Chapter 28

Molecular Basis of Inheritance

FACT/DEFINITION TYPE QUESTIONS

1. The two strands of DNA are held together by
(a) peptide bonds (b) phosphodiester bonds
(c) hydrogen bonds (d) S – S bonds

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

3. Chargaff's rules are applicable to
(a) single stranded RNA.
(b) single stranded DNA and RNA.
(c) single stranded DNA.
(d) double stranded DNA.

4. One turn of DNA possesses
(a) one base pair (b) two base pairs
(c) five base pairs (d) ten base pairs

5. Which of the following is correct for Watson and Crick's model of DNA. It is duplex with
(a) 10 base pairs and 3.4 Å distance for every turn.
(b) 10 base pairs and 3.4 Å distance for each turn of spiral.
(c) 20 base pairs and 34 Å for each turn.
(d) None of the above

6. Information flow or central dogma of modern biology is
(a) RNA → Proteins → DNA
(b) DNA → RNA → RNA
(c) RNA → DNA → Proteins
(d) DNA → RNA → Proteins

7. Nucleosome is
(a) intron interrupted DNA.
(b) double helix DNA.
(c) negatively charged DNA wrapped around positively charged histone octomer.
(d) satellite DNA.

8. Genetic information is carried out by long chain molecule made up of
(a) amino acids (b) enzymes
(c) nucleotides (d) histone proteins

9. Histones are rich in
(a) alanine and glycine (b) lysine and arginine
(c) histidine and serine (d) cysteine and tyrosine

10. In Meselson and Stahl's experiments, heavy DNA was distinguished from normal DNA by centrifugation in
(a) CsOH gradient (b) $^{14}NH_4Cl$
(c) $^{15}NH_4Cl$ (d) CsCl gradient

11. In *Streptococcus pneumoniae*
(a) virulent form is smooth.
(b) virulent form is rough.
(c) nonvirulent form is capsulated.
(d) all forms are rough.

12. The scientists involved in discovery of DNA as chemical basis of heredity were
(a) Hershey and Chase
(b) Griffith and Avery
(c) Avery, Mac Leod and McCarty
(d) Watson and Crick

13. During infection of *E. coli* cells by bacteriophage T_2,
(a) proteins are the only phage components that actually enter the infected cell.
(b) both proteins and nucleic acids enter the cell.
(c) only proteins from the infecting phage can also be detected in progeny phage.
(d) only nucleic acids enter the cell.

14. If a double stranded DNA has 20% of cytosine, what will be the percentage of adenine in it?
(a) 20% (b) 40%
(c) 30% (d) 60%

15. In some viruses, RNA is present instead of DNA indicating that
(a) their nucleic acid must combine with host DNA before replication.
(b) they cannot replicate.
(c) there is no hereditary information.
(d) RNA can act to transfer heredity.

16. A bacterium grown over medium having radioactive ^{35}S incorporates radioactivity in
(a) carbohydrates (b) proteins
(c) DNA (d) RNA

17. Leading strand during DNA replication is formed
(a) continuously.
(b) in short segments.
(c) first.
(d) ahead of replication.

18. DNA replication is
(a) conservative and discontinuous.
(b) semi-conservative and semi-discontinuous.
(c) semi-conservative and discontinuous.
(d) conservative.

19. Methyl guanosine triphosphate is added at 5' end of hn-RNA in a process of
(a) tailing (b) splicing
(c) capping (d) None of these

20. Genetic code is
(a) triplet, universal, ambiguous and degenerate.
(b) triplet, universal, non-ambiguous and non-degenerate.
(c) triplet, universal, non-ambiguous and degenerate.
(d) triplet, universal, ambiguous and non-degenerate.

21. Segments of mRNA removed during splicing are called _____.
(a) introns (b) exons
(c) promotor regions (d) integrator regions

22. Frame shift mutation occurs when
(a) base is deleted or added.
(b) base is added.
(c) base is deleted.
(d) anticodons are not present.

