bp/s

[NEET Oct. 2020]

9. The term 'Nuclein' for the genetic material was used by:

(A) Franklin (B) Miescher
(C) Chargaff (D) Mendel. **[NEET Oct. 2020]**

10. If the distance between two consecutive base pairs is 0.34 nm and the total number of base pairs of a DNA double helix in a typical mammalian cell is 6.6×10^9 bp, then the length of the DNA is approximately:

(A) 2.5 meters (B) 2.2 meters

(C) 2.7 meters (D) 2.0 meters.

[NEET Sept. 2020]

11. Which of the following statements is correct?

(A) Adenine pairs with thymine through one H-bond.

(B) Adenine pairs with thymine through three H-bonds.

(C) Adenine does not pair with thymine.

(D) Adenine pairs with thymine through two H-bonds.

[NEET Sept. 2020]

12. Purines found both in DNA and RNA are:

(A) guanine and cytosine

(B) cytosine and thymine

(C) adenine and thymine

(D) adenine and guanine **[NEET National 2019]**

13. DNA fragments are:

(A) positively charged

(B) negatively charged

(C) neutral

(D) either positively or negatively charged depending on their size. **[NEET 2017]**

14. The association of histone H_1 with a nucleosome indicates:

(A) transcription is occurring

(B) DNA replication is occurring

(C) the DNA is condensed into chromatin fibre

(D) the DNA double helix is exposed. **[NEET 2017]**

15. In sea urchin DNA, which is double stranded 17% of the bases were shown to be cytosine. The percentages of the other three bases expected to be present in this DNA are:

(A) G/34%, A/24.5%, T/24.5%

(B) G/17%, A/16.5%, T/32.5%

(C) G/17%, A/33%, T/33%

(D) G/8.5%, A/50%, T/24.5%.

[AIPMT Cancelled 2015]

16. Which one of the following is not applicable to RNA?

(A) Complementary base pairing

(B) 5' phosphoryl and 3' hydroxyl ends

(C) Heterocyclic nitrogenous bases

(D) Chargaff's rule **[AIPMT Latest July 2015]**

17. Identify the correct order of organisation of genetic material from largest to smallest.

(A) Chromosome, gene, genome, nucleotide

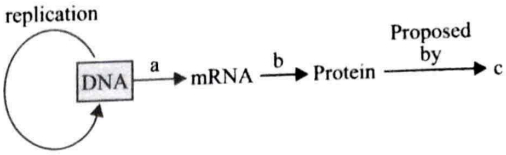
(B) Genome, chromosome, nucleotide, gene

(C) Genome, chromosome, gene, nucleotide

(D) Chromosome, genome, nucleotide, gene

[AIPMT Latest July 2015]

18. The diagram shows an important concept in the genetic implication of DNA. Fill in the blanks a to c.



(A) a-transcription, b-replication, c-James Watson

(B) a-translation, b-transcription, c-Erwin Chargaff

(C) a-transcription, b-translation, c-Francis Crick

(D) a-translation, b-extension, c-Rosalind Franklin

[NEET 2013]

19. What are the structures called that give an appearance as 'beads on string' in the chromosomes when viewed under electron microscope?

(A) Nucleosomes (B) Genes

(C) Base pairs (D) Nucleotides

[AIPMT 2011]

20. Which one of the following does not follow the central dogma of molecular biology?

(A) Pea

(B) *Mucor*

(C) *Chlamydomonas*

(D) HIV **[AIPMT Screening 2010]**

21. The 3'-5' phosphodiester linkages inside a polynucleotide chain serve to join:

(A) one DNA strand with the other DNA strand

(B) one nucleoside with another nucleoside

(C) one nucleotide with another nucleotide

(D) one nitrogenous base with pentose sugar.

[AIPMT Mains 2010]

22. In the DNA molecule

(A) the total amount of purine nucleotides and pyrimidine nucleotides is not always equal

(B) there are two strands, which run parallel in the 5′→3′ direction

(C) the proportion of adenine in relation to thymine varies with the organism

(D) there are two strands, which run anti parallel-one in 5′→3′ direction and other in 3′→5′.

[AIPMT Screening 2008]

23. The length of DNA molecule greatly exceeds the dimensions of the nucleus in eukaryotic cells. How is this DNA accommodated?
(A) Super-coiling in nucleosomes
(B) DNase digestion
(C) Through elimination of repetitive DNA
(D) Deletion of non-essential genes. **[AIPMT 2007]**

24. The two polynucleotide chains in DNA are:
(A) discontinuous (B) antiparallel
(C) semiconservative (D) parallel. **[AIPMT 2007]**

25. One turn of the helix in a B-form DNA is approximately:
(A) 2 nm (B) 20 nm
(C) 0.34 nm (D) 3.4 nm. **[AIPMT 2006]**

26. Antiparallel strands of a DNA molecule means that:
(A) one strand turns clockwise
(B) one strand turns anti-clockwise
(C) the phosphate groups of two DNA strands, at their ends, share the same position
(D) the phosphate groups at the start of two DNA strands are in opposite position (pole). **[AIPMT 2006]**

27. Which one of the following makes use of RNA template to synthesize DNA?
(A) DNA polymerase
(B) RNA polymerase
(C) Reverse transcriptase
(D) DNA dependent RNA polymerase **[AIPMT 2005]**

28. Which one of the following hydrolyses internal phosphodiester bonds in a polynucleotide chain?
(A) Protease (B) Lipase
(C) Endonuclease (D) Exonuclease
[AIPMT 2005]

29. The following ratio is generally constant for a given species:
(A) A + G / C + T (B) T + C / G + A
(C) G + C / A + T (D) A + C / T + G.
[AIPMT 2004]

30. If the DNA percentage of thymine is 20%, then what is the percentage of guanine?
(A) 20% (B) 40%
(C) 30% (D) 60% **[AIPMT 2002]**

31. One of the similarities between DNA and RNA is that both:
(A) are capable of replicating
(B) are polymers of nucleotides
(C) have similar pyrimidine bases
(D) have similar sugars **[AIPMT 2000]**

32. In DNA when AGCT occurs, their association is as per which of the following pair?
(A) ACGT (B) AGCT
(C) TCGA (D) All of these
[AIPMT 2000, 1999]

33. Which one contains four pyrimidine bases?
(A) GATCAATGC (B) GCUAGACAA
(C) UAGCGGUAA (D) TGCCTAACG
[AIPMT 1994]

34. Out of A = T, G ≡ C pairing, bases of DNA may exist in alternate valency state owing to arrangement called:
(A) Point mutation
(B) Analogue substitution
(C) Tautomerisational mutation
(D) Frame shift mutation **[AIPMT 1994]**

35. A DNA with unequal nitrogen bases would most probably be:
(A) single stranded (B) double stranded
(C) triple stranded (D) four stranded
[AIPMT 1993]

36. In RNA, thymine is replaced by:
(A) adenine (B) guanine
(C) cytosine (D) uracil. **[AIPMT 1992]**

37. A nucleotide is formed of:
(A) purine, pyrimidine and phosphate
(B) purine, sugar and phosphate
(C) pyrimidine, sugar and phosphate
(D) nitrogen base, sugar and phosphate **[AIPMT 1991]**

38. A segment of DNA has 120 adenine and 120 cytosine bases. The total number of nucleotides present in the segment is:
(A) 120 (B) 240
(C) 60 (D) 480 **[AIPMT 1991]**

39. An octamer with 4 histones complexed with DNA forms:
(A) Centromere (B) Endosome
(C) Mesosome (D) Nucleosome
[AIPMT 1990]

5.2. The Search for Genetic Material

40. Unequivocal proof that DNA is the genetic material was first proposed by:
(A) Avery, Macleod and McCarty
(B) Wilkins and Franklin
(C) Frederick Griffith
(D) Alfred Hershey and Martha Chase **[NEET 2023]**

41. Given below are two statements:

Statement I: RNA mutates at a faster rate.

Statement II: Viruses having RNA genome and shorter life span mutate and evolve faster.

In the light of the above statements, choose the correct answer from the options given below:

(A) Statement I is true but Statement II is false.

(B) Statement I is false but Statement II is true.

(C) Both Statement I and Statement II are true.

(D) Both Statement I and Statement II are false

[NEET 2023]

42. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage?

(A) Beadle and Tatum

(B) Meselson and Stahl

(C) Hershey and Chase

(D) Jacob and Monod **[NEET Odisha 2019]**

43. A molecule that can act as a genetic material must fulfill the traits given below, except:

(A) it should provide the scope for slow changes that are required for evolution.

(B) it should be unstable structurally and chemically.

(C) it should be able to generate its replica.

(D) it should be able to express itself in the form of 'Mendelian characters'. **[NEET Phase-II 2016]**

44. Transformation was discovered by:

(A) Meselson and Stahl

(B) Hershey and Chase

(C) Griffith

(D) Watson and Crick. **[AIPMT 2014]**

45. The unequivocal proof of DNA as the genetic material came from the studies on a:

(A) bacterium (B) fungus

(C) viroid (D) bacterial virus.

[AIPMT Mains 2011]

46. On which bacteria was the transformation experiment first performed?

(A) *Pasteurella pestis*

(B) *Salmonella*

(C) *Diplococcus pneumoniae*

(D) *E. coli* **[AIPMT 2002]**

47. How does a eukaryotic genome differs from the prokaryotic genome?

(A) Repetitive sequences are present in eukaryotes.

(B) The DNA is circular and single stranded in prokaryotes.

(C) The DNA is complexed with histones in prokaryotes.

(D) Genes in the former case are organized into operons.

[AIPMT 1998]

48. Who proved that DNA is basic genetic material?

(A) Watson (B) Griffith

(C) Hershey and Chase (D) Boveri and Sutton

[AIPMT 1993]

49. The transforming principle of *Pneumococcus* as found out by Avery, Mac Leod and McCarty was:

(A) DNA (B) *m*RNA

(C) protein (D) polysaccharide.

[AIPMT 1993]

5.3. RNA World

50. Sequence of which of the following is used to know the phylogeny?

(A) *m*RNA (B) *r*RNA

(C) *t*RNA (D) DNA **[AIPMT 2002]**

5.4. Replication

51. Match List I with List II:

List I	List II
(a) Frederick Griffith	(i) Genetic code
(b) Francois Jacob and Jacques Monod	(ii) Semi-conservative mode of DNA replication
(c) Har Gobind Khorana	(iii) Transformation
(d) Meselson & Stahl	(iv) *Lac* operon

Choose the correct answer from the options given below:

	(a)	(b)	(c)	(d)
(A)	(iii)	(iv)	(i)	(ii)
(B)	(ii)	(iii)	(iv)	(i)
(C)	(iv)	(i)	(ii)	(iii)
(D)	(iii)	(ii)	(i)	(iv)

[NEET 2024]

52. Ten *E. coli* cells with ^{15}N-*ds*DNA are incubated in a medium containing ^{14}N nucleotide. After 60 minutes, how many *E. coli* cells will have DNA totally free from ^{15}N?

(A) 40 cells (B) 60 cells

(C) 80 cells (D) 20 cells **[NEET 2022]**

53. Choose the correct pair from the following.

(A)	Polymerases	(i)	Break the DNA into fragments
(B)	Nucleases	(ii)	Separate the two strands of DNA
(C)	Exonucleases	(iii)	Make cuts at specific positions within DNA
(D)	Ligases	(iv)	Join the two DNA molecules

[NEET Sept. 2020]

54. During DNA replication, Okazaki fragments are used to elongate:

(A) the leading strand towards replication fork

(B) the lagging strand towards replication fork

(C) the leading strand away from replication fork

(D) the lagging strand away from the replication fork.

[NEET 2017]

55. DNA replication in bacteria occurs:

(A) during S-phase

(B) prior to mission

(C) just before transcription

(D) within nucleolus **[NEET 2017]**

56. Taylor conducted the experiments to prove semi conservative mode of chromosome replication on:

(A) *Vinca rosea*

(B) *Vicia faba*

(C) *Drosophila melanogaster*

(D) *E. coli.* **[NEET Phase-II 2016]**

57. When cell has stalled DNA replication fork, which checkpoint should be predominantly activated?

(A) G_1/S (B) G_2/M

(C) M (D) Both G_2/M and M

[NEET Phase-II 2016]

58. The Okazaki fragments in DNA chain growth:

(A) polymerise in the 3' to 5' direction and replication fork

(B) prove semi-conservative nature of DNA replication

(C) polymerize in the 5' to 3' direction and explain 3' to 5' DNA replication

(D) result in transcription. **[AIPMT 2007]**

59. During replication of a bacterial chromosome DNA synthesis starts from a *ori* site and

(A) RNA primers are involved

(B) is facilitated by telomerase

(C) moves in one direction of the site

(D) moves in bi-directional way. **[AIPMT 2004]**

60. Which of the following enzymes are used to join bits of DNA?

(A) Ligase (B) Primase

(C) DNA polymerase (D) Endonuclease

[AIPMT 2002]

61. During replication of DNA, its two strands separate. Each of these serves as a template for the formation of new strands. Such type of replication is called:

(A) flexible (B) non-conservative

(C) conservative (D) semi-conservative

[AIPMT 2000]

62. The hereditary material present in the bacterium *E. coli* is:

(A) double stranded RNA

(B) double stranded DNA

(C) single stranded RNA

(D) single stranded DNA **[AIPMT 1997]**

63. Okazaki fragments are seen during:

(A) transduction (B) transcription

(C) translation (D) replication **[AIPMT 1996]**

64. Which protein helps in the opening of DNA double helix in the form of replication fork?

(A) DNA polymerase I (B) DNA topoisomerase

(C) DNA gyrase (D) DNA ligase

[AIPMT 1994]

65. During DNA replication, the strands separate by:

(A) unwindase/helicase (B) gyrase

(C) DNA polymerase (D) topoisomerase

[AIPMT 1993]

66. Experimental material in the study of DNA replication has been:

(A) *Escherichia coli* (B) *Neurospora crassa*

(C) *Pneumococcus* (D) *Drosophila melanogaster.*

[AIPMT 1992]

67. *Escherichia coli* fully labelled with N^{1} is allowed to grow in N^{14} medium. The two strands of DNA molecule of the first generation bacteria have:

(A) different density and do not resemble parent DNA

(B) different density but resemble parent DNA

(C) same density and resemble parent DNA

(D) same density but do not resemble parent DNA

[AIPMT 1992]

68. DNA replication is:

(A) conservative

(B) conservative and discontinuous

(C) semi-conservative and semi-discontinuous

(D) semi-conservative and discontinuous **[AIPMT 1989]**

5.5. Transcription

69. Given below are two statements regarding RNA polymerase in prokaryotes.

Statement I: In prokaryotes, RNA polymerase is capable of catalysing the process of elongation during transcription.

Statement II: RNA polymerase associate transiently with 'Rho' factor to initiate transcription.

In the light of the given statements, choose the correct answer from the options given below.

