CHAPTER 6

Molecular Basis of Inheritance

6.1 The DNA

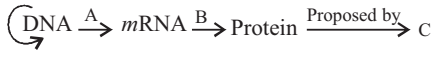
1. Which of the following statements is correct?
(a) Adenine pairs with thymine through two H-bonds.
(b) Adenine pairs with thymine through one H-bond.
(c) Adenine pairs with thymine through three H-bonds.
(d) Adenine does not pair with thymine.
(NEET 2020)

2. Purines found both in DNA and RNA are
(a) cytosine and thymine
(b) adenine and thymine
(c) adenine and guanine
(d) guanine and cytosine. *(NEET 2019)*

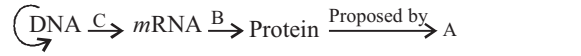
3. The association of histone H_1 with a nucleosome indicates that
(a) DNA replication is occurring
(b) the DNA is condensed into a chromatin fibre
(c) the DNA double helix is exposed
(d) transcription is occurring. *(NEET 2017)*

4. 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 17%, A 33%, T 33%
(b) G 8.5%, A 50%, T 24.5%
(c) G 34%, A 24.5%, T 24.5%
(d) G 17%, A 16.5%, T 32.5%. *(2015 Cancelled)*

5. The diagram shows an important concept in the genetic implication of DNA. Fill in the blanks A to C.



(a) A - Transcription, B -Translation, C - Francis Crick
(b) A - Translation, B - Extension, C - Rosalind Franklin
(c) A - Transcription, B - Replication, C - James Watson
(d) A - Translation, B - Transcription, C - Ervin Chargaff *(NEET 2013)*

6. 

The figure gives an important concept in the genetic implication of DNA. Fill the blanks A, B and C.
(a) A-Maurice Wilkins, B-Transcription, C-Translation
(b) A-James Watson, B-Replication, C-Extension
(c) A-Erwin Chargaff, B-Translation, C-Replication
(d) A-Francis Crick, B-Translation, C-Transcription *(Karnataka NEET 2013)*

7. What are the structures called that give an appearance as 'beads-on-string' in the chromosomes when viewed under electron microscope?
(a) Genes (b) Nucleotides
(c) Nucleosomes (d) Base pairs *(2011)*

8. Which one of the following does not follow the central dogma of molecular biology?
(a) Pea (b) *Mucor*
(c) *Chlamydomonas* (d) HIV *(2010)*

9. 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.
(Main 2010)

10. Which one of the following statements about the particular entity is true ?
(a) Centromere is found in animal cells, which produces aster during cell division.
(b) The gene for producing insulin is present in every body cell.
(c) Nucleosome is formed of nucleotides.
(d) DNA consists of core of eight histones.
(Main 2010)

11. In the DNA molecule,
(a) the proportion of adenine in relation to thymine varies with the organism
(b) there are two strands which run anti-parallel-one in 5′ → 3′ direction and other in 3′ → 5′
(c) the total amount of purine nucleotides and pyrimidine nucleotides is not always equal
(d) there are two strands which run parallel in the 5′ → 3′ direction. *(2008)*

12. Which one of the following pairs of nitrogenous bases of nucleic acids, is wrongly matched with the category mentioned against it?
(a) Guanine, Adenine - Purines
(b) Adenine, Thymine - Purines
(c) Thymine, Uracil - Pyrimidines
(d) Uracil, Cytosine - Pyrimidines *(2008)*

13. 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. *(2006)*

14. 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). *(2006)*

15. Which one of the following makes use of RNA template to synthesise DNA?
(a) DNA polymerase
(b) RNA polymerase
(c) Reverse transcriptase
(d) DNA dependant RNA polymerase *(2005)*

16. Which one of the following hydrolyses internal phosphodiester bonds in a polynucleotide chain?
(a) Lipase (b) Protease
(c) Endonuclease (d) Exonuclease *(2005)*

17. 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. *(2004)*

18. In a DNA percentage of thymine is 20% then what will be percentage of guanine?
(a) 20% (b) 40%
(c) 30% (d) 60% *(2002)*

19. Length of one loop of B-DNA
(a) 3.4 nm (b) 0.34 nm
(c) 20 nm (d) 10 nm. *(2000)*

20. DNA is mainly found in
(a) nucleolus (b) nucleus only
(c) cytoplasm only (d) none of these. *(1999)*

21. In prokaryotes, the genetic material is
(a) linear DNA without histones
(b) circular DNA without histones
(c) linear DNA with histones
(d) circular DNA with histones. *(1999)*

22. In DNA, when AGCT occurs, their association is as per which of the following pair?
(a) AT-GC (b) AG-CT
(c) AC-GT (d) All of these *(1999)*

23. The eukaryotic genome differs from the prokaryotic genome because
(a) the DNA is complexed with histone in prokaryotes
(b) the DNA is circular and single stranded in prokaryotes
(c) repetitive sequences are present in eukaryotes
(d) genes in the former case are organised into operons. *(1999)*

24. Genes are packaged into a bacterial chromosome by
(a) acidic protein (b) actin
(c) histones (d) basic protein. *(1997)*

25. Radiotracer technique shows that DNA is in
(a) multi-helix stage (b) single-helix stage
(c) double-helix stage (d) none of these. *(1996)*

26. Nucleosome core is made of
(a) H_0, H_2A, H_2B and H_3
(b) H_1, H_2A, H_2B, H_4
(c) H_1, H_2A, H_2B, H_3 and H_4
(d) H_2A, H_2B, H_3 and H_4. *(1993)*

27. A DNA with unequal nitrogen bases would most probably be
(a) single stranded (b) double stranded
(c) triple stranded (d) four stranded. *(1993)*

28. Nucleotide arrangement in DNA can be seen by
(a) X-ray crystallography (b) electron microscope
(c) ultracentrifuge (d) light microscope. *(1993)*

29. An octamer of 4 histones complexed with DNA forms
(a) endosome (b) nucleosome
(c) mesosome (d) centromere. *(1990)*

6.2 The Search for Genetic Material

30. The experimental proof for semi-conservative replication of DNA was first shown in a
(a) fungus (b) bacterium
(c) plant (d) virus. *(NEET 2018)*

31. Select the correct match.
(a) Ribozyme - Nucleic acid
(b) F_2 × Recessive parent - Dihybrid cross
(c) T.H. Morgan - Transduction
(d) G. Mendel - Transformation
(NEET 2018)

32. The final proof for DNA as the genetic material came from the experiments of
(a) Hershey and Chase
(b) Avery, MacLeod and McCarty
(c) Hargobind Khorana
(d) Griffith. *(NEET 2017)*

33. 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-II 2016)*

34. A molecule that can act as a genetic material must fulfill the traits given below, except
(a) it should be able to express itself in the form of 'Mendelian characters'
(b) it should be able to generate its replica
(c) it should be unstable structurally and chemically
(d) it should provide the scope for slow changes that are required for evolution. *(NEET-II 2016)*

35. Transformation was discovered by
(a) Meselson and Stahl (b) Hershey and Chase
(c) Griffith (d) Watson and Crick.
(2014)

36. The unequivocal proof of DNA as the genetic material came from the studies on a
(a) bacterium (b) fungus
(c) viroid (d) bacterial virus.
(Main 2011)

37. Semi-conservative replication of DNA was first demonstrated in
(a) *Escherichia coli*
(b) *Streptococcus pneumoniae*
(c) *Salmonella typhimurium*
(d) *Drosophila melanogaster.* *(2009)*

38. Transformation experiment was first performed on which bacteria?
(a) *E. coli*
(b) *Diplococcus pneumoniae*
(c) *Salmonella*
(d) *Pasteurella pestis* *(2002)*

39. The *Pneumococcus* experiment proves that
(a) bacteria do not reproduce sexually
(b) RNA sometime controls the production of DNA and proteins
(c) DNA is the genetic material
(d) bacteria undergo binary fission. *(1999)*

40. DNA synthesis can be specifically measured by estimating the incorporation of radio-labelled
(a) thymidine (b) deoxyribose sugar
(c) uracil (d) adenine. *(1997)*

41. The transforming principle of *Pneumococcus* as found out by Avery, MacLeod and McCarty was
(a) *m*RNA (b) DNA
(c) protein (d) polysaccharide. *(1993)*

42. Who proved that DNA is basic genetic material?
(a) Griffith (b) Watson
(c) Boveri and Sutton
(d) Hershey and Chase *(1993)*

43. *Escherichia coli* fully labelled with ^{15}N is allowed to grow in ^{14}N 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.
(1992)

6.3 RNA World

44. Which one of the following is not applicable to RNA?
(a) Heterocyclic nitrogenous bases
(b) Chargaff's rule
(c) Complementary base pairing
(d) 5' phosphoryl and 3' hydroxyl ends *(2015)*

45. Similarity in DNA and RNA is that
(a) both are polymer of nucleotides
(b) both have similar pyrimidine
(c) both have similar sugar
(d) both are genetic material. *(2000)*

6.4 Replication

46. During DNA replication, Okazaki fragments are used to elongate
(a) the lagging strand towards replication fork
(b) the leading strand away from replication fork
(c) the lagging strand away from the replication fork
(d) the leading strand towards replication fork.
(NEET 2017)

47. During replication of a bacterial chromosome DNA synthesis starts from a replication origin site and
(a) RNA primers are involved
(b) is facilitated by telomerase
(c) moves in one direction of the site
(d) moves in bidirectional way. *(2004)*

48. Method of DNA replication in which two strands of DNA separate and synthesise new strands is called
(a) dispersive (b) conservative
(c) semi-conservative (d) non conservative.
(2000)

49. There are special proteins that help to open up DNA double helix in front of the replication fork. These proteins are
(a) DNA ligase
(b) DNA topoisomerase I
(c) DNA gyrase
(d) DNA polymerase I. *(1994)*

50. During DNA replication, the strands separate by
(a) DNA polymerase (b) topoisomerase
(c) unwindase/helicase
(d) gyrase. *(1993)*