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

24. In eukaryotes, mRNA is synthesized with the aid of
(a) RNA polymerase III.
(b) RNA polmerase II.
(c) RNA polymerase I.
(d) reverse transcriptase.

25. Lactose operon produces enzymes
(a) β-galactosidase, permease and glycogen synthetase.
(b) β-galactosidase, permease and transacetylase.
(c) permease, glycogen synthetase and transacetylase.
(d) β-galactosidase, permease and phosphoglucose isomerase.

26. In *Escherichia coli*, *lac* operon is induced by
(a) lactose (b) promotor gene
(c) β-galactosidase (d) I-gene

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

28. *Lac* operon is
(a) arabinose operon (b) repressible operon
(c) inducible operon (d) overlapping genes

29. Satellite DNA
(a) is classified in many categories such as micro-satellites, minisatellites, etc. on the basis of base composition length of segments and number of repetitive units.
(b) normally does not code for any protein.
(c) shows polymorphism.
(d) All of the above

30. Which process is used for amplication or multiplication of DNA for finger printing ?
(a) Polymerse chain reaction (PCR)
(b) Nesslerisation
(c) Southern blotting
(d) Northern blotting

31. Polymorphism in DNA sequence
(a) is the basis of genetic mapping of human genome.
(b) arises due to mutation.
(c) is the basis of DNA finger printing.
(d) All of the above

32. VNTRs are
(a) Variable Number of Tandem Repeats.
(b) Very Narrow Tandem Repeats.
(c) Variable Non-cistronic Transposon Repeats.
(d) Valuable Non-cistronic Transposon Regions.

33. SNP which is pronounced as "snips" stands for
(a) Small Nuclear Protein
(b) Single Nucleotide Particle
(c) Single Nucleotide Polymorphism
(d) Small Nicking Points

34. Human Genome Project (HGP) is closely associated with the rapid development of a new area in biology called as
(a) biotechnology (b) bioinformatics
(c) biogeography (d) bioscience

STATEMENT TYPE QUESTIONS

35. Which of the following statement is correct about DNA polymerase ?
(a) DNA polymerase can synthesize mRNA in the 3' to 5' direction.

(b) DNA polymerase can synthesize DNA in the 5' to 3' direction.

(c) DNA polymerase can synthesize mRNA in the 5' to 3' direction.

(d) DNA polymerase can synthesize DNA in the 3' to 5' direction.

36. Which of the following statement forms the basis of DNA fingerprinting?

(a) The relative proportions of purines and pyrimidines in DNA.

(b) Satellite DNA occurring as highly repeated short DNA segments.

(c) The relative difference in the DNA occurrence in blood, skin and saliva.

(d) The relative amount of DNA in the ridges and grooves of the fingerprints.

37. Select the correct statement regarding protein synthesis.

(a) When the small subunit of the ribosome encounters an mRNA the process of translation begins.

(b) Peptidase catalyses the formation of peptide bond.

(c) UTRs are present between the start codon and stop codon.

(d) At the end of translation, the release factor binds to the initiation codon.

38. Which of the following statement is **incorrect**?

(a) VNTR belong to a class of mini satellite DNA.

(b) DNA sequences work on the principle developed by F. Sanger.

(c) HGP was coordinated by US Department of Energy and the National Institute of Health.

(d) DNA fingerprinting involves identifying similarities in repetitive DNA.

39. Identify the **incorrec**t statement about RNA.

(a) RNA was the first genetic material to evolve in the living systems.

(b) Apart from being a genetic material, it is also a catalyst.

(c) DNA evolved from RNA with chemical modifications.

(d) RNA being a catalyst is non-reactive and stable.

40. Identify the **incorrect** statement.

(a) In prokaryotes, the structural gene is polycistronic.

(b) In eukaryotes, structural genes have interrupted coding sequences.

(c) Eukaryotes have split gene arrangement.

(d) Intervening sequences appear in mature RNA.

41. Choose the **incorrect** statement regarding the observations drawn from the human genome project.

(a) Repetitive sequences are stretches of RNA.