(A) Statement I is true but Statement II is false.

(B) Statement I is false but Statement II is true.

(C) Both Statement I and Statement II are true.

(D) Both Statement I and Statement II are false.

[Re-NEET 2024]

70. Given below are two statements:

Statement I: In eukaryotes there are three RNA polymerases in the nucleus in addition to the RNA polymerase found in the organelles.

Statement II: All the three RNA polymerases in eukaryotic nucleus have different roles.

In the light of the above statements, choose the correct answer from the options given below:

(A) Statement I is correct but Statement II is incorrect.

(B) Statement I is incorrect but Statement II is correct.

(C) Both Statement I and Statement II are correct.

(D) Both Statement I and Statement II are incorrect.

[Re-NEET 2024]

71. A transcription unit in DNA is defined primarily by the three regions in DNA and these are with respect to upstream and down stream end:

(A) Structural gene, Transposons, Operator gene

(B) Inducer, Repressor, Structural gene

(C) Promoter, Structural gene, Terminator

(D) Repressor, Operator gene, Structural gene

[NEET 2022]

72. Which of the following statement is correct regarding the process of replication in *E. coli*?

(A) The DNA dependent RNA polymerase catalyses polymerization in one direction that is 5' → 3'.

(B) The DNA dependent DNA polymerase catalyses polymerization in 5' → 3' as well as 3' → 5' direction.

(C) The DNA dependent DNA polymerase catalyses polymerization in 5' → 3' direction.

(D) The DNA dependent DNA polymerase catalyses polymerization in one direction that is 3' → 5'.

[NEET 2024]

73. Which one is the correct product of DNA dependent RNA polymerase to the given template?

3'TACATGGCAAATATCCATTCA5'

(A) 5'AUGUAAAGUUUAUAGGUAAGU3'

(B) 5'AUGUACCGUUUAUAGGGAAGU3'

(C) 5'ATGTACCGTTTATAGGTAAGT3'

(D) 5'AUGUACCGUUUAUAGGUAAGU3'

[NEET 2024]

74. Match List I with List II:

List I	List II
(a) RNA polymerase III	(i) snRNPs
(b) Termination of transcription	(ii) Promoter
(c) Splicing of Exons	(iii) Rho factor
(d) TATA box	(iv) snRNAs, tRNA

Choose the correct answer from the options given below:

	(a)	(b)	(c)	(d)
(A)	(iii)	(ii)	(iv)	(i)
(B)	(iii)	(iv)	(i)	(ii)
(C)	(iv)	(iii)	(i)	(ii)
(D)	(ii)	(iv)	(i)	(iii)

[NEET 2024]

75. Which one of the following is the sequence on corresponding coding strand, if the sequence on *m*RNA formed is as follows.

5'AUCGAUCGAUCGAUCGAUCGAUCGAUCG 3'?

(A) 5' ATCGATCGATCGATCGATCGATCGATCG 3'

(B) 3' ATCGATCGATCGATCGATCGATCGATCG 5'

(C) 5' UAGCUAGCUAGCUAGCUAGCUAGCUAGC 3'

(D) 3' UAGCUAGCUAGCUAGCUAGCUAGCUAGC 5'

[NEET 2023]

76. What is the role of RNA polymerase III in the process of transcription in eukaryotes?

(A) Transcription of precursor of *m*RNA

(B) Transcription of only *sn*RNAs

(C) Transcription of *r*RNAs (28S, 18S and 5.8S)

(D) Transcription of *t*RNA, 5S *r*RNA and *sn*RNA

[NEET 2023]

77. Identify the correct statement.

(A) In capping methyl guanosine triphosphate is added to the 3' end of *hn*RNA.

(B) RNA polymerase binds with Rho factor to terminate the process of transcription in bacteria.

(C) The coding strand in a transcription unit is copied to an *m*RNA.

(D) Split gene arrangement is characteristic of prokaryotes.

[NEET 2021]

78. Which is the "Only enzyme" that has "Capability" to catalyse Initiation, Elongation and Termination in the process of transcription in prokaryotes?

(A) DNA dependent DNA polymerase

(B) DNA dependent RNA polymerase

(C) DNA Ligase

(D) DNase

[NEET 2021]

79. Which of the following RNAs is not required for the synthesis of protein?

(A) mRNA (B) tRNA

(C) rRNA (D) siRNA

[NEET 2021]

80. Name the enzyme that facilitates opening of DNA helix during transcription.

(A) DNA helicase (B) DNA polymerase

(C) RNA polymerase (D) DNA ligase

[NEET Sept. 2020]

81. In the process of transcription in eukaryotes, the RNA polymerase I transcribes:

(A) mRNA with additional processing, capping and tailing

(B) tRNA, 5S rRNA and snRNAs

(C) rRNAs-28S, 18S and 5.8S

(D) precursor of mRNA, hnRNA. **[NEET Odisha 2019]**

82. What initiation and termination factors are involved in transcription in Prokaryotes?

(A) σ and ρ, respectively

(B) α and β, respectively

(C) β and γ, respectively

(D) α and σ, respectively **[NEET Odisha 2019]**

83. Match the following RNA polymerases with their transcribed products.

(a)	RNA polymerase I	(i)	tRNA
(b)	RNA polymerase II	(ii)	rRNA
(c)	RNA polymerase III	(iii)	hnRNA

Select the correct option from the following:

	(a)	(b)	(c)
(A)	(i)	(iii)	(ii)
(B)	(i)	(ii)	(iii)
(C)	(ii)	(iii)	(i)
(D)	(iii)	(ii)	(i)

[NEET Odisha 2019]

84. The equivalent of a structural gene is:

(A) muton (B) cistron

(C) operon (D) recon.

[NEET Phase-II 2016]

85. Which of the following rRNAs act as structural RNA as well as ribozyme in bacteria?

(A) 5S rRNA (B) 18S rRNA

(C) 23S rRNA (D) 58S rRNA

[NEET Phase-II 2016]

86. DNA-dependent RNA polymerase catalyses transcription on one strand of the DNA which is called the:

(A) template strand (B) coding strand

(C) alpha strand (D) anti strand.

[NEET Phase-II 2016]

87. Which one of the following is wrongly matched?

(A) Transcription- Writing information from DNA to tRNA.

(B) Translation- Using information in mRNA to make protein.

(C) Repressor protein- Binds to operator to stop enzyme synthesis.

(D) Operon- Structural genes, operator and promoter.

[AIPMT 2014]

88. Removal of RNA polymerase III from nucleoplasm will affect the synthesis of:

(A) tRNA (B) hnRNA

(C) mRNA (D) rRNA.

[AIPMT Screening 2012]

89. Removal of introns and joining of exons in a defined order during transcription is called:

(A) looping (B) inducing

(C) slicing (D) splicing.

[AIPMT 2012, Screening 2009]

90. In eukaryotic cell transcription, RNA splicing and RNA capping take place inside the:

(A) ribosomes (B) nucleus

(C) dictyosomes (D) ER.

[AIPMT Mains 2010]

91. During transcription, RNA polymerase holoenzyme binds to a gene promoter and assumes a saddle-like structure. What is it's DNA-binding sequence?

(A) AATT (B) CACC

(C) TATA (D) TTAA

[AIPMT 2007, 05]

92. Molecular basis of organ differentiation depends on the modulation in transcription by:

(A) ribosome (B) transcription factor

(C) anticodon (D) RNA polymerase.

[AIPMT 2007]

93. DNA template sequence of CTGATAGC is transcribed over mRNA as:

(A) GACUAUCG (B) GUCTUTCG

(C) UACTATCU (D) GAUTATUG

[AIPMT 2004]

94. During transcription, the DNA site at which RNA polymerase binds is called:

(A) promoter (B) regulator

(C) receptor (D) enhancer. **[AIPMT 2003]**

95. Exon parts of mRNAs have code for:

(A) protein (B) lipid

(C) carbohydrate (D) phospholipid.

[AIPMT 2002]

96. Which of the following reunites the exon segments after RNA splicing?

(A) RNA polymerase (B) RNA primase

(C) RNA ligase (D) RNA proteases

[AIPMT 2002]

97. Which type of RNA polymerase is required in nucleus for RNA synthesis?

(A) 1 (B) 2

(C) 3 (D) 4 **[AIPMT 2001]**

98. In which direction *m*RNA is synthesized on DNA template?

(A) 5'→3' (B) 3'→5'

(C) Both (A) and (B) (D) Any of these

[AIPMT 2001]

99. In eukaryotes, after transcription of *m*RNA, some of its nucleotides are removed before it is translated into polypeptide. The nucleotides which are removed from *m*RNA are called:

(A) exons (B) introns

(C) upstream sequences (D) unusual bases.

[AIPMT 1997]

100. The coding sequences in split genes are called:

(A) introns (B) operons

(C) exons (D) cistrons. **[AIPMT 1995]**

101. Which is not involved in protein synthesis?

(A) Termination (B) Initiation

(C) Elongation (D) Transcription

[AIPMT 1994]

102. Reverse transcriptase is:

(A) RNA dependent RNA polymerase.

(B) DNA dependent RNA polymerase.

(C) DNA dependent DNA polymerase.

(D) RNA dependent DNA polymerase. **[AIPMT 1994]**

103. The process of transfer of genetic information from DNA to RNA/formation of RNA from DNA is:

(A) translation (B) transversion

(C) translocation (D) transcription.

[AIPMT 1991]

5.6. Genetic Code

104. **Statement I:** The codon 'AUG' codes for methionine and phenylalanine.

Statement II: 'AAA' and 'AAG' both codons code for the amino acid lysine.

In the light of the above statements, choose the correct answer from the options given below.

(A) Both Statement I and Statement II are true.

(B) Both Statement I and Statement II are false.

(C) Statement I is correct but Statement II is false.

(D) Statement I is incorrect but Statement II is true.

[NEET 2021]

105. What will be the sequence of *m*RNA produced by the following stretch of DNA?

3'-ATGCATGCATGCATG-5' Template strand

5'-TACGTACGTACGTAC-3' Coding strand

(A) 3'-AUGCAUGCAUGCAUG-5'

(B) 5'-UACGUACGUACGUAC-3'

(C) 3'-UACGUACGUACGUAC-5'

(D) 5' -AUGCAUGCAUGCAUG-3'

[NEET Odisha 2019]

106. From the following identify the correct combination of salient features of Genetic code.

(A) Universal, Non-ambiguous, Overlapping

(B) Degenerate, Overlapping, Commaless

(C) Universal, Ambiguous, Degenerate

(D) Degenerate, Non-overlapping, Non-ambiguous

[NEET Odisha 2019]

107. Under which of the following condition will there be no change in the reading frame of following mRNA - 5' AACAGCGGUGCUAUU:

(A) Deletion of GGU from 7^{th}, 8^{th} and 9^{th} positions.

(B) Insertion of G at 5^{th} position.

(C) Deletion of G from 5^{th} position.

(D) Insertion of A and G at 4^{th} and 5^{th} positions, respectively. **[NEET 2019]**

108. AGGTATCGCAT is a sequence from the coding strand of a gene. What will be the corresponding sequence of the transcribed *m*RNA?

(A) ACCUAUGCGAU

(B) UGGTUTCGCAT

(C) AGGUAUCGCAU

(D) UCCAUAGCGUA **[NEET 2018]**

109. If there are 999 bases in an RNA that codes for a protein with 333 amino acids and the base at position 901 is deleted such that the length of the RNA becomes 998 bases, how many codons will be altered?

(A) 1 (B) 11

(C) 33 (D) 333 **[NEET 2017]**

110. Which one of the following is the starter codon?

(A) UGA (B) UAA

(C) UAG (D) AUG

[NEET Phase-I 2016]

111. If one strand of DNA has the nitrogenous base sequence as ATCTG, what would be the complementary RNA strand sequence?

(A) TTAGU (B) UAGAC

(C) AACTG (D) ATCGU

[AIPMT Screening 2012]

112. Which one of the following is a wrong statement regarding mutations?

(A) Deletion and insertion of base pairs cause frame shift mutations.

(B) Cancer cells commonly show chromosomal aberrations.

(C) UV and gamma rays are mutagens.

(D) Change in a single base pair of DNA does not cause mutation. **[AIPMT Mains 2012]**

113. Whose experiments cracked the DNA and discovered unequivocally that a genetic code is a triplet?

(A) Nirenberg and Matthaei

(B) Hershey and Chase

(C) Morgan and Sturtevant

(D) Beadle and Tatum **[AIPMT Screening 2009]**

114. Point mutation involves:

(A) Insertion (B) Change in single base pair

(C) Duplication (D) Deletion

[AIPMT Screening 2009]

115. Which one of the following pair of codons is correctly matched with their function or the signal for the particular amino acid?

(A) UUA, UCA – Leucine

(B) GUU, GCU – Alanine

(C) UAG, UGA – Stop

(D) AUG, ACG – Start/methionine **[AIPMT 2008]**

116. After a mutation at genetic locus the character of an organism changes due to the change in:

(A) DNA replication (B) RNA transcription pattern

(C) protein structure (D) protein synthesis pattern.

[AIPMT 2004]

117. During transcription, if the nucleotide sequence of the DNA strand that is being coded is ATACG then the nucleotide sequence in the *m*RNA would be:

(A) TATGC (B) TCTGG

(C) UAUGC (D) UATGC. **[AIPMT 2004]**

118. Which form of RNA has a structure resembling clover leaf?

(A) *r*RNA (B) *hn*RNA

(C) *m*RNA (D) *t*RNA **[AIPMT 2004]**

119. After a mutation at a genetic locus the character of an organism changes due to change in:

(A) protein structure

(B) DNA replication

(C) protein synthesis pattern

(D) RNA transcription pattern **[AIPMT 2004]**

120. In the genetic code dictionary, how many codons are used for all the 20 essential amino acids?

(A) 20 (B) 64

(C) 61 (D) 60 **[AIPMT 2003]**

121. Degeneration of a genetic code is attributed to the:

(A) First member of a codon

(B) Second member of codon

(C) Entire codon

(D) Third member of a codon. **[AIPMT 2003]**

122. Which one of the following triplet codes, is correctly matched with its specificity for an amino acid in protein synthesis or as 'start' or 'stop' codon?

(A) UCG - start (B) UUU - stop

(C) UGU - leucine (D) UAC - tyrosine

[AIPMT 2003]

123. What would happen if in a gene encoding a polypeptide of 50 amino acids, 25^{th} codon (UAU) is mutated to UAA?

(A) A polypeptide of 49 amino acids will be formed

(B) A polypeptide of 25 amino acids will be formed

(C) A polypeptide of 24 amino acids will be formed

(D) Two polypeptides of 24 and 25 amino acids will be formed **[AIPMT 2003]**

124. Change in the sequence of nucleotide in DNA is called as:

(A) mutagen (B) mutation

(C) recombination (D) translation.