51. Experimental material in the study of DNA replication has been
(a) *Escherichia coli* (b) *Neurospora crassa*
(c) *Pneumococcus*
(d) *Drosophila melanogaster*. *(1992)*

52. DNA replication is
(a) conservative and discontinuous
(b) semi-conservative and semi-discontinuous
(c) semi-conservative and discontinuous
(d) conservative. *(1989)*

6.5 Transcription

53. Name the enzyme that facilitates opening of DNA helix during transcription.
(a) DNA ligase (b) DNA helicase
(c) DNA polymerase (d) RNA polymerase
(NEET 2020)

54. What will be the sequence of *m*RNA produced by the following stretch of DNA ?
3′ATGCATGCATGCATG5′TEMPLATE STRAND
5′ TACGTACGTACGTAC3′ CODING STRAND
(a) 3′AUGCAUGCAUGCAUG5′
(b) 5′UACGUACGUACGUAC 3′
(c) 3′ UACGUACGUACGUAC 5′
(d) 5′ AUGCAUGCAUGCAUG 3′
(Odisha NEET 2019)

55. Match the following RNA polymerase with their transcribed products :

1. RNA polymerase I	(i) *t*RNA
2. RNA polymerase II	(ii) *r*RNA
3. RNA polymerase III	(iii) hnRNA

Select the correct option from the following :
(a) 1-i, 2-iii, 3-ii (b) 1-i, 2-ii, 3-iii
(c) 1-ii, 2-iii, 3-i (d) 1-iii, 2-ii, 3-i
(Odisha NEET 2019)

56. Select the correct statement.
(a) Franklin Stahl coined the term "linkage".
(b) Punnett square was developed by a British scientist.
(c) Spliceosomes take part in translation.
(d) Transduction was discovered by S. Altman.
(NEET 2018)

57. AGGTATCGCAT is a sequence from the coding strand of a gene. What will be the corresponding sequence of the transcribed *m*RNA?
(a) AGGUAUCGCAU (b) UGGTUTCGCAT
(c) ACCUAUGCGAU (d) UCCAUAGCGUA
(NEET 2018)

58. Which of the following RNAs should be most abundant in animal cell?
(a) *t*RNA (b) *m*RNA
(c) miRNA (d) *r*RNA *(NEET 2017)*

59. Spliceosomes are not found in cells of
(a) fungi (b) animals
(c) bacteria (d) plants. *(NEET 2017)*

60. The equivalent of a structural gene is
(a) muton (b) cistron
(c) operon (d) recon. *(NEET-II 2016)*

61. Which of the following *r*RNAs acts as structural RNA as well as ribozyme in bacteria?
(a) 5S *r*RNA (b) 18S *r*RNA
(c) 23S *r*RNA (d) 5.8S *r*RNA
(NEET-II 2016)

62. 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) antistrand.
(NEET-II 2016)

63. Select the correct option.

Direction of RNA synthesis	**Direction of reading of the template DNA strand**
(a) 5′ – 3′	3′ – 5′
(b) 3′ – 5′	5′ – 3′
(c) 5′ – 3′	5′ – 3′
(d) 3′ – 5′	3′ – 5′ *(2014)*

64. Removal of introns and joining of exons in a defined order during transcription is called
(a) looping (b) inducing
(c) slicing (d) splicing. *(2012, 2009)*

65. 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 *(2012)*

66. Ribosomal RNA is actively synthesised in
(a) lysosomes (b) nucleolus
(c) nucleoplasm (d) ribosomes. *(2012)*

67. Which one of the following is not a part of a transcription unit in DNA?
(a) The inducer
(b) A terminator
(c) A promoter
(d) The structural gene *(2012)*

68. Removal of RNA polymerase III from nucleoplasm will affect the synthesis of
(a) *t*RNA (b) hnRNA
(c) *m*RNA (d) *r*RNA. *(2012)*

69. Which one of the following also acts as a catalyst in a bacterial cell?
(a) 5S *r*RNA (b) snRNA
(c) hnRNA (d) 23S *r*RNA *(2011)*

70. In eukaryotic cell transcription, RNA splicing and RNA capping take place inside the
(a) ribosomes (b) nucleus
(c) dictyosomes (d) ER. *(Main 2010)*

71. One gene-one enzyme hypothesis was postulated by
(a) Beadle and Tatum (b) R. Franklin
(c) Hershey and Chase (d) A. Garrod. *(2006)*

72. Telomerase is an enzyme which is a
(a) simple protein (b) RNA
(c) ribonucleoprotein (d) repetitive DNA. *(2005)*

73. During transcription holoenzyme RNA polymerase binds to a DNA sequence and the DNA assumes a saddle like structure at that point. What is that sequence called?
(a) AAAT box (b) TATA box
(c) GGTT box (d) CAAT box *(2005)*

74. Which form of RNA has a structure resembling clover leaf?
(a) *r*RNA (b) hnRNA
(c) *m*RNA (d) *t*RNA *(2004)*

75. 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. *(2004)*

76. During transcription, the DNA site at which RNA polymerase binds is called
(a) promoter (b) regulator
(c) receptor (d) enhancer. *(2003)*

77. Which of the following reunites the exon segments after RNA splicing?
(a) RNA polymerase (b) RNA primase
(c) RNA ligase (d) RNA proteoses *(2002)*

78. Exon part of *m*RNAs have code for
(a) protein (b) lipid
(c) carbohydrate (d) phospholipid. *(2002)*

79. *m*RNA is synthesised on DNA template in which direction?
(a) $5' \rightarrow 3'$ (b) $3' \rightarrow 5'$
(c) Both (a) and (b) (d) Any *(2001)*

80. Gene and cistron words are sometimes used synonymously because
(a) one cistron contains many genes
(b) one gene contains many cistrons
(c) one gene contains one cistron
(d) one gene contains no cistron. *(2001)*

81. Types of RNA polymerase required in nucleus of eukaryotes for RNA synthesis
(a) 1 (b) 2
(c) 3 (d) 4. *(2001)*

82. Anticodon occurs in
(a) *t*RNA (b) *m*RNA
(c) *r*RNA (d) DNA. *(2000)*

83. In three dimensional view the molecule of *t*RNA is
(a) L-shaped (b) S-shaped
(c) Y-shaped (d) E-shaped. *(2000)*

84. Genes that are involved in turning on or off the transcription of a set of structural genes are called
(a) redundant genes (b) regulatory genes
(c) polymorphic genes (d) operator genes. *(1998)*

85. DNA elements, which can switch their position, are called
(a) cistrons (b) transposons
(c) exons (d) introns. *(1998)*

86. The maximum formation of *m*RNA occurs in
(a) ribosome (b) nucleoplasm
(c) cytoplasm (d) nucleolus. *(1996)*

87. If the sequence of bases in DNA is ATTCGATG, then the sequence of bases in its transcript will be
(a) GUAGCUUA (b) AUUCGAUG
(c) CAUCGAAU (d) UAAGCUAC. *(1995)*

88. In split genes, the coding sequences are called
(a) exons (b) cistrons
(c) introns (d) operons. *(1995)*

89. The process of transfer of genetic information from DNA to RNA/formation of RNA from DNA is
(a) transversion (b) transcription
(c) translation (d) translocation. *(1991)*

6.6 Genetic Code

90. 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) 2.0 meters (b) 2.5 meters
(c) 2.2 meters (d) 2.7 meters.
(NEET 2020)

91. Under which of the following conditions there will be no change in the reading frame of following *m*RNA?
5' AACAGCGGUGCUAUU 3'
(a) Deletion of GGU from 7th, 8th and 9th positions
(b) Insertion of G at 5th position
(c) Deletion of G from 5th position
(d) Insertion of A and G at 4th and 5th position respectively *(NEET 2019)*

92. Which of the following features of genetic code does allow bacteria to produce human insulin by recombinant DNA technology?
(a) Genetic code is specific.
(b) Genetic code is not ambiguous.
(c) Genetic code is redundant.
(d) Genetic code is nearly universal. *(NEET 2019)*

93. If there are 999 bases in an RNA that code 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) 11 (b) 33
(c) 333 (d) 1 *(NEET 2017)*

94. Which one of the following is the starter codon?
(a) UAA (b) UAG
(c) AUG (d) UGA *(NEET-I 2016)*

95. Which of the following is not a property of the genetic code?
(a) Non-overlapping (b) Ambiguous
(c) Degeneracy (d) Universal
(Karnataka NEET 2013)

96. The one aspect which is not a salient feature of genetic code, is its being
(a) degenerate (b) ambiguous
(c) universal (d) specific. *(2010)*

97. Whose experiments cracked the DNA and discovered unequivocally that a genetic code is a "triplet"?
(a) Hershey and Chase
(b) Morgan and Sturtevant
(c) Beadle and Tatum
(d) Nirenberg and Mathaei *(2009)*

98. What is not true for genetic code?
(a) It is nearly universal.
(b) It is degenerate.
(c) It is unambiguous.
(d) A codon in *m*RNA is read in a non-contiguous fashion. *(2009)*

99. Which one of the following pairs of codons is correctly matched with their function or the signal for the particular amino acid?
(a) AUG, ACG - Start/methionine
(b) UUA, UCA - Leucine
(c) GUU, GCU - Alanine
(d) UAG, UGA - Stop *(2008)*

100. 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. *(2004)*

101. In mutational event, when adenine is replaced by guanine, it is a case of
(a) frame shift mutation (b) transcription
(c) transition (d) transversion. *(2004)*

102. What would happen if in a gene encoding a polypeptide of 50 amino acids, 25th codon (UAU) is mutated to UAA ?
(a) A polypeptide of 24 amino acids will be formed.
(b) Two polypeptides of 24 and 25 amino acids will be formed.
(c) A polypeptide of 49 amino acids will be formed.
(d) A polypeptide of 25 amino acids will be formed.
(2003)

103. 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
(2003)

104. 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. *(2003)*

105. In the genetic code dictionary, how many codons are used to code for all the 20 essential amino acids?
(a) 20 (b) 64
(c) 61 (d) 60 *(2003)*

106. 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) universility of codons. *(2002)*

107. Change in sequence of nucleotide in DNA is called
(a) mutagen (b) mutation
(c) recombination (d) translation. *(2002)*

108. Which of the following is initiation codon?
(a) UAG (b) AUC
(c) AUG (d) CCU *(2000)*

109. Initiation codon in eukaryotes is
(a) GAU (b) AGU
(c) AUG (d) UAG. *(1999, 1994)*

110. What base is responsible for hot spots for spontaneous point mutations?
(a) 5-bromouracil (b) 5-methylcytosine
(c) Guanine (d) Adenine *(1998)*

111. The codons causing chain termination are
(a) AGT, TAG, UGA (b) UAG, UGA, UAA
(c) TAG, TAA, TGA (d) GAT, AAT, AGT. *(1997)*

112. Which of the following serves as a terminal codon?
(a) UAG (b) AGA
(c) AUG (d) GCG *(1996)*

113. If the DNA codons are ATG ATG ATG and a cytosine base is inserted at the beginning, then which of the following will result?
(a) CAT GAT GAT G (b) A non-sense mutation
(c) C ATG ATG ATG (d) CA TGA TGA TG *(1995)*

114. Anticodon is an unpaired triplet of bases in an exposed position of
(a) *t*RNA (b) *m*RNA
(c) *r*RNA (d) both (b) and (c). *(1995)*

115. Initiation codon of protein synthesis (in eukaryotes) is
(a) GUA (b) GCA
(c) CCA (d) AUG. *(1993)*

116. Khorana first deciphered the triplet codons of
(a) serine and isoleucine
(b) cysteine and valine
(c) tyrosine and tryptophan
(d) phenylalanine and methinonine. *(1992)*

117. In the genetic dictionary, there are 64 codons as
(a) 64 amino acids are to be coded
(b) 64 types of *t*RNAs are present
(c) there are 44 nonsense codons and 20 sense codons
(d) genetic code is triplet. *(1990)*

118. Genetic code consists of
(a) adenine and guanine (b) cytosine and uracil
(c) cytosine and guanine (d) all of these. *(1988)*

6.7 Translation

119. The first phase of translation is
(a) binding of *m*RNA to ribosome
(b) recognition of DNA molecule
(c) aminoacylation of *t*RNA
(d) recognition of an anti-codon. *(NEET 2020)*

120. Many ribosomes may associate with a single *m*RNA to form multiple copies of a polypeptide simultaneously. Such strings of ribosomes are termed as
(a) polysome (b) polyhedral bodies
(c) plastidome (d) nucleosome. *(NEET 2018)*

121. A complex of ribosomes attached to a single strand of RNA is known as
(a) polypeptide (b) Okazaki fragment
(c) polysome (d) polymer. *(NEET-I 2016)*

122. Polysome is formed by
(a) a ribosome with several subunits
(b) ribosomes attached to each other in a linear arrangement
(c) several ribosomes attached to a single *m*RNA
(d) many ribosomes attached to a strand of endoplasmic reticulum. *(2008)*

123. The two sub-units of ribosome remain united at a critical ion level of
(a) magnesium (b) calcium
(c) copper (d) manganese. *(2008)*

124. Which antibiotic inhibits interaction between *t*RNA and *m*RNA during bacterial protein synthesis?
(a) Tetracycline (b) Erythromycin
(c) Neomycin (d) Streptomycin *(2006)*

125. Amino acid sequence, in protein synthesis is decided by the sequence of
(a) *r*RNA (b) *t*RNA
(c) *m*RNA (d) *c*DNA. *(2006)*

126. Using imprints from a plate with complete medium and carrying bacterial colonies, you can select streptomycin resistant mutants and prove that such mutations do not originate as adaptation. These imprints need to be used
(a) on plates with and without streptomycin
(b) on plates with minimal medium
(c) only on plates with streptomycin
(d) only on plates without streptomycin. *(2005)*

127. Protein synthesis in an animal cell occurs
(a) only on the ribosomes present in cytosol
(b) only on ribosome attached to the nuclear envelope and endoplasmic reticulum
(c) on ribosome present in the nucleolus as well as in cytoplasm
(d) on ribosomes present in cytoplasm as well as in mitochondria. *(2005)*

128. During translation initiation in prokaryotes, a GTP molecule is needed in
(a) formation of formyl-met-*t*RNA
(b) binding of 30S subunit of ribosome with *m*RNA
(c) association of 30S *m*RNA with formyl-met-*t*RNA
(d) association of 50S subunit of ribosome with initiation complex. *(2003)*

129. The RNA that pick up specific amino acid from amino acid pool in the cytoplasm to ribosome during protein synthesis is called
(a) *r*RNA (b) RNA
(c) *m*RNA (d) *t*RNA. *(1997)*

130. Which of the following step of translation does not consume a high energy phosphate bond?
(a) Peptidyl transferase reaction
(b) Aminoacyl *t*RNA binding to A-site
(c) Translocation
(d) Amino acid activation *(1997)*

131. Protein synthesis in an animal cell, takes place
(a) in the cytoplasm as well as endoplasmic reticulum
(b) only on ribose attached to nucleon
(c) only in the cytoplasm
(d) in the nucleolus as well as in the cytoplasm. *(1997)*

132. In protein synthesis, the polymerisation of amino acids involves three steps. Which one of the following is not involved in the polymerisation of protein ?
(a) Termination (b) Initiation
(c) Elongation (d) Transcription *(1994)*

133. Because most of the amino acids are represented by more than one codon, the genetic code is
(a) overlapping (b) wobbling
(c) degenerate (d) generate. *(1993)*

134. The process of translation is
(a) ribosome synthesis (b) protein synthesis
(c) DNA synthesis (d) RNA synthesis. *(1993)*

6.8 Regulation of Gene Expression

135. Match the following genes of the *Lac* operon with their respective products.

(A) *i* gene	(i) β-galactosidase
(B) *z* gene	(ii) Permease
(C) *a* gene	(iii) Repressor
(D) *y* gene	(iv) Transacetylase

Select the correct option.

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

(NEET 2019)

136. Select the correct match.
(a) Alec Jeffreys - *Streptococcus pneumoniae*
(b) Alfred Hershey and Martha Chase - TMV
(c) Matthew Meselson and F. Stahl - *Pisum sativum*
(d) Francois Jacob and Jacques Monod - *Lac* operon *(NEET 2018)*

137. All of the following are part of an operon except
(a) an operator (b) structural genes
(c) an enhancer (d) a promoter. *(NEET 2018)*

138. Which of the following is required as inducer(s) for the expression of *Lac* operon?
(a) Lactose (b) Lactose and galactose
(c) Glucose (d) Galactose *(NEET-I 2016)*

139. Gene regulation governing lactose operon of *E.coli* that involves the *lac* I gene product is
(a) negative and repressible because repressor protein prevents transcription
(b) feedback inhibition because excess of β-galactosidase can switch off transcription
(c) positive and inducible because it can be induced by lactose
(d) negative and inducible because repressor protein prevents transcription. *(2015 Cancelled)*

140. Which one of the following is wrongly matched?
(a) Transcription - Writing information from DNA to *t*RNA.
(b) Translation - Using information in *m*RNA to make protein.
(c) Repressor protein - Binds to operator to stop enzyme synthesis.
(d) Operon - Structural genes, operator and promoter. *(2014)*

141. Which enzyme will be produced in a cell if there is a nonsense mutation in the *lac* Y gene?
(a) Transacetylase
(b) Lactose permease and transacetylase
(c) β-galactosidase
(d) Lactose permease *(NEET 2013)*

142. 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 expresser. *(Karnataka NEET 2013)*

143. Select the two correct statements out of the four (i – iv) statements 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). *(2010)*

144. 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. *(Main 2010)*

145. *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 synthesise functional beta galactosidase
(c) in the presence of glucose, *E.coli* cells do not utilise lactose
(d) they cannot transport lactose from the medium into the cell. *(2005)*

146. 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 *(2003)*

147. Jacob and Monod studied lactose metabolism in *E. coli* and proposed operon concept. 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. *(2002)*

148. In *E. coli*, during lactose metabolism repressor binds to
(a) regulator gene (b) operator gene
(c) structural gene (d) promoter gene. *(2002)*

149. 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 have negative effect on *lac* operon. *(2001)*

150. In operon concept, regulator gene functions as
(a) inhibitor (b) repressor
(c) regulator (d) all of these. *(1999)*

151. The wild type *E.coli* cells are growing in normal medium with glucose. They are transferred to a medium containing only lactose as sugar. Which of the following changes take place?
(a) The lac operon is induced.
(b) *E.coli* cells stop dividing.
(c) The lac operon is repressed.
(d) All operons are induced. *(1995)*

152. The *lac* operon is an example of
(a) repressible operon (b) overlapping genes
(c) arabinose operon (d) inducible operon. *(1995)*

153. An environmental agent, which triggers transcription from an operon, is a
(a) depressor (b) controlling element
(c) regulator (d) inducer. *(1995)*

154. '*Lac* operon' in *E. coli*, is induced by
(a) 'I' gene (b) promoter gene
(c) β-galactosidase (d) lactose. *(1994)*

6.9 Human Genome Project

155. Expressed Sequence Tags (ESTs) refers to
(a) novel DNA sequences
(b) genes expressed as RNA
(c) polypeptide expression
(d) DNA polymorphism. *(NEET 2019)*

156. Identify the correct order of organisation of genetic material from largest to smallest.
(a) Genome, chromosome, gene, nucleotide
(b) Chromosome, genome, nucleotide, gene
(c) Chromosome, gene, genome, nucleotide
(d) Genome, chromosome, nucleotide, gene *(2015)*