[AIPMT 2002]

125. Out of 64 codons, 61 codons code for 20 types of amino acid, it is called:

(A) degeneracy of genetic code

(B) overlapping of gene

(C) wobbling of codon

(D) universality of codons. **[AIPMT 2002]**

126. Anticodon is an unpaired triplet of bases in an exposed position of:

(A) *m*RNA (B) *r*RNA

(C) *t*RNA (D) *s*RNA **[AIPMT 2000]**

127. The chain terminating codons are/ the translation termination triplet are:

(A) TAG, TAA. TGA (B) GAT, AAT. AGT

(C) AGT, TAG UGA (D) UAA, UAG, UGA

[AIPMT 1997, 96]

128. If the sequence of bases in DNA is ATTCGATG, then the sequence of bases in its transcript will be:

(A) CAUCGAAU (B) UAAGCUAC

(C) GUAGCUUA (D) AUUCGAUG

[AIPMT 1995]

129. The number of base substitution possible in amino acid codons is:
(A) 261 (B) 264
(C) 535 (D) 549 **[AIPMT 1994]**

130. Khorana first deciphered the triplet codons of:
(A) phenylalanine and methionine
(B) tyrosine and tryptophan
(C) threonine and histidine
(D) serine and isoleucine **[AIPMT 1992]**

131. In the genetic dictionary, there are 64 codons as:
(A) genetic code is a triplet
(B) 64 amino acids are to be coded
(C) 64 types of tRNAs are present
(D) there are 44 non-sense codons and 20 sense codons **[AIPMT 1990]**

132. Genetic code consists of:
(A) adenine and guanine
(B) cytosine and uracil
(C) cytosine and guanine
(D) all of the above **[AIPMT 1988]**

5.7. Translation

133. How many different proteins does the ribosome consist of?
(A) 40 (B) 20
(C) 80 (D) 60 **[NEET 2023]**

134. The process of translation of *m*RNA to proteins begins as soon as:
(A) the small subunit of ribosome encounters *m*RNA
(B) the larger subunit of ribosome encounters *m*RNA
(C) both the subunits join together to bind with *m*RNA
(D) the *t*RNA is activated and the larger subunit of ribosome encounters *m*RNA **[NEET 2022]**

135. Select the correct match:
(A) T.H. Morgan – Transduction
(B) F_2 × recessive parent – Dihybrid cross
(C) Ribozyme – Nucleic acid
(D) G. Mendel – Transformation **[NEET 2018]**

136. The mechanism that causes a gene to move from one linkage group to another is called:
(A) Inversion (B) Duplication
(C) Translocation (D) Crossing over
[NEET Phase-II 2016, AIPMT May 2015]

137. Which one of the following also acts as a catalyst in a bacterial cell?
(A) *sn*RNA (B) *hn*RNA
(C) 23S *r*RNA (D) 5S *r*RNA
[AIPMT Screening 2011, Mains 2010]

138. Amino acid sequence, in protein synthesis is decided by the sequence of:
(A) *r*RNA (B) *t*RNA
(C) *m*RNA (D) *c*DNA. **[AIPMT 2006]**

139. Because most of the amino acids are represented by more than one codon, the genetic code is:
(A) degenerate (B) generate
(C) overlapping (D) wobbling
[AIPMT 2002, 1993]

140. In translation, which step does not consume a high energy phosphate bond:
(A) Amino acid activation
(B) Aminoacyl *t*RNA binding to active ribosomal site
(C) Translocation
(D) Peptidyl-transferase reaction **[AIPMT 1997]**

5.8. Regulation of Gene Expression

141. Given below are two statements:
Statement I: In the *lac* operon, the *z* gene codes for beta-galactosidase which is primarily responsible for the hydrolysis of lactose into galactose and glucose.
Statement II: In addition to lactose, glucose or galactose can also induce *lac* operon.
In the light of the above statements, choose the correct answer from the given options:
(A) Statement I is true but Statement II is false.
(B) Statement I is false but Statement II is true.
(C) Both Statement I and Statement II are true.
(D) Both Statement I and Statement II are false.
[Re-NEET 2024]

142. The lactose present in the growth medium of bacteria is transported to the cell by the action of:
(A) Acetylase (B) Permease
(C) Polymerase (D) Beta-galactosidase
[NEET 2024]

143. Match List I with List II.

List I	List II
(a) Gene '*a*'	(i) β-galactosidase
(b) Gene '*y*'	(ii) Transacetylase
(c) Gene '*i*'	(iii) Permease
(d) Gene '*z*'	(iv) Repressor protein

Choose the correct answer from the options given below:

	(a)	(b)	(c)	(d)
(A)	(iii)	(iv)	(i)	(ii)
(B)	(iii)	(i)	(iv)	(ii)
(C)	(ii)	(i)	(iv)	(iii)
(D)	(ii)	(iii)	(iv)	(i)

[NEET 2023, NEET National 2019]

144. In an *E. coli* strain, *i* gene gets mutated and its product cannot bind the inducer molecule. If growth medium is provided with lactose, what will be the outcome?
(A) RNA polymerase will bind the promoter region
(B) *z*, *y*, *a* genes will be transcribed
(C) *z*, *y*, *a* genes will not be translated
(D) Only *z* gene will get transcribed **[NEET 2022]**

145. All of the following are parts of an operon except:
(A) an enhancer (B) structural genes
(C) an operator (D) a promoter. **[NEET 2018]**

146. Select the correct match:
(A) Matthew Meselson and F. Stahl – *Pisum sativum*
(B) Francois Jacob and Jacques Monad – *Lac* operon
(C) Alec Jeffreys – *Streptococcus pneumoniae*
(D) Alfred Hershey and Martha Chase – TMV
[NEET 2018]

147. Which of the following is required as inducer(s) for the expression of *lac* operon?
(A) Galactose
(B) Lactose
(C) Lactose and galactose
(D) Glucose **[NEET Phase-I 2016]**

148. Which enzyme(s) will be produced in a cell in which there is a non-sense mutation in the *lac y* gene?
(A) β-galactosidase
(B) Lactose permease
(C) Transacetylase
(D) Lactose permease and transacetylase **[NEET 2013]**

149. In an inducible operon, the genes are:
(A) usually not expressed unless a signal turns them "on"
(B) usually expressed unless a signal turns them "off"
(C) never expressed
(D) always expressed. **[NEET Karnataka 2013]**

150. Select the two statements out of the four (I-IV) given below about *lac* operon.
(I) Glucose or galactose may bind with the repressor and inactivate it.
(II) In the absence of lactose, the repressor binds with the operator region.
(III) The *z*-gene codes for permease.
(IV) This was elucidated by Francois Jacob and Jacques Monod.
The correct statements are:
(A) (II) and (III) (B) (I) and (III)
(C) (II) and (IV) (D) (I) and (II)
[AIPMT Screening 2010]

151. The *lac* operon consists of:
(A) four regulatory genes only
(B) one regulatory gene and three structural genes
(C) two regulatory genes and two structural genes
(D) three regulatory genes and three structural genes.
[AIPMT Mains 2010]

152. *E.coli* cells with a mutated *z* gene of the *lac* operon cannot grow in medium containing only lactose as the source of energy because:
(A) the *lac* operon is constitutively active in these cells
(B) they cannot synthesize functional galactosidase
(C) in the presence of glucose, *E.coli* cells do not utilize lactose
(D) they cannot transport lactose from the medium into the cell. **[AIPMT 2005]**

153. What does "*lac*" refer to in what we call the *lac* operon?
(A) lactose (B) lactase
(C) lac insect (D) the number 1,00,000
[AIPMT 2003]

154. In *E.coli*, during lactose metabolism repressor binds to:
(A) regulator gene (B) operator gene
(C) structural gene (D) promoter gene.
[AIPMT 2002]

155. Jacob and Monad studied lactose metabolism in *E. coli* and proposed the operon concept. The operon concept is applicable for:
(A) all prokaryotes
(B) all prokaryotes and some eukaryotes
(C) all prokaryotes and all eukaryotes
(D) all prokaryotes and some protozoans.
[AIPMT 2002]

156. In negative operon:
(A) co-repressor binds with repressor
(B) co-repressor does not bind with repressor
(C) co-repressor binds with inducer
(D) cAMP has negative effect on lac operon.
[AIPMT 2001]

157. The reason for the genes to regulate the process of organogenesis at different levels and at different time is due to:
(A) promoter (B) regulator
(C) intron (D) exon **[AIPMT 2001]**

158. In operon concept, regulator gene functions as:
(A) repressor (B) regulator
(C) inhibitor (D) all of these **[AIPMT 1999]**

159. The *lac* operon is an example of:
(A) repressible operon (B) overlapping genes
(C) inducible operon (D) arabinose operon
[AIPMT 1995]

160. An environmental agent, which triggers transcription from an operon, is a:
(A) depressor (B) controlling element
(C) regulator (D) inducer. **[AIPMT 1995]**

161. In *Escherichia coli*, *lac* operon is induced by:
(A) *i*-gene (B) lactose
(C) β-galactosidase (D) promoter gene
[AIPMT 1994]

5.9. Human Genome Project

162. Expressed Sequence Tags (ESTs) refers to:
(A) All genes whether expressed or unexpressed.
(B) Certain important expressed genes.
(C) All genes that are expressed as RNA.
(D) All genes that are expressed as proteins.
[NEET 2023, NEET National 2019]

163. If a geneticist uses the blind approach for sequencing the whole genome of an organism, followed by assignment of function to different segments, the methodology adopted by him is called as:
(A) bioinformatics (B) sequence annotation
(C) gene mapping (D) expressed sequence tags
[NEET 2022]

164. Commonly used vectors for human genome sequencing are:
(A) T-DNA (B) BAC and YAC
(C) Expression vectors (D) T/A cloning vectors.
[AIPMT 2014]

165. In history of biology, human genome project led to the development of:
(A) biotechnology (B) biomonitoring
(C) bioinformatics (D) biosystematics.
[AIPMT Mains 2011]

166. Genetic map is one that:
(A) establishes sites of the genes on a chromosomes
(B) establishes the various stages in gene evolution
(C) shows the stages during the cell division
(D) shows the distribution of various species in a region.
[AIPMT 2003]

167. How many base pairs (bp) does the haploid genome of humans contain?
(A) 2.9×10^9 (B) 4×10^8
(C) 7×10^9 (D) 3×10^9 **[AIPMT 1999]**

5.10. DNA Fingerprinting

168. DNA polymorphism forms the basis of:
(A) DNA fingerprinting
(B) translation
(C) genetic mapping
(D) both genetic mapping and DNA fingerprinting
[NEET 2022]

169. DNA fingerprinting involves identifying differences in some specific regions in DNA sequence, called as:
(A) Satellite DNA (B) Repetitive DNA
(C) Single nucleotides (D) Polymorphic DNA.
[NEET 2021]

170. Which is the basis of genetic mapping of human genome as well as DNA fingerprinting?
(A) Polymorphism in DNA sequence
(B) Single nucleotide polymorphism
(C) Polymorphism in hnRNA sequence
(D) Polymorphism in RNA sequence **[NEET Oct. 2020]**

171. Satellite DNA is important because it:
(A) codes for proteins needed in cell cycle
(B) shows high degree of polymorphism in population and also the same degree of polymorphism in an individual, which is heritable from parents to children
(C) does not code for proteins and is same in all members of the population
(D) codes for enzymes needed for DNA replication.
[AIPMT Latest July 2015]

172. One of the most frequently used techniques in DNA fingerprinting is:
(A) VNTR (B) SSCP
(C) SCAR (D) AFLP.
[NEET Karnataka 2013]

173. What is it that forms the basis of DNA fingerprinting?
(A) The relative proportions of purines and pyrimidines in DNA.
(B) The relative difference in the DNA occurrence in blood, skin and saliva.
(C) The relative amount of DNA in the ridges and grooves of the fingerprints.
(D) Satellite DNA occurring as highly repeated short DNA segment. **[AIPMT Mains 2012]**

174. Satellite DNA is a useful tool in:
(A) organ transplantation (B) sex determination
(C) forensic science (D) genetic engineering.
[AIPMT 2010 Screening]

175. DNA fingerprinting refer to:
(A) molecular analysis of profiles of DNA samples
(B) analysis of DNA samples using imprinting devices
(C) techniques used for molecular analysis of different specimens of DNA
(D) techniques used for identification of fingerprints of individuals. **[AIPMT 2004]**

1. (D) Histones are positively charged basic proteins. Nucleosomes are DNA wrapped around histone octamer. Euchromatin is loosely packed chromatin. Heterochromatin is densely packed chromatin.

2. (B) In prokaryotes, the DNA is held with some proteins in a region called nucleoid, but the proteins are not necessarily negatively charged. In fact, some of the proteins are positively charged, such as histone-like proteins, which can interact with the negatively charged DNA.

3. (A) Heterochromatin is more densely packed, dark stained and transcriptionally inactive chromatin. A typically nucleosome contains 200 base pairs (bp) of DNA helix, instead of 400.

4. (D) If the length of DNA double helix in a typical mammalian cell is calculated (by multiplying the total no. of base pairs with distance between two consecutive base pairs), it will be 3.3×10^9.

Length between the two base pairs = 0.34 nm

The total length of the double helix of DNA

= Total no. of base pairs × Distance between the two base pairs

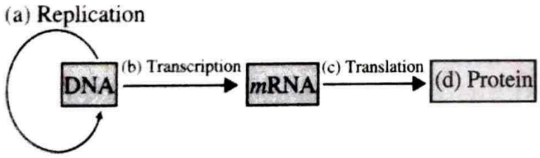
Let us consider the total no. of base pairs as X

$$1.1 \text{ m} = X \times 3.4 \times 10^{-10} \text{ m}$$

$$X = 3.3 \times 10^9 \text{ base pairs}$$

So, in a 1.1 m length of DNA, there will be about 3.3×10^9 base pairs.

5. (C) Central dogma:



Related Theory

➥ *Crick said that once information had gone from DNA into the protein, it could not get out of the protein and go back into the genetic code. This is the central dogma.*

6. (C) According to Chargaff rule, A + G = C + T and A = T; G = C.

Given: [A] = 30%

To find [T], [C], [G]

[A] = [T], [C] = [G]

A = 30%

[T] = 30%

also [A] + [T] + [C] + [G] = 100%

30% + 30% + 2[C] = 100

60% + 2[C] = 100

2[C] = 100 – 60

2[C] = 40

[C] = 20%

7. (A) Histones are positively charged basic proteins, rich in the basic amino acid residues lysine and arginine. They are organized to form a unit of 8 molecules called histone octamer. The negatively charged DNA is wrapped around the positively charged histone octamer to form a structure called nuleosome. Hence, histones are a family of basic proteins that associate with DNA in the nucleus and help condense it into chromatin, they are alkaline (basic pH) proteins, and their positive charges allow them to associate with DNA.