157. Satellite DNA is important because it
(a) does not code for proteins and is same in all members of the population
(b) codes for enzymes needed for DNA replication
(c) codes for proteins needed in cell cycle
(d) shows high degree of polymorphism in population and also the same degree of polymorphism in an individual, which is heritable from parents to children. *(2015)*

6.10 DNA Fingerprinting

158. Which of the following is not required for any of the techniques of DNA fingerprinting available at present?
(a) Restriction enzymes
(b) DNA-DNA hybridisation
(c) Polymerase chain reaction
(d) Zinc finger analysis *(NEET-I 2016)*

159. One of the most frequently used techniques in DNA fingerprinting is
(a) VNTR (b) SSCP
(c) SCAR (d) AFLP.
(Karnataka NEET 2013)

160. What is it that forms the basis of DNA finger-printing?
(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 segments. *(Mains 2012)*

161. 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. *(2004)*

ANSWER KEY

1.	(a)	**2.**	(c)	**3.**	(b)	**4.**	(a)	**5.**	(a)	**6.**	(d)	**7.**	(c)	**8.**	(d)	**9.**	(c)	**10.**	(b)
11.	(b)	**12.**	(b)	**13.**	(d)	**14.**	(d)	**15.**	(c)	**16.**	(c)	**17.**	(c)	**18.**	(c)	**19.**	(a)	**20.**	(b)
21.	(b)	**22.**	(a)	**23.**	(b)	**24.**	(d)	**25.**	(c)	**26.**	(d)	**27.**	(a)	**28.**	(a)	**29.**	(b)	**30.**	(b)
31.	(a)	**32.**	(a)	**33.**	(b)	**34.**	(c)	**35.**	(c)	**36.**	(d)	**37.**	(a)	**38.**	(b)	**39.**	(c)	**40.**	(a)
41.	(b)	**42.**	(d)	**43.**	(a)	**44.**	(b)	**45.**	(a)	**46.**	(c)	**47.**	(d)	**48.**	(c)	**49.**	(b)	**50.**	(c)
51.	(a)	**52.**	(b)	**53.**	(d)	**54.**	(b)	**55.**	(c)	**56.**	(b)	**57.**	(a)	**58.**	(d)	**59.**	(c)	**60.**	(b)
61.	(c)	**62.**	(a)	**63.**	(a)	**64.**	(d)	**65.**	(b)	**66.**	(b)	**67.**	(a)	**68.**	(a)	**69.**	(d)	**70.**	(b)
71.	(a)	**72.**	(c)	**73.**	(b)	**74.**	(d)	**75.**	(c)	**76.**	(a)	**77.**	(c)	**78.**	(a)	**79.**	(a)	**80.**	(c)
81.	(c)	**82.**	(a)	**83.**	(a)	**84.**	(d)	**85.**	(b)	**86.**	(d)	**87.**	(d)	**88.**	(a)	**89.**	(b)	**90.**	(c)
91.	(a)	**92.**	(d)	**93.**	(b)	**94.**	(c)	**95.**	(b)	**96.**	(b)	**97.**	(d)	**98.**	(d)	**99.**	(d)	**100.**	(a)
101.	(c)	**102.**	(a)	**103.**	(d)	**104.**	(d)	**105.**	(c)	**106.**	(a)	**107.**	(b)	**108.**	(c)	**109.**	(c)	**110.**	(c)
111.	(b)	**112.**	(a)	**113.**	(a)	**114.**	(a)	**115.**	(d)	**116.**	(b)	**117.**	(d)	**118.**	(d)	**119.**	(c)	**120.**	(a)
121.	(c)	**122.**	(c)	**123.**	(a)	**124.**	(c)	**125.**	(c)	**126.**	(c)	**127.**	(d)	**128.**	(c)	**129.**	(d)	**130.**	(a)
131.	(d)	**132.**	(d)	**133.**	(c)	**134.**	(b)	**135.**	(d)	**136.**	(d)	**137.**	(c)	**138.**	(a)	**139.**	(d)	**140.**	(a,d)
141.	(c)	**142.**	(a)	**143.**	(c)	**144.**	(b)	**145.**	(b)	**146.**	(a)	**147.**	(c)	**148.**	(b)	**149.**	(a)	**150.**	(b)
151.	(a)	**152.**	(d)	**153.**	(d)	**154.**	(c)	**155.**	(b)	**156.**	(a)	**157.**	(d)	**158.**	(d)	**159.**	(a)	**160.**	(d)
161.	(a)																		

Hints & Explanations

1. (a) : Adenine pairs with thymine by forming two hydrogen bonds, A = T.

2. (c)

3. (b) : Histones help in packaging of DNA. In eukaryotes, DNA packaging is carried out with the help of positively charged basic proteins called histones. Histones are of five types – H_1, H_2A, H_2B, H_3 and H_4. The association of H_1 histone with nucleosome indicates that DNA remains in its condensed form. Nucleosome is the unit of compaction. H_1 is attached over the linker DNA. The linker DNA, consisting of H_1 histone connects two adjacent nucleosomes. They together consititute chromatosome. It gives rise to a chromatin fibre after further condensation.

4. (a) : According to Chargaff's rule, the amount of adenine is always equal to that of thymine and the amount of guanine is always equal to that of cytosine, *i.e.*, A = T and G = C. Also, the purines and pyrimidines are always in equal amounts, *i.e.*, A + G = T + C. Now, given dsDNA has 17% cytosine and hence guanine will be also 17%. So, A + T must be 66%, therefore, percentage of adenine or thymine would be 66/2 = 33%.

5. (a) : The expression of the genetic material occurs normally through the production of proteins. This involves two consecutive steps. These are transcription and translation. The DNA codes for the production of messenger RNA (*m*RNA) during transcription. Messenger RNA carries coded information to ribosomes. The ribosomes read this information and use it for protein synthesis. This process is called translation. F.H.C. Crick described this unidirectional flow of information in 1958 as the 'central dogma of molecular biology'.

6. (d) : *Refer to answer 5.*

7. (c) : Nucleosomes appear as 'beads-on-string' in the chromosome when viewed under electron microscope. The beads in 'beads-on-string' arrangement are complexes of histones and DNA. The bead plus the connecting DNA leads to the next bead from the nucleosome. Nucleosome is the fundamental unit of organisation on which the higher-order packaging of chromatin is built. The bead of each nucleosome contains eight histone molecules in which two copies each of H_2A, H_2B, H_3 and H_4 are found.

8. (d) : $\text{DNA} \xrightarrow{\text{Transcription}} m\text{RNA} \xrightarrow{\text{Translation}} \text{Protein}$

This one-way flow of information from DNA to *m*RNA and then to protein is called the central dogma of molecular biology by F.H.C. Crick (1958). But later on two American workers H. Temin and D. Baltimore reported that DNA is also formed from RNA in retroviruses, *e.g.*, HIV. This is called reverse transcription or teminism, *i.e.*,

$$\text{DNA} \underset{\text{Reverse transcription}}{\overset{\text{Transcription}}{\rightleftharpoons}} m\text{RNA} \xrightarrow{\text{Translation}} \text{Protein}$$

This reverse transcription occurs under the influence of reverse transcriptase enzyme. So, HIV viruses does not follow central dogma.

9. (c) : The phosphodiester bonds is formed between the phosphate group, which is connected to carbon 5′ of the sugar residue of one nucleotide and carbon 3′ of the sugar residue of the next nucleotide.

10. (b) : Insulin gene is found in every body cell but is not expressed in all cells. It is nucleosome which consists of a core of eight histones. DNA is composed of nucleotides. Centriole is found in animal cells, which produces aster during cell division.

11. (b) : A DNA molecule has two unbranched complementary strands which are spirally coiled. The two chains are antiparallel, *i.e.*, they run parallel but in opposite direction. One chain has the polarity 5′ → 3′ whereas, other has 3′ → 5′. Both are held together by hydrogen bonds between their bases, *i.e.*, A = T and G ≡ C and the amount of adenine is equal to thymine and guanine equals to cytosine. The base ratio A + T / G + C may vary from one species to another but is constant for a given species. The purine and pyrimidines are always in equal amount (A + G = T + C) but A + T is not necessarily equal to G + C.

12. (b) : The two DNA chains are held together by hydrogen bonds between their nitrogenous bases. Adenine (A), a purine of one chain lies exactly opposite thymine (T), a pyrimidine of the other chain. Similarly, cytosine (C), a pyrimidine lies opposite guanine (G), a purine. Three hydrogen bonds occur between cytosine and guanine (C ≡ G) at positions 1′, 2′, and 6′ and two hydrogen bonds between adenine and thymine (A = T) at positions 1′ and 6′.

13. (d) : DNA or deoxyribonucleic acid is the largest macromolecule made of the helically twisted two antiparallel polydeoxyribonucleotide strands held together by hydrogen bonds. The two strands of DNA are together called DNA duplex. It has a diameter of 20Å. One turn spiral has a distance of 34 Å or 3.4 nm.

14. (d) : DNA is a type of nucleic acid that forms genetic material in many organisms. It consists of a long polymer of nucleotides which transcribes the coded information in the form of a triplet code of nucleotides in *m*RNA. It is a double helical molecule. The two strands of DNA run in opposite directions to one another with the hydrogen bonds between them. One strand of DNA has 5′-3′ direction and the other strand has 3′-5′ direction. So they are antiparallel. This direction is determined by the presence of a free phosphate or OH group at the end of the strand.

15. (c) : *Refer to answer 8.*

16. (c) : Endonucleases hydrolyse the internal phosphodiester bond. Exonucleases cleave the terminal nucleotides. Lipase digest fats and proteases break down proteins.

17. (c) : *Refer to answer 11.*

18. (c) : In a DNA, the percentage of thymine is 20%. So, as it pairs with adenine, it is also 20%. So, the guanine and cytosine together forms 60% of DNA and hence, guanine is 30%.

19. (a) : B-DNA is an antiparallel double helix. The double strand or duplex is coiled plectonemically in right handed fashion around a common axis like a rope stair case twisted in a spiral. The coiling produces alternate major and minor grooves. One turn of spiral has a distance between two adjacent nucleotides is 3.4 nm.

20. (b) : DNA is mainly found in nucleus. It is associated with RNA and proteins to form compact chromosomes. But some amount of DNA is also found in chloroplasts and mitochondria. This DNA is called extra-chromosomal DNA.

21. (b) : The genetic material of prokaryotes is circular and single stranded DNA. It has no association of histones. The eukaryotic genetic material is linear and double stranded DNA. It is associated with histone proteins to form nucleosome unit.

22. (a) : DNA molecule has four bases - adenine, guanine, cytosine and thymine. Adenine always pairs with thymine and guanine pairs with cytosine. Their association is A-T and G-C.

23. (b) : Genome refers to the total sets of chromosomes carried by each cell of the organism. In prokaryotes the genetic material is circular and single stranded DNA. It has no association of histones. The eukaryotic genetic material is linear and double stranded DNA. It is associated with histone proteins to form nucleosome unit.

24. (d) : In bacteria, DNA is highly charged molecule. The adjacent bases are linked by phosphate groups, each with an ionized hydroxyl group. It results in negative charges which are therefore balanced by an equivalent number of cationic groups.
These charges are balanced by histones which are basic proteins in case of eukaryotes. Histones are absent in bacterial cells. In bacteria the charges are neutralised by polyamines such as spermine and spermidine and by Mg^{2+} ions.

25. (c) : ^{14}C and ^{3}H are incorporated in bases like thymidine, uridine and amino acids to study the structure of DNA and proteins. Radiotracer technique shows that DNA is in double helical form.

26. (d) : Nucleosome core is made up of H_2A, H_2B, H_3 and H_4. It is about 7-10 nm in diameter, consisting of histones around which a DNA strand, about 120 base pair long is wrapped in chromosomes.

27. (a) : A DNA with unequal nitrogen bases would most probably be single stranded. Nitrogenous bases are unequal in number in single stranded DNA, because they do not possess complementary base pairs.

28. (a) : Nucleotide arrangement in DNA can be seen by X-ray crystallography. Watson and Crick, 1953 proposed the double helical model for DNA. They were awarded Nobel Prize in 1962. This model was developed by them on the basis of several previous observations including the *d*-helix of Pauling, 1951 and X-ray reflection studies of Franklin and Gosling, 1953.

29. (b) : An octamer of 4 histones complexed with DNA forms nucleosome. The association of histones with DNA is very characteristic. It involves the formation of linear array of spherical structures called nucleosomes. These structures contains four pairs of histones (H_2A, H_2B, H_3 and H_4) in a ball; around which is wrapped a stretch of about 150 base pairs of DNA.

30. (b) : Semi-conservative replication of DNA was proved by the work of Matthew Meselson and Franklin Stahl (1958) using bacterium *Escherichia coli*.

31. (a) : Ribozymes (ribonucleic acid enzymes) are RNA molecules that are capable of catalysing specific biochemical reactions similar to the action of protein enzymes.

32. (a)

33. (b) : Taylor *et al.* (1957) conducted experiment on *Vicia faba* (broad bean) to prove semi-conservative replication of DNA. He fed dividing cells of root tips of *Vicia faba* with radioactive ^{3}H containing thymine instead of normal thymine and found that all the chromosomes became radioactive. Labelled thymine was then replaced with normal one. Next generation

came to have radioactivity in one of the two chromatids of each chromosome while in subsequent generation radioactivity was present in 50% of the chromosomes. This is possible only if out of the two strands of a chromosome, one is formed afresh while the other is conserved at each replication.

34. (c) : Genetic material should be structurally and chemically stable otherwise its expression will change and lead to loss of several metabolic functions, etc.

35. (c) : Transformation was first studied by S.F. Griffith in 1928 while studying *Streptococcus pneumoniae*. He found that R-type non-virulent bacteria pick up virulence from heat killed virulent S-type bacteria and transform into virulent forms. It was this experiment which indicated presence of a 'transforming principle' which was later found out to be DNA, by Avery *et al.*

36. (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.

37. (a) : Mathew Meselson and Franklin Stahl (1958) conducted various experiments using isotopically labelled DNA of *Escherichia coli* to provide evidence in favour of semi-conservative mode of DNA replication.

38. (b) : Transformation involves transfer of genetic material of one bacterial cell into another bacterial cell by some unknown mechanism and it converts one type of bacterium into another type. This was first studied by Griffith (1928) in *Diplococcus pneumoniae* and hence is known as Griffith effect.

39. (c) : Transformation was first discovered by Griffith (1928), in *Pneumococcus* (*Streptococcus pneumoniae*), that causes pneumonia. Griffith injected a group of mice with non-encapsulated, rough (R), pneumococci; a second group with heat-killed encapsulated pneumococci cells and a third group a mixture consisting of a few living non-encapsulated, rough pneumococci derived from a type S culture, and heat-killed encapsulated cells (S type). Griffith observed that the mice in the first two groups were not infected, and the mice in the third group died within a few days. The mice of the third group should have survived as the organisms which could kill them had been killed and the cell of R type were incapable of causing disease. However, the mice died and living virulent encapsulated cells of the type S were recovered from their dead bodies. It was observed by Griffith, that killed encapsulated pneumococci had liberated some substance which favoured non-capsulated cells (R type) to produce a capsular substance. This substance in later experiments was proved to be DNA. These experiments showed that DNA is the genetic material.

40. (a) : Autoradiography is the study of labelled precursors like ^{3}H by knowing the movement of radioactivity with the help of photographic films and emulsions at short intervals. Radioactive material like tritiated thymidine which is formed by replacing normal hydrogen of thymidine with H^{3} (heavy isotope of hydrogen). Thymidine only is used for this purpose because RNA will not be labelled by this.

41. (b) : The transforming principle of *Pneumococcus* as found out by Avery, MacLeod and McCarty was DNA. In 1944, Avery, MacLeod and McCarty repeated Griffith's experiment successfully. They separated the proteins, carbohydrates and DNA of S III strains and separately mixed them in the pure cultures of R II. Only DNA could bring about transformation of R II type into S III and not the proteins or the carbohydrates.

42. (d) : Hershey and Chase proved that DNA is a basic genetic material. Hershey and Chase, 1952, by using ^{32}P and ^{35}S with a T-2 type phage concluded that DNA is the genetic material.

43. (a) : Experimental material in the study of DNA replication has been *Escherichia coli*. *E. coli* fully labelled with ^{15}N is allowed to grow in ^{14}N medium. The two strands of DNA molecule of the first generation bacteria have different density and do not resemble parent DNA. Meselson and Stahl, 1958 by using ^{14}N and ^{15}N confirmed that the replication of DNA in *E. coli* is semi-conservative in nature.

44. (b) : Chargaff's rules are applicable only for double stranded DNA molecule. These are not applicable for single stranded DNA or RNA molecules. Chargaff's rules state that DNA helices contain equal molar ratios of A and T, G and C. This is because in a dsDNA molecule, complementary base pairing occurs between A and T, and C and G base pairs. This complementary base pairing is not possible in case of single stranded RNA molecule. Thus, Chargaff's rules are not applicable to RNA.

45. (a) : Deoxyribonucleic acid and ribonucleic acid as the name suggests are made up of several nucleotide monomers. Each nucleotide consists of pentose sugar, phosphate group and nitrogenous bases. DNA has deoxyribose sugar whereas RNA has ribose sugar. The bases in DNA molecule are A, T, G and C whereas in RNA, thymine is absent and instead uracil is found.

46. (c) : Lagging strand is a replicated strand of DNA which is formed in short segments called Okazaki fragments. Its growth is discontinuous. The direction of growth of the lagging strand is 3' $\rightarrow$ 5' though in each Okazaki fragment it is 5' $\rightarrow$ 3'.

47. (d) : Prokaryotic DNA acts as a single replicating unit called replicon. Each replicon has a particular region where replication starts. It is called origin of replication or *ori*. In the region of *ori*, there is a particular nucleotide sequence called autonomic replicating sequence or ARS. Replication proceeds bidirectionally from each *ori*. A replication fork is produced on each side of *ori*. Replication will continue till a replication fork meets another replication fork.

48. (c) : The method of DNA replication is semi-conservative. According to the semi-conservative model proposed by Watson and Crick, each strand of the two double helices formed would have one old and one new strand. So, the parental identity is conserved upto half extent and hence DNA replication is semi-conservative.

49. (b) : DNA is a double helical molecule and it opens to form a replication fork for its replication. The two strands of DNA are joined with the help of H-bonds between the strands. Topoisomerases are specialised to cause nicks or breaks in the double helix and helps separate the DNA stands. Helicase unwinds the DNA helix from that nick caused by the topoisomerase and this separates the two strands. DNA gyrase introduces negative supercoils in DNA strands of prokaryotes. DNA polymerase adds nucleotide units to the 3′ end of a DNA chain. DNA ligase joins the ends of DNA.

50. (c) : During DNA replication, the strands separate by unwindase/helicase. The molecule is unwound by DNA unwinding proteins called helicases. The helicases II and III get attached to lagging strand and protein to the leading strand. The formation of bands is avoided by single stranded DNA binding proteins (SSB).

51. (a) : *Refer to answer 43.*

52. (b) **53. (d)** **54. (b)** **55. (c)**

56. (b) : Franklin Stahl along with Matthew Meselson proved semi-conservative mode of replication in DNA. Punnett square was developed by a British geneticist, Reginald C. Punnett. Spliceosome formation is part of post-transcriptional change in eukaryotes. Transduction was discovered by Joshua Lederberg and Norton Zinder in the bacterium *Salmonella*.

57. (a) : Coding strand and *m*RNA have same nucleotide sequence except, 'T' - Thymine is replaced by 'U' - Uracil in *m*RNA.