Related Theory

➥ *Below pH 4, the histones become partially unfolded, lose specific secondary and tertiary structure, and undergo non-specific aggregation.*

8. (C) *E. coli* has 4.6×10^6 base pairs. It completes replication process in 18 minutes *i.e.*, 18 × 60 seconds.

Rate of polymerisation

$$= \frac{4.6 \times 10^6 \text{ bp}}{18 \times 60 \text{ s}}$$

$$= \frac{4.6 \times 10^5}{18 \times 6} = \frac{46 \times 10^4}{108}$$

$$= \frac{460000}{108}$$

= 4259.2 bp/s or approximately 4000 bp/s

9. (B) Friedrich Miescher isolated "nuclein". DNA with associated proteins, from white blood cell nuclei (pus). He was the first to identify DNA as a distinct molecule. Rosalind Franklin discovered the molecular structures of DNA and RNA using X-ray crystallography. Erwin Chargaff discovered that DNA contains equal amounts of adenine and thymine and equal amounts of cytosine and guanine (A=T, C=G). Gregor Mendel discovered the basic principles of heredity and laid the mathematical foundation of the science of genetics.

Related Theory

➥ *DNA molecule is a polynucleotide chain. Each nucleotide consists of a deoxyribose sugar molecule attached to a phosphate group and a nitrogenous base- purines (adenine and guanine) and pyrimidines (cytosine and thymine). The nucleotides are joined covalently by the phosphate of one nucleotide and the sugar of the next, forming a phosphate-sugar*

backbone from which the nitrogenous bases protrude. Both strands are held together with the help of hydrogen bonding between complementary base pairs i.e., adenine - thymine, and cytosine - guanine.

10. (B) Total number of base pairs = 6.6×10^9

The distance between each base pair = 0.34 nm

$= 0.34 \times 10^{-9}$ m

So, the distance between 6.6×10^9 base pairs

$= 6.6 \times 10^9 \times 0.34 \times 10^{-9}$ m

$= 2.2$ m

Thus, the length of DNA is 2.2 m.

Related Theory

Helix sence	A Right handed	B Right handed	Z Left handed
Repeating unit	1 bp	1 bp	2 bp
Rotating/bp	33.6°	35.9°	60°/2°
Mean bp/turn	10.7	10.0	12
Inclination of bp to axis	+ 19°	– 1.2°	– 9°
Rise/bp along axis	2.3 Å	3.32 Å	3.8 Å
Pitch/turn of helix	24.6 Å	33.2 Å	45.6 Å

11. (D) Adenine forms complementary base pairs with thymine with the help of double hydrogen bonds (A = T) and cytosine forms complementary base pairs with guanine with the help of triple hydrogen bonds (C ≡ G). C ≡ G bond is stronger than A = T bond due to presence of triple hydrogen bonds.

12. (D) The purines found in DNA and RNA are adenine and guanine. The pyrimidines in DNA are cytosine and thymine; in RNA, uracil is found instead of thymine.

Mnemonics

Students usually confuse between purines and pyrimidines. They can be learned using the following trick:

For Purin:

Please Ask me about Gravity

Please – ***Purines***

Ask – ***Adenine***

Gravity – ***Guanine***

For Pyrimidines:

Powerful Chefs Use Top – *notch ingredients.*

Powerful – ***Cytosine***

Use – ***Uracil***

Top – ***Thymine***

13. (B) DNA is negatively charged due to the presence of phosphate groups in the DNA backbone that carry negatively-charged oxygen molecules giving the phosphate-sugar backbone of DNA an overall negative charge.

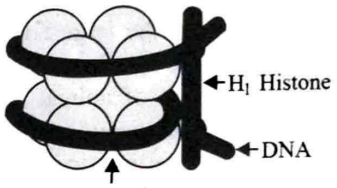
Related Theory

During the formation of phosphodiester bond, nucleotides retain one of the two negative charge, while other is lost to form ester bond.

14. (C) The association of H_1 histone with nucleosome indicates that DNA remains in its condensed form. Thus, DNA cannot be in open helix form. Histone proteins plays no role in transcription or replication of DNA.

Related Theory

Histones are a family of basic proteins that associate with DNA in the nucleus and help condense it into chromatin, they are alkaline (basic pH) proteins, and their positive charges allow them to associate with DNA. They are found inside the nucleus of eukaryotic cells. There are 5 types of histone proteins. One pairs of each H_2A, H_2B, H_3 and H_4 forms the histone octamers while H_1 is the linker DNA which binds to the entry/exit sites of DNA on the surface of the nucleosomal core particle and completes the nucleosome.



Structure of Nucleosome

15. (C) Chargaff's rule states that purine and pyrimidine base pairs are present in equal amount, *i.e.*, A = T, G = C.

$$(A + T) = (G + C)$$

$$\frac{A+T}{G+C} = 1$$

Cytosine = 17%

If A + G + C + T = 100 and G = C, A = T then

A + 17 + G + T = 100

G = 17%

A + T + 34 = 100

A + T = 100 – 34%

A + T = 66%

A = T = 33%

Hence, if cytosine is 17%, then G = 17% A and T will be 33% each.

16. (D) Chargaff's rule generalised about the structure of DNA. It is not applicable for RNA. However, RNA shows other characteristics similar to DNA such as complementary base pairing, 5' phosphoryl and 3' hydroxyl ends and presence of heterocyclic nitrogenous bases, *i.e.*, purines and pyrimidines (except thymine).

Related Theory

➥ *According to Chargaff's rules of base pairing:*

(1) The amount of adenine is always equal to the amount of thymine (A=T) and the amount of guanine is always equal to the amount of cytosine (C=G).

(2) Adenine is joined to thymine with two hydrogen bonds (A=T) and guanine is joined to cytosine by three hydrogen bonds (C≡G).

(3) The ratio of adenine to thymine and that of guanine to cytosine is always equal to one, i.e., $\frac{A}{T} = \frac{G}{C} = 1$.

(4) The ratio of $\frac{A}{G}$ *and* $\frac{T}{C}$ *changes with every species.*

Caution

➥ *Students should remember that RNA does not possess pyrimidine nitrogenous base, thymine. Instead, it consists of uracil, which is a demethylated derivative of thymine.*

17. (C) A genome is an organism's complete set of DNA including all of its genes. Each genome contains all of the information needed to build and maintain that organism. This is the largest in the given options. Chromosomes are the thread-like structures located inside the nucleus of animal and plant cells. The building blocks of nucleic acids are the nucleotides. A gene is the basic physical and functional unit of heredity. Genes are made up of DNA.

18. (C) DNA $\xrightarrow{\text{Transcription}}$ mRNA $\xrightarrow{\text{Translation}}$ protein

Francis Crick suggested that there is unidirectional flow of information from DNA to RNA to protein.

19. (A) Under electron microscope, the nucleosomes on chromatin appear as 'beads on a string' in chromosome, due to the wrapping of DNA over a core of histone proteins. The nucleosome is a fundamental subunit of chromatin. Each nucleosome is composed of a little less than two turns of DNA wrapped around a unit of 8 molecules called histone octamer. A single nucleosome consists of about 150 base pairs of DNA sequence wrapped around a core of histone proteins. They are repeatedly folded among themselves to form a chromosome.

20. (D) HIV belongs to Retrovirus group which show reverse central dogma or reverse transcription.

Related Theory

➥ *The biggest revolution in the central dogma was the discovery of retroviruses, which transcribe RNA into DNA through the use of a special enzyme called reverse transcriptase. This has resulted in an exception to the central dogma.*

21. (C) 3′ → 5′ phosphodiester bond is formed between carbon 3' of one nucleotide and carbon 5' of the other nucleotide.

Related Theory

➥ *A strand of DNA or RNA consists of nucleotides linked together by phosphodiester bonds. A phosphodiester bond exists between the phosphate of one nucleotide and the sugar 3′ carbon of the next nucleotide. This forms a backbone of alternating sugar and phosphate molecules known as the sugar-phosphate backbone. The two strands of DNA are also antiparallel (run in opposite directions) to one another. A strand of DNA can have direction 5′ → 3′ or 3′ → 5′. One strand of the DNA molecule is 5′ → 3′ and the other strand is 3′ → 5′. A DNA strand is assigned direction based on what is found at the end of the strands.*

➥ *The end of the strand with a free phosphate is the 5′ end because phosphate attaches to the 5′ carbon of the sugar. The end with a free OH group is the 3′ end because the OH group is attached to the 3′ carbon of the sugar.*

22. (D) According to Watson and Crick DNA molecule consists of two such polynucleotide chains wrapped helically around each other, with the sugar phosphate chain on the outside and purine and pyrimidine on the inside of the helix. The two strands run antiparallel, *i.e.*, one strand has phosphodiester linkage in 3′ → 5′ direction while other strand has phosphodiester linkage in 5′ → 3′ direction. Chargaff suggested that despite wide compositional variations exhibited by different types of DNA the total amount of purines is equal to the total amount of pyrimidines (A + G = T + C). However, the ratio of A/T and G/C is specific for every species.

23. (A) The nucleosome model explains the packaging of histone proteins and DNA in the chromatin material which forms the chromosome.

Related Theory

➥ *A nucleosome is the basic structural unit of DNA packaging in eukaryotes. The structure of a nucleosome consists of a segment of DNA wound around eight histone proteins and resembles thread wrapped around a spool.*

24. (B) Watson and Crick through their DNA model has shown that the two strands of DNA are antiparallel. One chain grows in 5′ → 3′ direction and the other chain grows in the 3′ → 5′ direction.

Caution

➥ *Students should remember that DNA is not semi-conservative, but the replication process is.*

25. (D) B-DNA is a helical structure with a diameter of 20 Å and the distance between the two base pairs is 3.4 Å. There are 10 base pairs in each turn; hence, one turn of the helix (pitch of each helix) is approximately 34 Å or 3.4 nm (10 = 1.0 nm).

Related Theory

➥ *There are three different DNA types:*

(1) A-DNA: *It is a right-handed double helix similar to the B-DNA form. Dehydrated DNA takes an A form that protects the DNA during extreme condition such as desiccation.*

(2) ***B-DNA:*** *The most common DNA conformation which is a right-handed helix in normal physiological conditions.*

(3) ***Z-DNA:*** *Z-DNA is a left-handed DNA where the double helix winds to the left in a zig-zag pattern and play some role in gene regulation.*

26. (D) The antiparallel strands of a DNA molecule means that the phosphate groups at the start of two DNA strands are in the opposite directions. One polynucleotide chain grows in the 5′ → 3′ direction and the other chain grows in the 3′ → 5′ direction.

27. (C) Reverse transcriptase use an RNA template and a short primer complementary to the 3' end of the RNA to direct the synthesis of the first strand of cDNA.

28. (C) Endonuclease hydrolyses internal phosphodiester bonds in a polynucleotide chain. A nuclease is an enzyme capable of cleaving the phosphodiester bonds between the nucleotide subunits of a nucleic acid. They are of two types endonucleases and exonucleases. The former hydrolyzes internal phosphodiester bonds in a polynucleotide chain, while the latter works by cleaving nucleotides one at a time from the ends of the polunucleotide chain. Lipase is an enzyme that is used in the hydrolysis of lipids (fats). Protease enzyme hydrolyse proteins and peptides.

29. (C) The C+G/A+T ratio varies from organism to organism among the prokaryotes, but within the same species, it is constant as A = T and C = G.

Related Theory

➥ *Erwin Chargaff discovered that the number of nitrogenous bases in the DNA was present in equal quantities. The amount of A is equal to T, whereas the amount of C is equal to G, i.e., A=T; C=G.*

30. (C) According to Chargaff's Rule, the DNA molecule should have an equal ratio of pyrimidine (cytosine and thymine) and purine (adenine and guanine). It means that the number of adenine molecules is equal to thymine molecules and the number of guanine molecules is equal to cytosine molecules.

A complement with T, and G complement with C.

Thus, $T = A = 20\%$.

And, $A + T = 40\%$

Since, $G = C$

and, remaining of $G + C = 60\%$

So, $G = C = 30\%$

31. (B) Both DNA and RNA are polymers of nucleotides. DNA is capable of replicating in all cases because it functions as hereditary material. RNA is formed from DNA by the process of transcription, only in few cases (RNA viruses) it functions as a hereditary material. The nitrogenous bases found in DNA are adenine and guanine (both purines) and cytosine and thymine (both pyrimidines), whereas in RNA purine bases are the same (*i.e.*, adenine, guanine), but in pyrimidines, the bases are uracil and cytosine, where thymine is replaced by uracil. DNA contains deoxyribose sugar, while RNA contains ribose sugar.

32. (C) The association of AGCT is with TCGA in DNA. In a DNA molecule, purine always binds with complementary pyrimidine. Adenine on one strand always binds with pyrimidine, thymine on the other strand. Similarly purine, guanine links with pyrimidine cytosine on the other strand.

33. (A) Pyrimidines are nitrogenous bases in the nucleotide components. There are three pyrimidines, cytosine (C), thymine (T) and uracil (U). In GATCAATGC, there are four pyrimidine bases.

34. (C) Tautomerisation occurs due to rearrangement of electrons and protons of the molecules. Due to tautomerisation, purines and pyrimidines in DNA and RNA may exist in several alternate forms or tautomers.

Related Theory

➥ *Tautomers are the type of structural isomers, formed by shifting pi-bonds between functional groups. They are interconvertible and also called keto-enol isomers. Tautomerisation converts the amino ($-NH_2$) group of cytosine and adenine into amino ($-NH$) group and keto group ($C = O$) of thymine and guanine into enol ($-OH$) group. This results in the pairing of tautomeric thymine with normal guanine and of cytosine with adenine, causing mutation. Such mutations are called tautomeric mutations.*

35. (A) A DNA with single strand will not possess its complementary base pairs. Hence, nitrogenous bases are unequal in number.

Related Theory

➥ *Watson and Crick gave the double helix model for the structure of DNA. The main criteria of their proposition was base pairing between the two strands of a polynucleotide chains. Later, Erwin Chargaff's rule stated that for a double stranded DNA, the ratio between adenine and thymine, and guanine and cytosine are constant and equal. The base pairing confers a very unique property of the polynucleotide chains. They are said to be complementary to each other. Therefore, if the sequence of bases in one strand is known then the sequence of other strand can be predicted.*

36. (D) In both RNA and DNA, purines are the same. The two purines are adenine and guanine. The two pyrimidines are cytosine and thymine in DNA but in RNA thymine is replaced by uracil.

37. (D) Nucleotide is the basic unit of nucleic acids (DNA and RNA). A nucleotide is made up of three components nitrogen bases, a pentose sugar and a

phosphate group. The two nitrogenous bases are purines and pyrimidines, which form the backbone of the nucleotide.

38. (D) According to Chargaff's rule, amount of adenine is equal to that of thymine and, cytosine is equal to that of guanine. A + G = T + C. If DNA segment has 120 bases of adenine and 120 cytosine bases, then the number of bases in the guanine and thymine base will also be the same as A = T and C = G. Therefore, there are 120 guanine bases and 120 thymine bases. So, the total number of nucleotides in a sequence are 480.