58. (d) : *r*RNA (ribosomal RNA) is the most abundant of all types of RNA (70-88%). Hence, it will be present in highest amount. Percentage of *t*RNA and *m*RNA is 15% and 2-5% respectively. miRNA (micro RNA) are 21-22 bp long RNA that bring degeneration of *m*RNA.

59. (c) : Spliceosomes help in removal of introns. They will not occur in prokaryotes because prokaryotes do not have introns and thus, processing does not require splicing of *m*RNA.

60. (b) : Cistron (or gene) is a length of DNA that contains the information for coding a specific polypeptide chain or a functional RNA molecule (*i.e.*, transfer RNA or ribosomal RNA). Hence, cistron is a unit of function. Currently such a gene is called structural gene.

61. (c) : 23S *r*RNA acts as structural RNA as well as ribozyme in bacteria.

62. (a) : The strand of DNA on which RNA polymerase binds to catalyse transcription is called template strand. It is also known as master or antisense strand. It has the polarity of $3' \rightarrow 5'$.

63. (a) : RNA polymerase initiates and extends the RNA (chain elongation) and functions always in 5′ to 3′ direction. The structural component of DNA has 3′ to 5′ polarity. It is also called template DNA strand or antisense (–) strand.

64. (d) : Introns, which occur principally in eukaryotes, are transcribed into messenger RNA (*m*RNA) but are subsequently removed from the transcription before translation. In certain cases, removal of the introns is an autocatalytic process (self-splicing) whereby the RNA itself has the properties of an enzyme.

65. (b) : In RNA, thymine is substituted with uracil thus, the RNA strand complementary to DNA strand ATCTG will be UAGAC.

66. (b) : Nucleolus is the centre for synthesis of ribosomal RNA (*r*RNA) that form ribosomal subunits. Ribosomal proteins migrate to the nucleolus from their assembly sites in the cytoplasm and are packaged into ribonucleoproteins. These return to the cytoplasm where they become mature ribosome particles.

67. (a) : A transcription unit is a part of DNA that is able to transcribe a complete RNA. It consists of a promoter region (where RNA polymerase binds to start transcription), the structural gene (coding region) and the terminator region (that signals release of RNA polymerase and newly formed RNA strand).

68. (a) : In eukaryotes, RNA polymerase enzymes (Type I, II, III) catalyse the synthesis of RNA using as a template either an existing DNA strand or an RNA strand. Type I is responsible for synthesis of *r*RNA, type II for *m*RNA and type III for *t*RNA synthesis.

69. (d) : The 23S *r*RNA is a component of the large prokaryotic (bacterial cell) subunit (50S). The ribosomal peptidyl transferase activity resides in this *r*RNA and

acts as a ribozyme (catalytic RNA). In eukaryotic cells, the 60S (28S component) ribosome subunit contains the peptidyl transferase component and acts as the ribozyme.

70. (b) : Unlike in prokaryotes where transcription and translation take place in the same compartment, in eukaryotes primary transcript is first processed in the nucleus and then transported outside of the nucleus. Since the primary transcripts of the eukaryotes contains both the expressing genes (exons) and non-expressing genes (introns), it undergoes splicing of introns and later capping and tailing at 5′-end and 3′-end respectively.

71. (a) : In 1948, Beadle and Tatum proposed one-gene one-enzyme hypothesis which states that a gene controls metabolic machinery of the organism through synthesis of an enzyme. This laid the foundation of biochemical genetics. Beadle and Tatum were awarded Nobel Prize in 1958. This one gene one enzyme theory has been changed to one gene one polypeptide hypothesis proposed by Yanofsky, *i.e.*, one gene synthesises one polypeptide and many polypeptides form one enzyme.

72. (c) : Telomerase is a ribonucleoprotein molecule that is enzymatic in nature.

73. (b) : After 25 bases from start of transcription point are TATA boxes. After 40 bases from TATA boxes appears CAAT boxes. Both of these sequences serve as recognition sites in eukaryotic promoters. Transcription in eukaryotic genes is a far more complicated process than in prokaryotes.

74. (d) : Transfer RNA (*t*RNA) are types of RNA responsible for the transfer of specific amino acids to the growing end of a polypeptide chain during translation. R.Holly in 1965 gave clover leaf model of *t*RNA for yeast alanyl *t*RNA. It has four major sites - AA binding site, anticodon site, TΨC loop and DHU loop. The chain is having unpaired base sequence CCA at 3′ end and G at 5′ end.

75. (c) : During transcription RNA synthesis from a DNA template takes place. It involves rewriting of the code without a change in its language. In *m*RNA, adenine pairs with uracil because thymine is not present in *m*RNA. So the nucleotide sequence in *m*RNA would be–

DNA template	A	T	A	C	G
	|	|	|	|	|
*m*RNA	U	A	U	G	C

76. (a) : Promoter is region on a DNA molecule upstream from the coding sequence, area to which RNA polymerase initially binds prior to the initiation of transcription. The promoter,or at least part of it, determines the nature of the polymerase that associates with it. Certain consensus sequences within the promoter region seem to be particularly important in the binding of RNA polymerase and these are known as CAAT and TATA boxes. The promoter region extends from some 40 nucleotides to about five nucleotides upstream from the start of the gene-coding region, the CAAT and TATA boxes being located within the promoter region as short six or seven nucleotide sequence.

77. (c) : RNA polymerase enzyme catalyses the synthesis of RNA. It is single in prokaryotes. There are three types of RNA polymerases in eukaryotes– I for 28S, 18S and 5.8S RNA, II for *m*RNA and snRNA and III for *t*RNA, 5S RNA and scRNA. Primase is an RNA polymerase that is used to initiate DNA synthesis. RNA ligase reunites the exon segment after RNA splicing.

78. (a) : DNA transcribes to form *m*RNA. Its function is to carry coded information from DNA for the synthesis of proteins. The RNA consists of a coding region called exon and non-coding region called introns. The exons are thus the functional part that have code for proteins.

79. (a) : *m*RNA is synthesised on DNA template in 5′ → 3′ direction. Synthesis of *m*RNA exhibits several features that are synonymous with DNA replication. RNA synthesis requires accurate and efficient initiation, elongation proceeds in the 5′ → 3′ direction (*i.e.*, the polymerase moves along the template strand of DNA in the 5′ → 3′ direction) and RNA synthesis requires distinct and accurate termination. Transcription exhibits several features that are distinct from replication.

80. (c) : A gene is a hereditary unit consisting of a sequence of DNA and occupying a specific position or locus within the genome. Gene activity ultimately affects the phenotype of the organism possessing the gene. Thus gene is a physical and functional unit of genetic information. A cistron is a unit of genetic function. In prokaryotes, there is one gene one enzyme correspondence. It means that in these organisms genes and cistrons are equivalent.

81. (c) : *Refer to answer 77.*

82. (a)

83. (a) : 3-D model of *t*RNA looks like flattened L-shaped molecule. *t*RNA acts as adapter molecule which carries amino acids to the site of protein synthesis (*i.e.*, ribosomes). Most accepted model for *t*RNA structure is clover leaf model.

84. (d) : Operator genes are a region of DNA sequence capable of interacting with a specific repressor molecule and in doing so it affects the activity of other genes downstream from it.

85. (b) : Transposons are portable genetic elements which can insert themselves at random into a plasmid or any chromosome independently of the host cell

recombination system. It was discovered by Barbara Mc Clintock (1940) in maize and termed as jumping genes. Later Hedges and Jacob termed them as transposons. Introns are nontranslated sequences within the coding sequence of a gene. Such sequences are transcribed into hnRNA but are then spliced out and are not represented in the message. The non-intron sequences of the gene are referred to as exons. Cistron sequence of nucleotides in a DNA molecule code for one particular polypeptide chain.

86. (d) : Nucleolus is a plasmosome body that is formed around the nucleolus organiser and is located in the secondary constriction on that chromosome. It is made up of RNA and proteins. The associated nucleolar chromatin contains DNA. It forms *m*RNA that has low molecular weight. Ribosomes are mainly concerned with protein synthesis. They are sites for synthesis of *r*RNA and *t*RNA is synthesised in the cytoplasm.

87. (d) : In transcription, *m*RNA is formed from DNA template and thymine of DNA is replaced by uracil of RNA. Uracil pairs with adenine.

DNA	A	T	T	C	G	A	T	G
	|	|	|	|	|	|	|	|
*m*RNA	U	A	A	G	C	U	A	C

(transcript)

88. (a) : Split genes are those genes that consist of continuous sequence of nucleotide (coding sequence) interrupted by intervening sequences. Most eukaryotic genes are split as are genes of some animal viruses. The continuous coding sequences are called exons and the intervening non-coding sequence are called introns. These introns are not represented in *m*RNA transcribed from the gene and are not utilised for the synthesis of proteins.

89. (b) : The process in living cells in which the genetic information of DNA is transferred to a molecule of messenger RNA (*m*RNA) is the first step in protein synthesis. Transcription takes place in the cell nucleus or nuclear region and is regulated by transcription factors.

90. (c) : If the distance between two consecutive base pairs is 0.34 nm *i.e.,* 0.3×10^{-9} m and the total number of base pairs of a DNA double helix in a typical mammalian cells is 6.6×10^9 bp the length of DNA is calculated by multiplying the total number of base pairs with distance between two consecutive(approx.) base pair *i.e.,* 6.6×10^9 bp = 0.34 nm = 2.2 m

91. (a) : Insertion or deletion of three or its multiple bases insert or delete in one or multiple codon hence one or multiple amino acids, and reading frame remains unaltered from that point onwards.

92. (d) : As genetic code is nearly universal means almost all organisms (from a virus, bacteria to a tree or human being) will have amino acids coded by same kind of codons as given in checkerboard. So, this property is utilised to produce human insulin using bacteria.

93. (b) : 1 codon consists of 3 bases. Therefore, a deletion on 901 position will affect 33 codons.