39. (D) Histones are organised to form a unit of 8 molecules called histone octamer. The negatively charged DNA is wrapped around the positively charged histone octamer to form a structure called nucleosome. An octamer of 4 histones complexed with DNA forms nucleosomes (H_2A, H_2B, H_3 and H_4). Centromere links a pair of sister chromatids together during cell division. Endosomes are a collection of intracellular sorting organelles in eukaryotic cells. They regulate trafficking of proteins and lipids among other subcellular compartments of the secretory and endocytic pathway. Mesosomes are folded invaginations in the plasma membrane of bacteria.

40. (D) Alfred Hershey and Martha Chase in 1952 provided evidence that DNA, and not protein, was the genetic material of viruses. They used radioactive labeling to track the transfer of genetic material from viruses to bacteria.

Related Theory

- *Wilkins and Franklin contributed to the understanding of the structure of DNA through their work on X-ray crystallography. Their data was used by Watson and Crick to propose the double helix structure of DNA.*
- *Frederick Griffith's experiment in 1928 demonstrated the phenomenon of transformation, where genetic material from dead bacteria can be taken up by living bacteria and change their phenotype.*

41. (C) RNA molecules are inherently less stable than DNA, and are more prone to mutations during replication due to the lack of proofreading mechanisms.

RNA viruses, such as influenza and HIV, have shorter life spans and replicate at a much faster rate than DNA viruses. This leads to a higher mutation rate and faster evolution of the virus.

42. (C) Alfred Hershey and Martha Chase (1952) experimentally proved that DNA is the sole genetic material in bacteriophage. They showed that when bacteriophages, which are composed of DNA and protein, infect bacteria, their DNA enters the host bacterial cell, but most of their protein does not. This proved that DNA is the hereditary material. Beadle and Tatum experimentally showed that one gene-one enzyme hypothesis using *Neurospora*. Meselson and Stahl first showed that DNA replicates semi-conservatively through experiments on *E. coli*. Jacob and Monod were first to explain *lac* operon.

43. (B) Genetic material should be structurally and chemically stable. A molecule that can act as a genetic material must fulfill the following criteria:

(1) It should be able to generate its replica (Replication).

(2) It should be stable chemically and structurally.

(3) It should provide a scope for slow changes (mutations) that are required for evolution.

(4) It should be able to express itself in the form of 'Mendelian characters'.

44. (C) Frederick Griffith discovered transformation using *Streptococcus pneumoniae* bacteria and mice. Meselson and Stahl demonstrated semi-conservative replication of DNA. Hershey and Chase concluded that DNA, not protein, was the genetic material. James D. Watson and Francis H.C. Crick discovered the double-helix structure of DNA.

45. (D) The unequivocal proof that DNA is the genetic material came from the experiments of Alfred Hershey and Martha Chase (1952). They worked with viruses that infect bacteria called bacteriophages.

46. (C) Transformation is the transfer of genetic material from one bacterial cell into another. In 1928, Frederick Griffith performed series of experiments with *Diplococcus pneumoniae* and witnessed miraculous transformation in the bacteria.

47. (B) Genome refers to the total sets of chromosomes carried by each cell of an organism. The genetic material of a cell is its genome. Eukaryotic genomes are composed of one or more linear, double-stranded DNA chromosomes. The eukaryotes are diploid. DNA is divided into several linear chromosomes in the nucleus. It is combined with histone proteins to form nucleosome groups. Prokaryotes are characterised by lack of nucleus or other membrane bound organelles. The genetic material in prokaryotes is a circular and single stranded DNA. It has no association of histones. It remains in direct contact with the cytoplasm.

48. (C) Alfred Hershey and Martha Chase in 1952 worked on *E.coli* and proved that DNA is the genetic material. They worked with bacteriophages (the virus that infect the bacteria) and attached them to the *E. coli* and found that its genetic material entered the bacterial cell. The bacterial cell treats the viral genetic

material as its own and start manufacturing more virus particles. They worked to discover whether it was protein or DNA from the viruses that entered the bacteria and experimentally proved that the genetic material that passed from virus to bacteria was DNA. Watson and Crick studied the double helix model for the structure of DNA. Frederick Griffith studied the transforming principle in his experiment with *Streptococcus pneumoniae*. Boveri and Sutton gave the chromosomal theory of inheritance.

49. (A) Frederick Griffith studied the transforming principle in his experiment with *Streptococcus pneumoniae* but could not discover the nature of genetic material. The genetic material was thought to be protein, prior to the work of Avery, Mac Leod and McCarty. They further worked on the Griffith's experiment to determine the biochemical nature of the transforming principle. They isolated protein, DNA and RNA from the heat killed S-cells to find out that which one could transform the R cells into S cells and proved that DNA is the transforming principle of *Pneumococcus*.

Related Theory

Frederick Griffith cultured Streptococcus pneumoniae, where some strains produced smooth shiny colonies (S), while others had rough (R) colonies. This happened due to the presence of polysaccharide coat on S-strain, which was virulent. R-strains were without coat and were non-virulent. S-strain infected mice died and R-strain infected ones did not develop pneumonia. After heat treatment, when bacterial cells were killed, S-strain injected into the mice did not kill them. But when a mixture of heat killed S- and live R-strains was injected, the mice died. The R-strain had been transformed into S-strained and had enabled the R-strain to synthesize a polysaccharide coat.

50. (B) The genes for *r*-RNAs tend to be highly conserved and are therefore, often employed for phylogenetic studies.

51. (A) (a) In 1928, Frederick Griffith, in a series of experiments with *Streptococcus pneumoniae* (bacterium responsible for pneumonia), witnessed a miraculous transformation in the bacteria.

(b) Francois Jacob and a biochemist, Jacques, Monod were the first to elucidate a transcriptionally regulated system, lac operon.

(c) Har Gobind Khorana developed a chemical method that was instrumental in synthesising RNA molecules with defined combinations of bases (homopolymers and copolymers). He was awarded for their interpretation of the genetic code and its function in protein synthesis.

(d) Matthew Meselson and Franklin Stahl showed semi-conservative DNA replication first in *Escherichia coli*.

52. (B) DNA replicates semi-conservatively. It was first shown in *E. coli* by Matthew Meselson and Franklin Stahl in 1958. *E. coli* cells with ^{15}N-dsDNA are incubated in a medium containing ^{14}N nucleotide. As each division of *E. coli* takes 20 minutes, in every 20 minutes 2 strands of DNA gets separated and a new DNA strand is synthesized using ^{14}N medium. DNA extracted from the culture after 40 minutes (*i.e.*, in the second generation, after 40 minutes) had two hybrid density DNA and two light density DNA. After, next 20 minutes (*i.e.*, 60 minutes IIIrd generation) each of these 4 DNAs will synthesize new DNA strands with 2/8 DNA of hybrid density and 6/8 DNA of light density. Thus after 60 minutes, 1 *E. coli* will form 6 *E. coli* cells, totally free from ^{15}N. Therefore, 10 *E. coli* will produce $10 \times 6 = 60$ *E. coli* cells free from ^{15}N.

53. (D) Ligases are the enzymes that join two DNA fragments. DNA polymerase enzyme is used to synthesise DNA using dNTPs. Nucleases hydrolyse the phosphodiester bonds of DNA and RNA. Exonucleases are broad classification of enzymes that cleave off the nucleotides one at a time from the 3' or 5' ends of DNA and RNA chains.

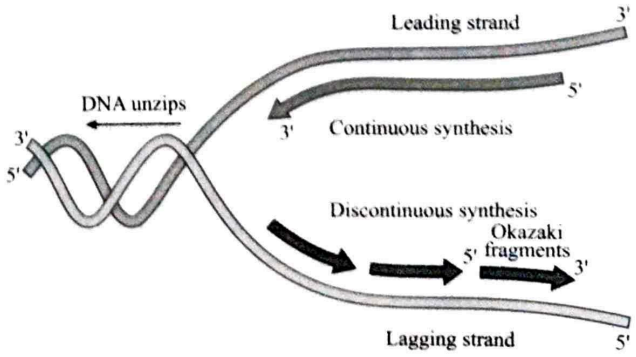
Related Theory

Both endonuclease and exonuclease are nuclease enzymes which can hydrolyze polynucleotide chains such as DNA and RNA. The main difference between these enzymes is that endonucleases cleave the phosphodiester bond in the polynucleotide present internally in the polynucleotide chain, whereas exonucleases cleave the phosphodiester bond from the ends. Accordingly, exonucleases require a free 3' or 5' end for their action, and release individual nucleotides after the hydrolytic reaction; while endonucleases do not require such a free end and release oligonucleotide chains after hydrolysis.

54. (D) Okazaki fragments are short segments of replicating DNA. They elongate the lagging strand away from replication fork. The leading strand is replicated towards the replication fork.

Related Theory

DNA polymerases can synthesize DNA in the 5' to 3' direction. One strand, which runs 5' to 3' towards the replication fork, is made continuously, because the DNA polymerase is moving in the same direction as the replication fork. This continuously synthesized strand is called the leading strand. The lagging strand is synthesized discontinuously in the form of short fragments called Okazaki fragments that are later connected covalently by DNA ligase to form a continuous strand.



DNA Replication

55. (B) In the DNA replication process new DNA arises from the parent DNA. Since bacteria is a prokaryote, it lacks a cell nucleus, so due to their primitive nature, they lack a well defined S-phase. DNA replication is bidirectional from the site of origin of replication. Therefore, in bacteria DNA replication occurs before fission. For propagation, bacteria mostly depends on binary fission. This is a simple process where a cell grows twice its size and then divide into two daughter cells.

Related Theory

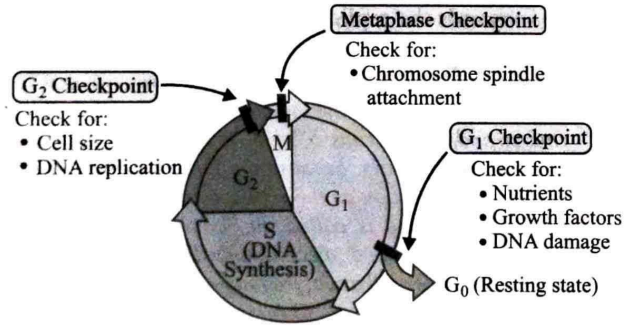
DNA is replicated by unwinding the helix. For this, unwinding enzyme. DNA helicase breaks the Hydrogen bonds between nitrogenous base pairs of two strands of DNA and separate them at the origin of replication, forming a replication fork in the form of Y.

56. (B) J.H. Taylor used radioactive thymine to detect semi-conservative mode of replication in DNA and chromosomes in *Vicia faba*. T.H. Morgan discovered linkage in *Drosophila melanogaster*.

57. (A) Stalled forks activate checkpoints signalling and pause replication. G_1/S checkpoint is activated and checks DNA damage and cell size prior to S-phase.

Related Theory

It is essential that the daughter cells produced be exact duplicates of the parent cell. Mistakes in the duplication of the chromosomes lead to mutations which can be lethal for an organism. To prevent this, the internal control mechanisms operate at three cell cycle checkpoints which halt the cell cycle until conditions are favourable. These checkpoints occur near the end of G_1, at the G_2/M transition, and during metaphase.



Cell Cycle

58. (C) Okazaki fragments in DNA are linked up by the enzyme DNA ligase after replacing the RNA primers with deoxyribonucleotides solution of the Okazaki fragments in DNA chain growth. Replication occurs always in 5' → 3' direction. However, Okazaki fragments are synthesized on 3' → 5' DNA template, join to form lagging strand which grows in 3' → 5' direction.

59. (A) The events for initiation of DNA replication in prokaryotes may be classified into:

(1) pre-priming (occurring only at the origin);

(2) priming recurring with the initiation of each Okazaki fragment during elongation phase.

Unwinding of DNA is followed by the synthesis of RNA primers by RNA primase.

60. (A) DNA ligase joins pieces of DNA together, mainly joins Okazaki fragments with the main DNA piece. DNA polymerase is responsible for forming new copies of DNA, in the form of nucleic acid molecules. DNA primase catalyses the synthesis of a short RNA segment called a primer complementary to a ssDNA template. Endonucleases are enzymes that cleave the phosphodiester bond within a polynucleotide chain.

61. (D) Matthew Meselson and Franklin Stahl in 1958 experimented on *E. coli* and proved that DNA replicates semi-conservatively. In semi-conservative replication of DNA, in each replica one half is the old strand and the other half is a new strand synthesized over it, wherein one strand is synthesized continuously and the other one is discontinuous. Since, each daughter DNA molecule contains one strand of the parent DNA double helix (only one strand synthesized is fresh), the process of replication is called semi-conservative method.

62. (B) The hereditary material present in bacterial chromosome is a circular, double stranded DNA molecule. The DNA is called a naked DNA as it is not associated with any histone proteins. This DNA is circular with no free ends.

Related Theory

The DNA is the genetic material and is present in all types of organisms either prokaryotes or eukaryotes in the form of chromosomes. It acts as a messenger of genetic information transferred to different generations. The DNA of all types of cells (prokaryotes or eukaryotes) duplicates itself by the process called DNA replication. This replicated DNA is divided into two daughter nuclei equally and transferred to the offsprings. After the division of the nucleus, the cell cytoplasm is divided and produces two daughter cells.

63. (D) Okazaki fragments are formed during DNA replication. DNA replication is discontinuous over the lagging strand, which means that on this strand DNA polymerase synthesize only short stretches of DNA due to opposite running of DNA template. These short DNA segments are called Okazaki particles. DNA ligase joins these Okazaki fragments and forms the continuous complementary strand.

Related Theory

Transcription is the process of copying genetic information from one strand of DNA into RNA. Translation refers to the process of polymerization of amino acids to form a polypeptide. Transduction is the process by which a virus or viral vector transfers genetic material from one bacterial cell to another.

64. (C) DNA gyrase unwinds the DNA helix during replication. Gyrases or topoisomerases II are enzymes that remove the super coiling in DNA strands during replication. These enzymes cut the phosphodiester bonds on both DNA strands and releases the supercoil.

65. (A) Enzyme DNA helicase separate two DNA strands. It functions by melting the hydrogen bonds that holds the DNA in a double helix structure. It is also known as 'Unwindase'. It opens up the DNA to allow for replication. In prokaryotes, helicase or unwindase is assisted by gyrase in this function. DNA polymerase uses a DNA template to catalyse the polymerisation of deoxynucleotides. Gyrase helps in the opening of DNA double helix in the form of replication fork and topoisomerases are enzymes that remove the super coiling in DNA strands during replication.

66. (A) Meselson and Stahl (1958) cultured *Escherichia coli* on ammonium chloride having heavy isotope of nitrogen for several generations to study the semi-conservative replication of DNA. *Pneumococcus* was used as an experimental material by Frederick Griffith in transforming principle to identify the nature of the genetic material. *Neurospora crassa* was used by Beadle and Tatum to postulate one gene one enzyme theory. *Drosophila melanogaster* was used by T. H. Morgan, who formulated chromosomal theory of inheritance.

67. (B) When *Escherichia coli* fully labelled with N^{15} is allowed to grow in N^{14} medium, then after the first generation of replication, the strands will have intermediate density between heavy and light bands due to the semi-conservative replication of DNA. One of the two strand would have N^{15} and the other strand would have N^{14}. Therefore, these two molecules of DNA will be similar but not same in density.

68. (D) DNA replication is semi-conservative and discontinuous. The two strands of DNA would separate and act as a template for the synthesis of new complementary strands. After the completion of replication, each DNA molecule would have one parental and one newly synthesized strand. This is semi-conservative DNA replication. During replication the strand formed in leading strand is continuous, while the lagging strand is discontinuous and breaks up into small fragments or pieces, called Okazaki fragments. These discontinuously synthesized fragments are later joined by the enzyme DNA ligase.

69. (A) RNA polymerase associate transiently with Rho factor, a bacterial protein to terminate the transcription, not to initiate the transcription.

70. (C) In eukaryotic nuclei, RNA Pol I transcribes rRNA genes, RNA Pol II synthesis mRNA and regulatory RNAs like snRNAs and mi RNAs, and RNA Pol III transcribes tRNAs, 5S rRNA, and other small regulatory RNAs.

Each polymerase specialises in producing specific type of RNA crucial for cellular processes, such as RNA regulation and protein synthesis.

71. (C) A transcription unit in DNA typically includes three regions - Promoter, structural gene, terminator, with the promoter located towards 5' end (upstream) initiating transcription, the structural gene encoding the protein, and the terminator located towards 3' end (downstream) signaling the end of transcription.

72. (C) In *E.coli* during replication, the DNA dependent DNA polymerase catalyse polymerisation only in one direction, that is 5' → 3'.

⚠ Caution

➥ *Some students think that in the leading strand, DNA is synthesised in the 5' → 3' direction, while in the lagging strand, DNA is synthesised in the 3' → 5' direction. But in both strands, DNA is synthesised in the 5' → 3' direction.*

73. (D) The given sequence represents the template strand that is to be coded.

3' TACATGGCAAATATCCATTCA 5'

5' ATGTACCGTTTATAGGTAAGT 3' (Coding strand)

The sequence of coding strands with polarity (5' → 3') is same as RNA (except thymine at the place of uracil).

Therefore, the correct product of DNA dependent RNA polymerase will be:

5' AUGUACCGU

UUAUAGGUAAGU 3'

74. (C) In eukaryotes, RNA polymerase III codes for *sn*RNAs, tRNA and 5S *r*RNA. Rho factor is responsible for termination of transcription. Splicing of exons is performed by *sn*RNPs. TATA box is present in the promoter region of transcription unit.

75. (A) To determine the sequence on the corresponding coding strand, we need to remember that DNA strands are complementary and antiparallel. This means that the sequence on the coding strand will be complementary to the mRNA sequence, read in the 5' to 3' direction. Also, RNA contains uracil (U) instead of thymine (T).

Given mRNA sequence:

5' AUCGAUCGAUCGAUCGAUCGAUCG 3'

Complementary DNA sequence:

3' TAGCTAGCTAGCTAGCTAGCTAGC TAGC 5'

Coding DNA strand:

5' ATCGATCGATCGATCGATCGATCG 3'

76. (D) RNA polymerase III (Pol III) is responsible for the transcription of several types of RNA molecules, including transfer RNA (*t*RNA), 5S ribosomal RNA (*r*RNA), and small nuclear RNA (*sn*RNA).

Pol III is one of three RNA polymerases in eukaryotic cells that is responsible for transcribing DNA into RNA. Pol III is responsible for transcribing genes that code for small functional RNAs, which are generally less than 300 nucleotides in length.

Transfer RNA (*t*RNA) molecules are involved in protein synthesis, and carry amino acids to the ribosome, where they are incorporated into the growing protein chain. The 5S ribosomal RNA (*r*RNA) is a component of the large ribosomal subunit, while snRNAs are involved in RNA splicing and other RNA processing events.

Related Theory

The genes transcribed by RNA Pol III fall in the category of "housekeeping" genes whose expression is required in all cell types and most environmental conditions.

Caution

Students usually get confused with RNAs transcribed by various polymerases. RNA polymerase I transcribes rRNA s(28S, 18S, 58S), RNA polymerase II transcribes precursor of mRNA, heteronuclear RNA (hnRNA) and RNA polymerase III transcribes tRNA and 5S rRNA and snRNAs.

77. (B) Rho factor attaches to the mRNA transcript and uses its helicase function to track along the transcript toward the moving RNA polymerase. Upon catching up with the polymerase, Rho catalyses the dissociation of mRNA from genomic DNA and the RNA polymerase.

Related Theory

A sigma factor is a protein needed for initiation of RNA synthesis. It is a bacterial transcription initiation factor that enables specific binding of RNA polymerase to gene promoter. Rho is an ATP-dependent RNA-stimulated helicases that disrupt the nascent RNA-DNA complex.

78. (B) The DNA dependent RNA polymerase is only capable of catalysing the process of elongation. It associates transiently with initiation-factor (σ) and termination-factor (ρ) to initiate and terminate the transcription respectively.

Related Theory

Rho factor attaches to the mRNA transcript and uses its helicase function to track along the transcript toward the moving mRNA polymerase.

79. (D) siRNAs are highly specific and usually synthesized to reduce the translation of specific messenger RNAs (mRNAs). This is done to reduce the synthesis of particular proteins. They form from double-stranded RNA transcribed and then cut to size in the nucleus before releasing into the cytoplasm. mRNA, tRNA and rRNA are the major types of RNA needed to synthesize a protein in a cell.

Related Theory

The siRNA is an exogenous double-stranded RNA uptaken by cells, while miRNA is single-stranded and comes from endogenous non-coding RNA. Besides, the siRNA is present in lower animals and plants, but not found in mammals; whereas miRNAs are present in all the animal and plant.

80. (C) During transcription, RNA polymerase binds to the promoter sequence near the beginning of a gene, to initiate the transcription process. RNA polymerase is also responsible for the unwinding of DNA helix and activates the process of elongation. DNA helicase is responsible for unwinding of DNA helix during replication process. DNA polymerase functions during replication. DNA ligase joins the DNA fragments.

81. (C) RNA polymerase I transcribes rRNAs (28S, 18S and 5.8S). RNA polymerase II transcribes hnRNA (or precursor of mRNA). RNA polymerase III transcribes tRNA, 5S rRNA and snRNA.

82. (A) In prokaryotic transcription, initiation and termination factors includes σ factor and ρ factor. To begin transcription, the RNA polymerase holoenzyme assembles at the promoter. The dissociation of σ allows the core enzyme to proceed along the DNA template, synthesizing mRNA by adding RNA nucleotides. While Rho-dependent termination is controlled by the rho protein, which tracks along behind the polymerase on the growing mRNA chain. Near the end of the gene, the polymerase interact with rho releases the mRNA from the transcription bubble. In eukaryotic transcription, initiation factors include TF-IIA, TF-II H and termination factors includes TTF-I.

Related Theory

Both prokaryotes and eukaryotes perform fundamentally the same process of transcription, with the important difference of the membrane-bound nucleus in eukaryotes. With the genes bound in the nucleus, transcription occurs in the nucleus of the cell and the mRNA transcript must be transported to the cytoplasm. In prokaryotes, which lack membrane-bound nuclei and other organelles, transcription occurs in the cytoplasm of the cell.

83. (C) RNA polymerase I transcribes rRNA. RNA polymerase II transcribes precursor of mRNA, hnRNA (heterogeneous nuclear RNA) and RNA polymerase III is responsible for the transcription of tRNA, 5srRNA and snRNAs (small nuclear RNAs).

84. (B) Cistron is equivalent to structural gene. Cistron is a segment of DNA coding for a polypeptide. Muton is a small segment of DNA in which mutation occurs. Operon is the functional unit of a DNA having number of genes. Recon is the unit of DNA for recombination.

Caution

- *Students should remember that eukaryotic structural gene is monocistronic while prokaryotic is polycistronic.*

85. (C) In bacteria, 23S rRNA act as structural RNA, for the synthesis of proteins as well as ribozyme.

Caution

- *Students should remember that ribozyme is the only known non-proteinaceous enzyme.*

86. (A) DNA dependent RNA polymerase catalyses transcription on template strand of DNA. It decodes its information directly through RNA polymerase.

Related Theory

- *Transcription is the process of transfer of genetic information from DNA to mRNA. It is done by formation of RNA over the template of DNA. It creates single stranded RNA which has a coded information similar to the sense or coding strand of DNA (with the exception of U in place of T). The DNA strand which function as template for RNA synthesis is the template or antisense strand. It has 3′ → 5′ polarity and transcription proceeds in 5′ → 3′. The segment of DNA that takes part in transcription is called transcription unit.*
- *Template strand runs in 3′ → 5′. It contains the same nucleotide sequence as the tRNA and is made up of complementary nucleotide sequence as the mRNA. Coding strand runs in 5′ → 3′. It contains the complementary nucleotide sequence as the tRNA and also contains the same nucleotide sequence to mRNA, except thymine.*

87. (A) Transcription is a process of writing information from DNA to *m*RNA, not *t*RNA. In translation, the *m*RNA is used to form protein. Repressor protein is a protein which binds to operator to stop enzyme synthesis. Operon consists of structural genes, operator and promoter.

Caution

- *Students should remember that in eukaryotes, transcription occurs in nucleus whereas in prokaryotes it occurs in the cytoplasm. In eukaryotes, RNA processing is required as its structural gene is monocistronic whereas in prokaryotes it does not require because its structural gene is polycistronic.*

88. (A) RNA polymerase III transcribe *t*RNA, RNA polymerase II transcribe *hn*RNA which modified to form *m*RNA and RNA polymerase I form *r*RNA.

Related Theory

- *Bacteria contain a single type of RNA polymerase, while eukaryotes (multicellular organisms and yeasts) contain three distinct types- RNA polymerase I, II, III.*

89. (D) During the process of splicing, introns are removed from the pre-*m*RNA by the spliceosome and exons are spliced back together. If the introns are not removed, the RNA would be translated into a non-functional protein. Splicing occurs in the nucleus before the RNA migrates to the cytoplasm.

Related Theory

- *The spliceosome controls mRNA splicing. The spliceosome is composed of particles made up of both RNA and protein.*

90. (B) Messenger RNA production requires synthesis of a pre-*m*RNA by RNA Pol II and processing of the nascent precursor by 5' capping, splicing of introns, and 3' cleavage or poly-adenylation to make mature *m*RNA. This occurs in nucleoplasm of the cell (or inside nucleus).

Related Theory

- *In molecular biology, splicing refers to editing of the precursor messenger RNA (pre-mRNA) transcript into a mature messenger RNA (mRNA) wherein introns are removed and exons are joined together i.e., they are ligated. Splicing occurs within the nucleus after transcription.*

91. (C) The DNA binding sequence for RNA polymerase is called TATA box. The TATA box is present in the eukaryotic promoter region. It is a 7-bp long region located 20 bp upstream to the start point. It is surrounded by GC rich sequences. During the process of transcription, the RNA polymerase (a holoenzyme which has a core unit and a sigma factor for proper initiation of transcription) binds to the TATA box because of which DNA assumes a saddle-like structure at this place.

Related Theory

- *In molecular biology, the TATA box (also called the Goldberg-Hogness box) is a sequence of DNA found in the core promoter region of genes in archaea and eukaryotes. The bacterial homolog of the TATA box is called the Pribnow box which has a shorter consensus sequence.*

92. (B) Molecular basis of organ differentiation depends on the modulation in transcription by transcription factor. A transcription factor regulates and controls the process of transcription by binding to specific sequences in the DNA.

93. (A) During transcription, complementary *m*RNA is formed on DNA template, where thymine is replaced by uracil. So, GACUAUCG will be the sequence.

94. (A) Promoter region is the proximal area of transcription unit, which provides site for attachment of transcription factors (σ factor) and RNA polymerase. It is present upstream at 5′ end of coding strand. It has special structure; an AT rich area called TATA box or Pribnow box.

95. (A) An exon is the portion of a gene that codes for amino acids. In the cells of plants and animals, most gene sequences are broken up by one or more DNA sequences called introns. The parts of the gene sequence that are expressed in the protein are called exons, because they are expressed, while the parts of the gene sequence that are not expressed in the protein are called introns, because they come in between or interfere with the exons.

Related Theory

➥ *Exons usually include both the 5′ and 3′ untranslated regions of mRNA, which contain start and stop codons, in addition to any protein coding sequences.*

96. (C) RNA ligase rejoines the exon segments after RNA splicing is finished.

97. (C) Eukaryotes have three types of RNA polymerases:

(1) **RNA polymerase I:** It transcribes rRNAs (28S, 18S and 5.8S). It is found in the nucleus and responsible for rRNA synthesis.

(2) **RNA polymerase II:** It is responsible for mRNA synthesis and found in the nucleoplasm.

(3) **RNA polymerase III:** It is responsible for the transcription of tRNA, 5S rRNA and snRNAs. It is also found in the nucleoplasm.

98. (A) The enzyme polymerase catalyse the polymerization of the bases only in 5′ → 3′ direction. The strand that has the polarity 3′ → 5′ acts as a template and is referred to as template strand, while the former is called the coding strand.

99. (B) The RNA in case of eukaryotes contains non-coding intervening sequences called introns. In the splicing process, introns are removed through cutting and exons (the essential coding sequences) are joined in a definite order.

100. (C) In eukaryotes, the monocistronic structural genes have interrupted coding sequences, thus the genes are called split genes. These split genes have protein coding regions called exons, which are interrupted by non-coding DNA segments called introns. Exons are transcribed into RNA and further translated into proteins. Introns do not code for any proteins synthesis. Cistron is a segment of DNA coding for a polypeptide. The operon is a cluster of genes that are regulated by a single promoter. It has regulatory gene and structural genes.

101. (D) Protein synthesis involves initiation, elongation and termination. It does not involve transcription, which is the process of synthesis of RNA from DNA.

102. (D) Reverse transcription is the process of making DNA over RNA with the help of enzyme reverse transcriptase. This enzyme is present in certain viruses which have genetic material as RNA, to duplicate their genome. Here, RNA segment is the template which synthesises cDNA. The second strand of cDNA is synthesised to make a double-stranded structure of viral DNA. The enzyme used is RNA-dependent DNA polymerase.