94. (c) : Polypeptide synthesis is signalled by two initiator codons or start codons *i.e.*, AUG (methionine codon) and rarely by GUG (valine codon).

95. (b) : Genetic code is non-ambiguous. Non-ambiguous code means that there is no ambiguity about a particular code. One codon specifies only one amino acid and not any other. There are 64 codons. Out of 64, 3 are stop codons or non-sense codons, *i.e.*, these do not code for any amino acid and rest 61 code for one of the 20 amino acids. Neither of them code for more than one amino acids except GUG which normally code for valine but in certain conditions it also codes for N-formyl methionine as initiation codon.

96. (b) : *Refer to answer 95.*

97. (d) : Genetic code was deciphered in 1960's by Crick, Ochoa, Nirenberg, Mathaei and Khorana.

98. (d) : The relationship between the sequence of amino acids in a polypeptide and nucleotide sequence of DNA or *m*RNA is called genetic code**.** The genetic code is continuous and does not possess pause after the triplets. So, a codon in *m*RNA is present in contiguous fashion. If a nucleotide is deleted or added, the whole genetic code will read differently.

99. (d) : AUG codes for methionine and is initiation or start codon which starts the synthesis of polypeptide. UAA (ochre), UAG (amber) and UGA (opal) do not specify any amino acid so they are called termination codons. CUU, CUC, CUA and CUG codes for leucine whereas GCU, GCC, GCA and GCG codes for alanine.

100. (a) : 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 synthesised 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 acid.

101. (c) : Transition mutant is one in which a purine is substituted by a different purine, or a pyrimidine by a different pyrimidine. Such a change involves a base pair change between a G–C pair and an A–T pair in the DNA whereas transversion results when one nitrogen base is replaced by another different type, *e.g.*, C-G and A-T. Transcription is the formation of *m*RNA on DNA template.

102. (a) : UGA, UAG and UAA are three non-sense (or termination) codon which do not code for any amino acid. If in a gene encoding a polypeptide of 50 amino acid, 25th codon is mutated to UAA or any of the termination codon, then the chain will be terminated at that place because it will become difficult for *t*RNA to bring amino acid from amino acid pool. So in that case a polypeptide of 24 amino acids will be formed.

103. (d) : Codon UAC is correctly matched as it codes for amino acid tyrosine. UCG codes for serine, UUU codes for phenylalanine and UGU codes for cysteine. Start codon is AUG and stop codons are UAA, UAG and UGA.

104. (d) : In a triplet, for a particular amino acid more than one word (synonyms) can be used. This phenomenon is described by saying that the code is degenerate. A degenerate code would be one where there is one to one relation between amino acids and the codons that 44 codons out of 64 will be useless or non-sense codons. A code is degenerate because of the third base of the codon. It has been shown that the same *t*RNA can recognize more than one codons differing only at the third position. For example GCU, GCC and GCA all code for alanine amino acids.

105. (c) : *Refer to answer 95.*

106. (a)

107. (b) : 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 synthesised 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 acid.

108. (c) : *Refer to answer 99.*

109. (c) : *Refer to answer 99.*

110. (c) : Mutations are rare events in nature and are then described as spontaneous mutations. Some of these mutations originate from mistakes in normal duplication of DNA. Transitions may be produced by tautomeric shift or ionisation of bases which leads to mistaken A – C base pairing and more frequently mistaken G – T base pairing. Guanine pairs with the rare enol form of thymine and is thus considered as hotspot for spontaneous point mutations.

111. (b) : *Refer to answer 99.*

112. (a) : *Refer to answer 99.*

113. (a) : Non-sense mutation is a mutation which interconverts a nonsense to or from a sense-coding triplet, resulting in an abnormally foreshortened or elongated polypeptide chain. But in this example cytosine is added at the beginning so CAT GAT GAT G will result.

114. (a) : Anticodon is the sequence of three nucleotides in a transfer RNA molecule that pairs with a complementary sequence of three nucleotides (codon) on a molecule of messenger RNA. *t*RNA has clove like shape or L shape (three dimensional). It has G at 5′ end CCA at 3′ end. CCA at 3′ end is meant for attaching to a specific amino acid (AA-binding site). On the opposite side lies an anticodon that is complementary to a specific codon of *m*RNA. The two are called recognition sites.

115. (d) : *Refer to answer 99.*

116. (b) : Khorana synthesised a chain of alternate nucleotide GUGUGUGUGU. He found that it stimulated synthesis of a peptide having alternate valine-cysteine-valine-cysteine.

117. (d)

118. (d) : The genetic information is transferred from DNA to *m*RNA to protein. The proteins are made up of some 20 amino acids whose sequence is hidden in the sequence of nucleotides of *m*RNA. Hence, genetic code consists of all 20 amino acids. Thus genetic code is the relationship of amino acids sequence in a polypetide and nucleotide/base sequence in *m*RNA antisense strand and DNA.

119. (c) : Translation is the process of polymerisation of amino acids to form a polypeptide. The order and sequence of amino acids are defined by the sequence of bases in the *m*RNA. The amino acids are joined by a bond that is known as a peptide bond. Formation of a peptide bond requires energy. So, in the first phase itself amino acids are activated in the presence of ATP and linked to their cognate *t*RNA–a process commonly called as charging of *t*RNA or aminoacylation of *t*RNA.

120. (a) : The association of many ribosomes with single *m*RNA leads to formation of polyribosomes or polysomes. It occurs during translation process of protein synthesis.

121. (c)

122. (c) : *Refer to answer 120.*

123. (a) : Ribosomes are very small organelles having a diameter of 150 Å – 250 Å. Each ribosome is made up of two subunits, a smaller subunit and another larger subunit. These two subunits are associated with the help of Mg^{2+} ions (at 0.001 M concentration). If the Mg^{2+} ions concentration is less in cytoplasm, the two units of ribosome separate but when the Mg^{2+} ions concentration is increased ten times, the two unites and form a dimer.

124. (c) : Neomycin is a broad spectrum antibiotic which was first isolated from a strain of *Streptomyces fradiae*. It is effective against Gram positive as well as Gram

negative bacteria. Its mechanism of action is by selective inhibition of protein synthesis on the 70S (prokaryotic) ribosome by inhibiting the interaction of *m*RNA and *t*RNA during translation process.

125. (c) : Messenger RNA or *m*RNA has been named so because it carries the coded information from DNA for the synthesis of proteins. It carries the coded information in a number of base triplets called codons. It is transcribed on DNA by the enzyme RNA polymerase. Hence, its base sequence is complementary to DNA on which it has been synthesised. In eukaryotes, each gene transcribes its own *m*RNA, therefore the number of *m*RNAs corresponds to the number of genes. *r*RNA is a type of RNA that forms structural and functional components of ribosomes. *t*RNA is a class of RNA having structures with triplet nucleotide sequences that are complementary to the triplet nucleotide coding sequences of *m*RNA. It binds with amino acids and transfers them to ribosomes.

126. (c) : Streptomycin is broad spectrum (active against both Gram-positive and Gram-negative bacteria) and was the first really effective drug against tuberculosis, but its use is limited by the development of resistant strains and by toxic side-effects. The bactericidal action of streptomycin, as with other aminoglycoside antibiotics (*e.g.*, neomycin) is through selective inhibition of protein synthesis on 70S ribosomes. To check resistance of mutants against streptomycin they must be grown on plates with streptomycin. Only those bacterial colonies will propagate from the master that are resistant to the antibiotic.

127. (d) : The mitochondria contains its own set of ribosomes which synthesise proteins, so protein synthesis occurs both in mitochondria and cytoplasm.

128. (c) : The initiation of polypeptide chain in prokaryotes is always brought about by the amino acid methionine but it has to be formylated to form *t*RNA f^{met}. Then methionine binds with *t*RNA f^{met} to form f-^{met}-*t*RNA f^{met}. This f^{met}-*t*RNA f^{met} complex binds with the *m*RNA-30S subunit complex using initiation factors IF-2 and IF-1 and GTP.

129. (d) : Transfer RNA or *t*RNA help in transfer of amino acids to ribosomes. *m*RNA complex to form the polypeptide chain. It has four key regions a carrier and recognition end, enzyme site and ribosome site. This recognition end has three anticodons with the help of which amino acids are identified. *r*RNA forms 67% of 70S ribosomes and 50% of 80S ribosomes. *m*RNA carries the coded information from DNA for the synthesis of proteins.

130. (a) : Protein synthesis or translation consists of ribosomes, amino acids, *m*RNA, *t*RNAs and aminoacyl *t*RNA synthetases. The ribosomes have two binding sites namely aminoacyl site or A-site and peptide site or P-site. The starting amino acid methionine lies at the P-site of the ribosome. The next incoming *t*RNA is called amino acyl *t*RNA, it is bound to A-site. A peptide bond is formed between COOH group of the *t*RNA at P-site and NH_2 group of aminoacyl *t*RNA. This is facilitated by the enzyme peptidyl transferase and does not require high energy phosphate bonds.

131. (d) : Protein synthesis in an animal cell, takes place in the nucleolus as well as in the cytoplasm. Main part of protein synthesis (transcription and translation) occurs in nucleolus. Chain elongation occurs in cytoplasm.

132. (d) : Transcription is the mechanism of copying the message of DNA on RNA with the help of enzyme RNA polymerase. It is meant for taking the coded information from DNA to the site where it is required for protein synthesis. Translation or protein synthesis is a complicated process involving several steps such as – activation of amino acid, transfer of amino acid to *t*RNA, initiation of polypeptide synthesis, elongation of polypeptide chain and termination of polypeptide chain.

133. (c) : Certain amino acids are identified by more than one codons. This phenomenon is called as degeneracy, *e.g.*, phenylalanine is code by UUU and UUC.

134. (b) : The process of translation is protein synthesis. Emil Fischer, a German chemist established that the proteins are polymers of amino acids. There are some twenty amino acids involved in protein synthesis. In translation, the message coded by DNA on *m*RNA is translated into a specific protein.