Related Theory

➥ *The enzymes are encoded and utilized by infections to reverse the replication. For e.g., reteroviruses, utilize the enzyme to reverse translate their RNA genomes into DNA, which then gets incorporated into the host genome and reproduces there. HIV infections are also the example of reverse transcriptase. Without reverse transcriptase, viral genome does not have the option to enter the host cell and reproduce there.*

103. (D) Transcription is the process of copying genetic information from one strand of DNA into RNA. Translation refers to the process of polymerization of amino acids to form a polypeptide. Transversion is a mutation in which a purine nucleotide is changed into a pyrimidine nucleotide and vice-versa (A or G with T or C). Translocation is a type of rearrangement, where a block of genes from one chromosome are transferred to other non-homologous chromosome. It required an elongation factor and GTP (energy molecule).

Related Theory

➥ *Central dogma of protein synthesis explains a unidirectional flow of information from DNA to RNA (Transcription) and from RNA to polypeptide (Translation).*

104. (D) The ribosome reads the mRNA in three nucleotide codons, beginning with the start codon, AUG, which codes for the amino acid methionine.

Related Theory

➥ *The start codon marks the site at which translation into protein sequence begins, and the stop codon marks the site at which translation ends. AUG is the most common START codon. There are 3 STOP codons in the genetic code – UAG, UAA, and UGA.*

Caution

➥ *Students should remember that AUG codes for the amino acid methionine (Met) in eukaryotes and formyl methionine (fMet) in prokaryotes.*

105. (B) The *m*RNA will be complementary to DNA template strand, but in RNA, thymine is replaced by uracil. Thus,

3' ATGCATGCATGCATG 5'-DNA template strand

5' UACGUACGUACGUAC 3'- Transcripted *m*RNA strand.

Caution

- *Students usually forget that RNA is always synthesised in 5' → 3' direction and template strand used for the transcription is always 3' → 5' direction.*

106. (D) Characteristics of the genetic codon:

(1) It is a triplet code.

(2) It is comma free and *m*RNA read three bases at a time without skipping any bases.

(3) It is non-overlapping.

(4) It is non-ambiguous (one codons code for only one amino acid).

(5) It is universal.

(6) It is degenerate (some amino acids are coded by more than one codon).

(7) The code has start (AUG) and stop signals (UAG, UAA, and UGA).

107. (A) Deletion of GGU from 7^{th}, 8^{th} and 9^{th} position will not change the reading frame of *m*RNA: AAC AGC GGU GCU AUU. There is no change in the reading frame occurs after removing three nucleotide pairs.

Related Theory

- *Insertion of G at 5^{th} position will be read as AAC AGG CGG UGC UAU U. In this case leaving out a single U won't give the same reading frame.*
- *Deletion of G at 5^{th} position will be read as AAC ACG GUG CUA UU. In this case UU as a pair of two is left out. Hence, it will also not give the same reading frame.*
- *Adding A and G at 4^{th} and 5^{th} position will be read as AAC AGA GCG GUG CUA UU. Again in this case the last UU is a pair of two. Hence, the option is wrong.*

108. (C) The corresponding sequence of transcribed *m*RNA by template or non-coding strand (complementary to RNA) is AGGUAUCGCAU.

Related Theory

- *The only difference between the coding strand and the new mRNA strand is instead of thymine, uracil takes its place in the mRNA strand. The coding strand is also called the sense strand. The coding strand runs in a 5' → 3' direction, while template strand runs in a 3' → 5' direction.*

Caution

- *Students usually get confused between coding strand and template strand. Coding strand is the one that codes for mRNA. It has same nucleotides sequence as that of mRNA, except thymine (T) is replaced by uracil (U) in mRNA. Template strand is the one from which mRNA is transcripted. In this, mRNA consist of complementary base pairs to that of template strand.*

109. (C) 1 codon consists of 3 bases.

Thus, for 999 bases, no. of codons $= \frac{999}{3} = 333$

If 901^{st} base is deleted, the codons after 901 base will be affected.

Number of bases left $= 999 - 901 = 98$

Thus, number of codons affected $= \frac{98}{3} = 33$ codons.

110. (D) AUG (codes for methionine) is a initiation codon while UGA, UAA and UAG are terminating codons during the process of translation.

Related Theory

- *Translation is the mechanism by which the triplet base sequences of mRNA molecules (codons) are converted into a specific sequence of amino acids in a polypeptide chain. It occurs on ribosomes. The order and sequence of amino acids is defined by the sequence of bases in mRNA. The amino acids are transferred to the ribosomes by the tRNA. The initiation of formation of polypeptide chain is brought about by AUG codon which codes for methionine. The termination of polypeptide is signalled by one of the three stop codons in the mRNA (UAA, UAG, UGA).*

111. (B) In RNA, Thymine base is replaced by Uracil.

Hence,

ATCTG	—	Template DNA
TAGAC	—	Coding DNA strand
UAGAC	—	Complementary RNA strand

112. (D) Change in a single base pair of DNA causes mutation. Such mutations are called point mutations. Cancer is an uncontrolled process of cell division, caused by the mutation in the DNA of the cell. A frame shift mutation is a genetic mutation caused by the deletion or insertion in a DNA sequence that shifts the way the sequence is read. UV and gamma rays are the mutagens that causes mutation.

113. (A) Nirenberg and Matthaei deciphered the first of the 64 triplet codons in the genetic code by using nucleic acid homopolymers to translate specific amino acids. Hershey and Chase concluded that protein was not a genetic material, and that DNA was the genetic material. T.H. Morgan studied linkage in *Drosophila*. Alfred Henry Sturtevant developed a technique for genetic mapping in the fruit fly, *Drosophila*. Beadle and Tatum gave one gene-one enzyme hypothesis.

Related Theory

- *If genes are located in a consistent linear order along a chromosome, then the distance between any two genes and the amount of crossing over should be in direct proportion. The percentage of crossing over therefore gives direct measure of the chromosomal crossing over. In turn, it directly measure the distance between the genes involved.*

114. (B) Point mutation involves change within a gene in which one base pair in the DNA sequence is altered. There are two types of point mutations: Substitution mutations cause a single base pair to be exchanged for another. Frame shift mutations occur when a base is added or removed, the entire codon sequence following the mutation changes. Insertion and deletion causes frame shift mutation.

Related Theory

Point mutations are frequently the result of mistakes made during DNA replication, although modification of DNA, such as through exposure to X- rays or to ultraviolet radiation also can induce point mutations.

115. (C) The three codons UAA, UAG and UGA are stop codons or terminator codons. In option (A) UUA is leucine but UCA is serine. So it is incorrectly matched. In option (B) GUU codes for valine, while GCU codes for alanine. This is also wrongly matched. In option (D) AUG is a start codon and also codes for methionine but ACG codes for threonine.

116. (C) According to the central dogma genetic information flows unidirectionally from DNA to *m*RNA and from *m*RNA to protein. DNA code determines the code in *m*RNA and *m*RNA determines the sequence of amino acids (building blocks of proteins). Mutation causes changes in the DNA sequence. Mutation at gene level causes a change in nucleotide (in DNA segment) sequence. Hence, any change in nucleotides (in DNA) would result in change in the *m*RNA coding and wrong *m*RNA will produce wrong chain of amino acids. Thus, the change in the structure of protein or enzyme might lead to the change in the character of an organism.

Related Theory

In some viruses, genetic information flows in reverse direction from RNA to DNA. This is reverse transcription and the enzymes catalyzing this reaction are reverse transcriptase or RNA dependent DNA polymerase.

117. (C) Template strand only serves as the template for transcription whereas coding strand contains the exact same sequence of nucleotides in the *m*RNA except thymine.

Coding DNA strand	—	5'-ATACG-3'
Template DNA strand	—	3'-TATGC-5'
*m*RNA synthesised	—	5'-UAUGC-3'

118. (D) The *t*RNA molecule has a distinctive folded structure with three hairpin loops that form the shape of a three-leafed clover. One of these hairpin loops contains a sequence called the anticodon, which can recognize and decode an *m*RNA codon. Each *t*RNA has its corresponding amino acid attached to its end.

119. (A) The genetic information flows from,

$$DNA \rightarrow mRNA \rightarrow protein$$

A mutation involves a change in the sequence of nucleotides in a nucleic acid molecule. This change will express itself in the form of a change in the sequence of amino acids in the protein molecule synthesized through the information encoded in nucleic acid segment. Therefore mutations at molecule level can be studied both by the study of the sequence of amino acids in a protein and also by the study of sequence of nucleotides in a segment of nucleic acids.

120. (B) There are 64 possible base triplets and only 20 amino acids. Some amino acids are encoded by more than one codon. In fact, 61 of the 64 possible triplets specify particular amino acids and 3 triplets (called stop codons) designate the termination of translation.

121. (D) Each codon is specific for only one amino acid (or one stop signal), yet the genetic code is described as degenerate, or redundant, because a single amino acid may be coded by more than one codon. The codons that code for one amino acid can differ in any of their places; nevertheless, the second or third codon is more frequent.

122. (D) Codon UAC is correctly matched as it codes for amino acid tyrosine. Stop codons are UAA, UAG and UGA. Start codon includes AUG (Methionine). UGC and UGU codes for cystine amino acid. UUC codes for phenylalanine. Codon UCG codes for serine.

123. (C) If UAU is mutated to UAA, the codon will stop. UAA is the stop codon. Therefore at 25^{th} amino acid the synthesis of polypeptide stops. The chain will not grow after 24^{th} amino acid. In the absence of a new initiating or start codon, other codons will not be able to translate.

Related Theory

There are 64 codons in total in a genetic code of which 61 codons code for amino acids and the three codons UAA, UAG and UGA do not code for any amino acids and are called terminator codons or stop codons. Protein synthesis terminates when stop codons are read.

124. (B) A mutation is a change in a DNA sequence. Mutations can result from DNA copying mistakes made during cell division, exposure to ionizing radiation, exposure to chemicals called mutagens, or infection by viruses.

Related Theory

Chromosome mutation is the process of change that results in rearranged chromosome parts, abnormal numbers of individual chromosomes, or abnormal numbers of chromosome sets.

125. (A) Degeneracy of codons is the redundancy of the genetic code, exhibited as the multiplicity of three-base pair codon combinations that specify an amino acid. The exceptions are methionine (AUG) and tryptophan (UGG).

126. (C) *t*RNA plays a role of an adapter molecule for carrying amino acid to the *m*RNA template during protein synthesis. It has anticodon loops that has bases complementary to the code, and it also has an amino acid acceptor end to which it binds to amino acids. *t*RNAs are specific for each amino acid.

127. (D) UAA, UAG, UGA are the chain terminating codons. They act as the stop codons and do not read for any amino acids. Protein synthesis terminates when stop codons are read.

128. (B) Transcription is the process of carrying genetic information from one strand of DNA into RNA. It is governed by the principle of complementarity, where *m*RNA is synthesized on DNA template by the complementary bases. In this condition, thymine replaces uracil in the RNA strand, so the sequence of bases will be UAAGCUAC.

129. (D) In a genetic code, the codon is a triplet, where 61 codons code for amino acid and 3 codons do not code for any amino acid, they are the stop codons. Each codon has three bases which can undergo transition and transversion. So, the number of base substitution possible in the amino acid codon is $61 \times 3^2 = 549$.

Related Theory

- *Base substitution is the result of mutation. Transversion is a mutation in which a purine nucleotide is changed into a pyrimidine nucleotide and vice-versa (A or G with T or C). Transition refers to a point mutation in which a purine nucleotide is replaced by another purine (A = G) or a pyrimidine nucleotide to another pyrimidine (C = T), resulting in the change in the number of base substitution.*

130. (C) Dr. Hargobind Khorana deciphered first triplet codon of threonine and histidine.

131. (A) Genetic code is a triplet, coding for one amino acid in a polypeptide chain. There are four different types of nucleotide bases: A, U, G and C. Sequence of 3 consecutive bases in a DNA molecule codes for one specific amino acid. Since the code is a triplet thus 64 ($4 \times 4 \times 4$) distinct triplet of bases determine the 20 amino acids. Out of these 64 triplets only 61 codons code for 20 amino acids. The three codons (UAA, UAG and UGA) do not code for any amino acids. They are called the stop codons or terminator codons. In 61 triplet codons, more than one codon codes for same amino acid.

132. (D) Genetic code directs the sequence of amino acids during protein synthesis. Therefore, genetic code is the relationship between amino acid sequence in a polypeptide chain and base sequence of *m*RNA (which store information for linking the amino acid in a definite sequence during protein synthesis). These nitrogenous bases are adenine, guanine, cytosine and uracil.

133. (C) The ribosome is composed of both proteins and RNA molecules. In prokaryotes, the small subunit of the ribosome consists of 21 proteins and a single RNA molecule, while the large subunit consists of 34 proteins and three RNA molecules. In eukaryotes, the small subunit consists of about 33 proteins and a single RNA molecule, while the large subunit consists of about 49 proteins and four RNA molecules. Therefore, the total number of different proteins that make up the ribosome can vary depending on the organism, but a general estimate would be around 80 different proteins.

134. (A) Translation is the process of polymerization of amino acids to form a polypeptide. Ribosomes is the cellular factory responsible for synthesizing proteins. The ribosome consists of structural RNAs and about 80 different proteins. It exists as two subunits in its inactive state, a larger and a smaller subunit. When the small subunit encounters an *m*RNA, the process of translation of the *m*RNA to protein begins.

135. (C) Ribozymes are RNA molecules having enzymatic activity, *i.e.*, they are capable of catalysing specific biochemical reactions. Hence, they are nucleic acids with enzymatic function.

136. (C) Translocation is the process in which one gene moves from one linkage group to the other. Inversion, duplication, transversion and translocation are the types of point mutations, which lead to variation. Crossing over is the exchange of genetic material between non-sister chromatids of two homologous chromosomes.

Related Theory

- *All the genes which are located on a single chromosome form one linkage group. The total number of linkage groups in an organism corresponds to the haploid number of chromosomes, i.e., to the number of chromosome pairs.*

137. (C) 23S rRNA in bacteria is the enzyme ribozyme which acts as a catalyst in splicing of RNA during protein synthesis. It is found in large sub-unit (70S) of ribosome of bacteria.

Related Theory

- *Ribozyme is the only non-protein enzyme known so far, rest all the enzymes are proteinaceous.*

138. (C) In the process of protein synthesis, messenger RNA is responsible for carrying the genetic code transcribed from DNA. The process is known as translation and it occurs in ribosomes. The sequence of amino acids in a particular protein is determined by the sequence of nucleotides in *m*RNA. Ribosomal RNA (*r*RNA) help translate the information in messenger RNA (*m*RNA) into protein. Transfer RNA, or *t*RNA bring amino acids to the ribosome for protein production in a specific order, and reads the codons from the messenger RNA or *m*RNA.

139. (A) The genetic code is degenerate. All amino acids are coded by more than one codon (except methionine and tryptophan, that has single code for each). Degeneracy means lack of specificity, so the presence of more than one codon for a single amino acid causes degeneracy. The maximum number of codons for an amino acid is six *e.g.*, serine (UCU, UCC, UCA, UCG, AGU and AGC). Degeneracy results in protection against mutation.

140. (D) Peptidyl transferase reaction does not require energy. The reaction is catalyzed by the enzyme peptidyl transferase and forms a peptide bond between adjacent amino acids. Aminoacyl *t*RNA bind to the larger ribosomal unit once *t*RNA is activated and involves elongation factor EF-G and energy (GTP). Amino acid activation requires energy, it involves the addition of amino acid to *t*RNA and the reaction is catalyzed by aminoacyl *t*RNA synthase and uses ATP (cleavage of ATP to AMP and PPi). Translocation is a type of rearrangement, where a block of genes from one chromosome are transferred to other non-homologous chromosome. It required an elongation factor and GTP (energy molecule).

141. (A) Glucose and galactose do not have binding sites for attaching the repressor protein so that they can never induce the *lac* operon.

142. (B) The lactose present in the growth medium of bacteria is transported into the cell primarily by a transporter protein known as permease. This protein facilitates the entry of lactose into bacterial cells by active transport.

143. (D) *Lac* operon of *E.coli*, regulates the metabolism of lactose. The genes of the *lac* operon include *lac z*, *lac y*, and *lac a*, which encode for the enzymes β-galactosidase, permease, and transacetylase, respectively. The expression of these genes is controlled by the regulatory gene *lac i*, which encodes for the repressor protein.

Mnemonics

➥ *Enzymes coded by the genes in lac operon model can be memorised as:*

Zeeshan ka Beta Yoyo lene Paris Aaya Train se

	Gene	***Enzyme***
Zeeshan ka Beta	Gene ***'z'***	*β-galactosidase*
Yoyo lene Paris	*Gene* ***'y'***	***Permease***
Aaya Train se	*Gene* ***'a'***	***Transacetylase***

144. (C) The *lac* operon consists of one regulatory gene (*i* gene) and three structural genes (*z*, *y* and *a*). These genes codes for β-galactosidase, permease and transacetylase, respectively. All the three genes of *lac* operon are required for lactose metabolism. The repressor of the operon is synthesised from the *i* gene. The repressor protein binds to the operator region of the operon and prevents RNA polymerase from transcribing the operon. In the presence of an inducer, such as lactose or allolactose, the repressor is inactivated by the interaction with the inducer. This allows RNA polymerase access to the promoter and the transcription proceeds. Now, if *i* gene gets mutated and its product cannot bind the inducer molecule, then the repressor will remain activated, thus blocking transcription. The repressor protein binds to operator region of operon and prevents RNA polymerase from binding to operon. Hence, *z*, *y* and *a* genes will not be translated.

145. (A) *Lac* operon is a regulatory unit of DNA containing cluster of genes in prokaryotes, consisting of structural genes, operator, promoter and regulatory gene. Enhancer are the sequences present in eukaryotes that help in the transcription of genes.

146. (B) Francois Jacob and Jacques Monad proposed the model of gene regulation termed as *lac* operon. In *lac* operon, a polycistronic structural gene is regulated by a common promoter and regulatory genes. Such arrangement is very common in bacteria and is referred to as operon.

147. (B) Allolactose/lactose is known as inducer because in its presence it turns on, or induces the expression of the *lac* genes.

Related Theory

➥ *When lactose is present outside the cell, it crosses the cell membrane and acts as an inducer of the operon. It does so once lactose is broken down to create allolactose. The lac operon is then membrane facilitating lactose transport into the cell, and β-galactosidase, which eats up lactose to make glucose molecules and β-galactosidase also makes allolactose. This leads to a positive feedback loop.*

148. (A) In non-sense mutation, the substitution of single codon results in the formation of stop codon, which terminate polypeptide synthesis. In *lac* operon, Gene *z* is transcribed, before gene *y* and then gene *a*. Hence, non-sense mutation in gene *y* will stop

transcription of gene *y* and gene *a* and only gene *z* will be functional. Thus, β galactosidase will be produced but no other enzyme will be produced.

149. (A) When *E. coli* is exposed to both lactose and glucose, the organism first metabolise glucose and then temporarily cease to grow until the genes of *lac* operon become included to provide the ability to metabolise lactose. Allolactose is called an inducer because in its presence it turns on, or induces the expression of the *lac* genes.

150. (C) Lactose in *lac* operon acts as an inducer that binds with the repressor and inactivates it.

z-gene codes for β-galactosidase. Permease is coded by y-gene.

151. (B) The *lac* operon consists of:

(1) Regulatory gene *i*: It codes for the repressor protein.

(2) Structural gene:

(i) *z* gene: codes for β-galactosidase which catalyses the hydrolysis of lactose into glucose and galactose.

(ii) *y* gene: codes for permease which regulates the lactose permeability in the cell.

(iii) *a* gene: codes for transacetylase which assists the enzyme β-galactosidase.

Related Theory

The operator is a short region of DNA that lies partially within the promoter and that interacts with a regulatory protein that controls the transcription of the operon.

152. (B) The *z* gene in the *lac* operon encodes for a galactosidase protein. This protein is an enzyme that is capable of breaking down the lactose into simpler sugars which can be absorbed by the bacteria. Hence a mutated *z* gene would result in a non-functional enzyme and thus the bacteria cannot grow.

Related Theory

Glucose is the preferred and most frequently available energy source for E. coli. The enzymes to metabolize glucose are made constantly by E. coli. When E. coli is exposed to both lactose and glucose, the organism first metabolise glucose and then temporarily cease to grow until the genes of lac operon become included to provide the ability to metabolise lactose.

153. (A) The *lactose* operon (*lac* operon) is an operon required for the transport and metabolism of lactose in *E. coli* and many other enteric bacteria. The gene product of *lac z* is β-galactosidase which cleaves lactose, a disaccharide, into glucose and galactose.

154. (B) The repressor can bind to a short sequence of the *lac* gene, called operator. When repressor binds to that sequence it physically blocks access by RNA polymerase to the DNA. As a result, as long as it is bound no *lac* *m*RNA can be initiated.

Related Theory

The regulatory gene codes for a regulatory protein. The lac repressor, encoded by the lac gene, is the regulatory protein of the lac operon.

155. (A) Regulation of transcription in prokaryotes typically involves an operon, such as the *lac* operon in *E. coli*. The *lac* operon is regulated by proteins that behave differently depending on whether lactose is present or absent.

156. (A) In negative or repressible operon, the repressor co-repressor complex binds with the operator. The free repressor cannot bind to the operator.

Related Theory

Operon is a functional unit of DNA, containing a set of genes under the control of a single promoter. In negative operons, the operon is turned off in the presence of a repressor.

157. (B) Regulator gene is involved in controlling the expression of one or more genes. Hence, regulator is responsible for regulating the process at different levels and at different time during organogenesis. Introns are the non-coding intervening sequences and exons are the coding sequences. Promoter is the binding site for RNA polymerase and it also defines the template and the coding strands in a transcriptional unit

158. (A) In *lac* operon, the *i* gene codes for the repressor of the *lac* operon. The *lac* operon consists of one regulatory gene (the *i* gene, *i.e.*, the inhibitor gene, not the inducer gene) along with three structural genes (*z*, *y* and *a*). Regulator gene produces a biochemical for suppressing the activity of the operator gene. This is because a repressor binds to the operator region of the DNA. The operator has an overlapping sequence with the promoter. This prevents RNA polymerase to bind to the promoter region and thus inhibits the transcription of the downstream structural genes. Hence, regulator gene acts as a repressor.

159. (C) Lactose is the substrate for enzyme β-galactosidase and it regulates the switching on and off of the operon. Hence, it is termed as inducer operon.

160. (D) An inducer binds within the regulatory region of an operon and helps RNA polymerase bind to the promoter, thereby it enhances the transcription of operon through interacting with a repressor or activator. Inducer promotes the production of an enzyme. Inducers are often substrates for the enzymes.

161. (B) Lac operon is an operon required for the metabolism of lactose in *E.coli*. *Lac* operon is an inducible operon, which becomes operational in the presence of an inducer lactose. Lactose is the substrate for the enzyme β-galactosidase and induces the operon.

162. (C) Expressed Sequence Tags (ESTs) are short stretches of cDNA (complementary DNA) sequences derived from the transcribed regions of a gene. These cDNA sequences are obtained by sequencing the *m*RNA (messenger RNA) molecules expressed in a particular tissue or cell type. Since *m*RNA represents the expressed form of a gene, ESTs provide a snapshot of the genes that are being actively transcribed and translated in a particular cell type or tissue.

163. (B) Sequence annotation is the blind approach used by a genetist for simply sequencing the whole set of genome that contained all the coding and non-coding sequence, and later assigning different regions in the sequence with functions. It is a process of marking specific features in a DNA, RNA or protein sequence with descriptive information about structure or function. For sequencing, the total DNA from the cell is isolated and converted into random fragments of smaller sizes and cloned in a suitable host using specialized vectors. The cloning resulted into amplification of each piece of DNA fragment so that it could be subsequently sequenced easily.

164. (B) Commonly used vectors for human genome sequencing are BAC and YAC. Bacterial Artificial Chromosomes (BAC) are obtained from naturally occurring f-plasmid and are able to accommodate large DNA sequence (300-3500 kb) to study genetic disorders. Yeast Artificial Chromosomes (YAC) are used to clone large genome of an organism (2500-300 kb).

Related Theory

- *The two types of 'biological tools' used in recombinant DNA technology are:*
  - *(1) **Enzymes:** These include restriction enzymes (Endonucleases), which acts as molecular scissors; Ligases, which are responsible for joining DNA fragments together and Reverse Transcriptase, which is used for converting mRNA to cDNA.*
  - *(2) **Vector:** They serve as a medium or vehicle to carry recombinant DNA into the host cell. The most commonly used vectors are Plasmids, Cosmids and Bacteriophages.*

165. (C) Human genome project (HGP) was an international scientific research project which was successfully completed in the year 2003 by sequencing the entire human genome of 3.3 billion base pairs. The HGP led to the growth of bioinformatics, the science of collecting and analysing; complex biological data such as genetic codes.

Related Theory

- *Goals of the human genome project include:*
  - *(1) Optimization of the data analysis.*
  - *(2) Sequencing the entire genome.*
  - *(3) Identification of the complete human genome.*
  - *(4) Creating genome sequence databases to store the data.*
  - *(5) Taking care of the legal, ethical and social issues that the project may pose.*

166. (A) A genetic map is a type of chromosome map that shows the relative locations of genes and other important features. The map is based on the idea of linkage, which means that the closer two genes are to each other on the chromosome, the greater the probability that they will be inherited together.

167. (D) The haploid human genome is said to have approximately 3×10^9 base pairs or 3.2 billion bases containing 20,000 to 25,000 genes.

Related Theory

- *The total length of a human genome is over 3 billion base pairs that make up a human DNA. The genome is organized into 22 paired chromosomes and the sex chromosomes (XY) with one X chromosome in males and two in females, and one Y chromosome in males only. The length of the chromosomes was estimated by multiplying the no. of base pairs by 0.34 nanometers, which is the distance between the base pairs in the DNA double helix. The size of the chromosome ranges from 45 to 275 mb, making the total genome size of 3286 Mb = 3.3 × 10^9 base pairs.*

168. (D) Polymorphism in DNA sequence is the basis of genetic mapping of human genome as well as of DNA fingerprinting. DNA fingerprinting is a technique to find out variations in individuals of a population at DNA level, which makes every individual unique in its phenotypic appearance. Polymorphism refers to variation at genetic level, it refers to the presence of two or more variant forms of a specific DNA sequence that can occur among different individuals or populations. It is a very useful tool in forensic applications, genetic biodiversity and evolutionary biology. It also forms the basis of paternity testing.

Related Theory

- *Gene mapping refers to the process of determining the location of genes on chromosomes. It involves sequencing of a genome and using computer programs to analyse the sequence to identify the location of genes.*

169. (B) DNA fingerprinting involves identifying differences in some specific regions in DNA sequence *i.e.*, repetitive DNA. These sequences normally do not code for any proteins, but they form a large portion of human genome.

Related Theory

- *Satellite DNA consists of very large arrays of tandemly repeating, non-coding DNA. Satellite DNA is the main component of functional centromeres, and form the main structural constituent of heterochromatin.*

170. (A) Polymorphism means variation at genetic level which arises due to mutation. It forms the basis of genetic mapping of human genome as well as DNA fingerprinting. Single nucleotide polymorphisms (SNPs) are a type of polymorphism involving variation of a single base pair.

Related Theory

➥ *Single nucleotide polymorphism (SNP), variation in a genetic sequence that affects only one of the basic building blocks—adenine (A), guanine (G), thymine (T), or cytosine (C)—in a segment of a DNA molecule and that occurs in more than 1 percent of a population. SNPs act as chromosomal tags to specific regions of DNA, and these regions can be scanned for variations that may be involved in a human disease or disorder.*

171. (B) Satellite DNA forms the minor peak after centrifugation of DNA. It consists of repetitive DNA sequences which does not code for any proteins. They show high degree of polymorphism and are heritable in nature. And hence are used in DNA fingerprinting.

172. (A) Variable Number of Tandem Repeats (VNTR) is an important source for many genetic markers like RFLP, as VNTR form bands that is unique in every individual. It is used in the DNA fingerprinting process that is useful in identifying criminals and even used to identify genetic relation between two individuals.

Related Theory

➥ *However, in recent studies, instead of VNTR, STR (Short Tandem Repeats) are used. They show high degree of polymorphism and relatively short length, comparative to VNTR.*

173. (D) A DNA that contains number of repetitive short DNA sequences is known as satellite DNA or tandemly repeated DNA. DNA fingerprinting is a technique that is used to identify the nucleotide sequence in the specific region of sample DNA. Fingerprint identification is the analysis of physical prints of fingers on surfaces; it does not include DNA study.

Related Theory

➥ *In organism, 99.9% of the genetic code is exactly same in each in dividual. Only 0.1% of it differs in every individual. Hence, if the technique of DNA fingerprinting is followed in reliable manner, without any manipulation, the chance of wrong result in highly unlikely. DNA fingerprinting can also be used in forensics to identify criminals, in medical situations to diagnose inherited disorders, in paternity tests, etc.*

174. (C) Satellite DNA is a useful tool in forensic science, it is used in DNA fingerprinting to identify suspects and resolve disputes.

175. (A) DNA fingerprinting involves determining the genetic makeup of a person. Determining and analysing the repeated sequences (as in STR), form the basis of DNA fingerprinting.

Related Theory

➥ *Sir Alec Jeffreys is the father of DNA fingerprinting. DNA (deoxyribonucleic acid) represents the blueprint of the human genetic makeup. A DNA fingerprint, therefore, is a DNA pattern that has a unique sequence such that it can be distinguished from the DNA patterns of other individuals. DNA fingerprinting is also called DNA typing.*