135. (d)

136. (d) : Alec Jeffreys (1984) invented the DNA fingerprinting technique. Alfred Hershey and Martha Chase proved that DNA is genetic material using T_2 bacteriophages in an experiment. Matthew Meselson and F. Stahl proved semiconservative mode of replication in bacterium *E. coli*.

137. (c) : Operon concept is for prokaryotes that consist of operator gene, promoter gene, regulator gene and structural gene. Structural, operator and regulator genes are also present in eukaryotic gene expression along with enhancer gene but enhancer gene is present only in eukaryotic gene expression. It changes the rate of transcription of structural genes.

138. (a) : In *Lac* operon, lactose is an inducer. It binds with suppressor and inactivates it. It allows RNA polymers access to the promoter and transcription proceeds.

139. (d) : The control of expression of *lac* operon is negative (as it is turned off normally) and inducible. Inducible operon is an operon which remains switched off normally but becomes operational in the presence

of an inducer (lactose, actually allolactose a metabolite of lactose, in case of *lac* operon). The inducible operon generally functions in catabolic pathways. In the presence of an inducer, the repressor has a higher affinity for the inducer than for the operator gene. When lactose is added, a few lactose molecules are carried into the cell by the enzyme lactose permease as small amount of this enzyme is present in the cell even when the operon is not working. These few lactose molecules are converted into allolactose molecules which act as an inducer and bind to the repressor (a product of regulator gene). The repressor-inducer complex fails to join with the operator gene, thus it is turned on.

140. (a, d) : Transcription is the process in living cells in which the genetic information of DNA is transferred to *m*RNA as first step of gene expression. An operon consists of structural genes, promoter, operator and regulator gene.

141. (c) : A non-sense mutation is the one which stops polypeptide synthesis due to the formation of termination or non-sense codon. In *lac* operon, sequence of structural genes is Z, Y and A, which respectively code for β-galactosidase, lactose permease and transacetylase. If the gene Y has non-sense mutation, gene expression will stop at it, resulting in non-expression of both gene Y and successive gene A. Thus, only β-galactosidase enzyme will be produced.

142. (a) : *Refer to answer 139.*

143. (c) : The two French scientists, Jacob and Monod proposed the *lac* operon of *E. coli*. The *lac* operon (an inducible operon) contains a promoter, an operator, a regulator gene and three structural genes *z*, *y*, and *a*, coding for the enzymes β-galactosidase, β-galactoside permease and β-galactoside transacetylase, respectively. β-galactoside permease "pumps" lactose into the cell, where β-galactosidase cleaves it into glucose and galactose. The function of the transacetylase is still not clear. The *lac* regulator gene, designated the *i* gene, codes for a repressor. In the absence of the inducer (*i.e.*, lactose, actually allolactose), the repressor binds to the *lac* operator sequence, preventing RNA polymerase from binding to the promoter and transcribing the structural genes. The inducer of the operon, allolactose, is derived from lactose in a reaction that is catalysed by β-galactosidase. Once formed, allolactose binds to the repressor, causing it to be released from the operator; in doing so, it induces transcription of the *z*, *y* and *a* structural genes. CAP is activator called catabolic activator protein. It exerts a positive control in *lac* operon because in its absence RNA polymerase is unable to recognise promotor gene. CAP activates *lac* genes only when glucose is absent. Such enzymes whose synthesis can be induced by adding the substrate are known as inducible enzymes and the genetic systems responsible for the synthesis of such an enzyme are known as inducible operons.

144. (b) : *Refer to answer 143.*

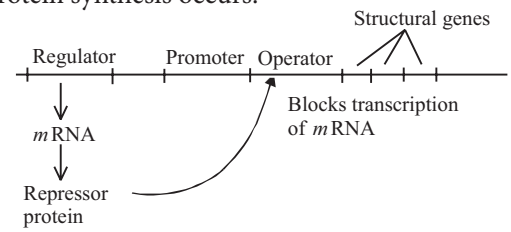
145. (b)

146. (a) : In *lac* operon, *lac* refers to lactose. The *lac* operator is a part of the structural genes (*lac* Z, *lac* Y, *lac* A and *lac* I). It is responsible for the uptake and initial catabolism of lactose.

$$\text{Lactose} \xrightarrow{\beta\text{-galactosidase}} \text{Glucose} + \text{Galactose}$$

147. (c) : Operon model was given by Jacob and Monod (1961) for regulation of protein synthesis in prokaryotes. In bacteria, the genes that contain the information for assembling the enzymes for a metabolic pathway are usually clustered together on the chromosome in a functional complex called an operon. Regulation of protein synthesis in eukaryotes is explained by gene battery model given by Britten and Davidson.

148. (b) : In the *lac* operon of *E.coli,* due to the activity of regulator gene synthesis of repressor molecules occurs. These repressor molecules get attached to the operator gene and thus check *m*RNA synthesis and because of this no protein synthesis occurs.



149. (a) : The tryptophan operon (trp operon) in bacteria is a repressible operon. Here, repressor is inactive and it becomes active as DNA binding protein only when complexed with a co-repressor (tryptophan). In absence of tryptophan, the operator site is open to binding by RNA polymerase, which transcribes the structural genes of tryptophan operon, leading to production of enzymes that synthesise tryptophan. When tryptophan becomes available, the enzymes of tryptophan synthetic pathway are no longer needed and tryptophan (co-repressor)-repressor complex blocks transcription. The regulation of this operon is also a negative control.

150. (b) : Regulator gene is a gene whose function is to control the transcriptional activity of other genes, either adjacent or distant in the genome. In the case of the *lac* operon of *E.coli* the regulator gene *lac i* produces a protein product that represses the operator gene of the operon. In bacteria the same regulator gene may affect a series of non-adjacent operons.

151. (a) : When *E.coli* bacteria are transferred to medium containing lactose, then the *lac* operon is induced. The *lac* operon consists of 3 structural gene (*lac* Z, *lac* Y and *lac* A). It involves the synthesis of β-galactosidase enzyme in *E.coli*, which hydrolyses lactose into glucose and galactose.

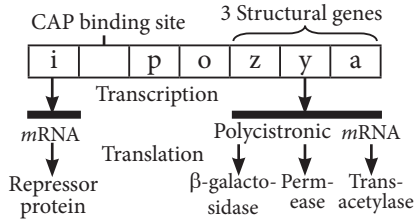
152. (d) : *Refer to answer 143.*

153. (d) : Inducer is a metabolite (or analogue of similar chemical structure), usually of low molecular weight, which promotes the production of an enzyme. Inducers are often substrates for the enzymes they induce, *e.g.*, lactose in case of the synthesis of β-galactosidase in *lac* operon.

154. (c) : *Lac* operon in *E. coli* is induced by β-galactosidase an enzyme meant for hydrolysis of lactose in glucose and galactose.

$$\text{Lactose} \xrightarrow{\beta\text{-galactosidase}} \text{Glucose + Galactose}$$

These enzymes are called as inducible enzymes, because the synthesis of such enzymes are induced by adding substrate such as lactose by 10, 000 times.



155. (b) : Expressed Sequence Tags (ESTs) are genes that are expressed as RNA. It is used in sequencing of human genome.

156. (a) : In genome all the genes are contained in a single set of chromosomes. The instructions in our genome are present in the form of DNA. DNA has a complicated structure in the form of a double helix. Single strands of DNA are coiled up into structures called chromosomes. Within the chromosomes, segments of DNA are "read" together to form genes. Thus, a gene is a segment of DNA or chromosome situated at a specific locus (gene locus) which carries coded information associated with a specific function and can undergo crossing over as well as mutation. A nucleotide is the basic unit of DNA made up of a pentose sugar, phosphoric acid and a nitrogenous base.

157. (d) : Satellite DNA is that part of repetitive DNA which has long repetitive nucleotide sequences in tandem that forms a separate fraction on density ultracentrifugation. DNA fingerprinting involves identifying differences in some specific regions in DNA sequence called as repetitive DNA, because in these sequences, a small stretch of DNA is repeated many times. These repetitive DNA sequences are separated from bulk genomic DNA as different peaks during density gradient centrifugation. The bulk DNA forms a major peak and the other small peaks are referred to as satellite DNA. Depending on base composition (A:T rich or G:C rich), length of segment, and number of repetitive units, the satellite DNA is classified into many categories, such as micro-satellites, mini-satellites, etc. These sequences normally do not code for any proteins, but they form a large portion of human genome. These sequences show high degree of polymorphism and form the basis of DNA fingerprinting. Since DNA from every tissue (such as blood, hair-follicle, skin, bone, saliva, sperm, etc.) from an individual show the same degree of polymorphism, they become very useful identification tool in forensic applications.

158. (d) : Any small, functional, freely folded domain in which coordination of one or more zinc ions is required to stabilise its structure is known as zinc finger. The zinc finger domains are widely dispersed in eukaryotic genomes and are actively involved in sequence specific binding to DNA/RNA and contribute in protein-protein recognitions.

159. (a)

160. (d) : DNA fingerprinting is a technique of determining nucleotide sequences of certain areas of DNA which are unique to each individual. The difference of about 0.1% or 3×10^6 base pairs (out of 3×10^9 bp) provides individuality to each human being. Human genome possesses numerous small noncoding but inheritable sequences of bases which are repeated many times. These sequences occur near telomere, centromeres, Y chromosome and heterochromatic area. The area with same sequence of bases repeated several times is called repetitive DNA. It is separated as satellite from the bulk DNA during density gradient centrifugation and hence called satellite DNA where, repetition of bases is in tandem. Satellite DNAs show polymorphism (the occurrence of mutations in a population at high frequency), which is the basis of genetic mapping of human genome as well as DNA fingerprinting. While mutations in genes produce alleles with different expressions, mutations in non-coding repetitive DNA have no immediate impact. These mutations which have piled up with time form the basis of polymorphism.

161. (a) : *Refer to answer 160.*