(b) Less than 2 per cent of the genome codes for protein.

(c) SNPs help in tracing human history.

(d) Repetitive sequences make up a very large portion of the human genome.

42. Find out the **incorrect** statement.

(a) Uracil is present in RNA at the place of thymine.

(b) The complex of DNA and protein in chromosome is called chromatin.

(c) Heterochromatin is the most highly condensed form of chromatin.

(d) The process involved in the RNA formation on the DNA template is called replication.

43. Select the two correct 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 Jacque Monod.

(a) (ii) and (iii) (b) (i) and (iii)

(c) (ii) and (iv) (d) (i) and (ii)

44. How many of the given statements (i-iv) is/are correct?

(i) In transcription, adenosine pairs with uracil.

(ii) Regulation of *lac* operon by repressor is referred to as positive regulation.

(iii) The human genome has approximately 50,000 genes.

(iv) Haemophilia is a sex-linked recessive disease.

(a) Two (b) Three

(c) Four (d) One

45. Which of the following statements are correct?

(i) r-RNA provides the template for synthesis of proteins.

(ii) t-RNA brings amino acids and reads the genetic code.

(iii) RNA polymerase binds to promoter and initiates transcription.

(iv) A segment of DNA coding for polypeptide is called intron.

(a) (i) and (iii) (b) (i) and (ii)

(c) (i), (ii) and (iii) (d) (ii) and (iii)

46. Which of the following statements about RNA polymerase are correct?

(i) RNA polymerase I transcribes rRNAs.

(ii) RNA polymerase II transcribes snRNAs.

(iii) RNA polymerase III transcribes hnRNA.

(iv) RNA polymerase II transcribes hnRNAs.

(a) (i) and (ii) (b) (i) and (iii)

(c) (ii) and (iii) (d) (i) and (iv)

47. Select the **incorrect** statement(s).

(i) Six codons do not code for any amino acid.

(ii) Codon is read in mRNA in a contiguous fashion.

(iii) Three codons function as stop codons.
(iv) The initiation codon AUG codes for methionine.
(a) (i) only (b) (ii) only
(c) (i), (ii) and (iv) (d) (i), (ii) and (iii)

48. Read the following statements and choose the **incorrect** statements.
(i) Nitrogenous base is linked to the pentose sugar through a N-glycosidic linkage.
(ii) Phosphate group is linked to 5′–OH of a nucleoside through phosphoester linkage.
(iii) Two nucleosides are linked through 3′–5′N-glycosidic linkage.
(iv) Negatively charged DNA is wrapped around positively charged histone octamer to form nucleosome.
(v) The chromatin that is more densely packed and stains dark is called euchromatin.
(a) (i) only (b) (iv) only
(c) (iii) and (v) (d) (i), (ii) and (iii)

ASSERTION/REASON TYPE QUESTIONS

In the following questions, a statement of Assertion is followed by a statement of Reason.
(a) If both Assertion and Reason are true and the Reason is the correct explanation of the Assertion.
(b) If both Assertion and Reason are true but the Reason is not the correct explanation of the Assertion.
(c) If Assertion is true but Reason is false.
(d) If both Assertion and Reason are false.

49. **Assertion :** Adenine cannot pair with cytosine
Reason : Adenine and cytosine do not have a perfect match between hydrogen donor and hydrogen acceptor sites. Hence, they cannot pair.

50. **Assertion :** A single mRNA strand is capable of forming a number of different polypetide chains.
Reason : The mRNA strand has terminator codon.

51. **Assertion :** The genetic code is degenerate.
Reason : Most amino acids are coded by more than one codon.

52. **Assertion :** Replication and transcription occur in the nucleus but translation takes place in the cytoplasm.
Reason : mRNA is transferred from the nucleus into cytoplasm where ribosomes and amino acids are available for protein synthesis.

53. **Assertion :** DNA fingerprinting is very well known for its application in paternity testing is case of disputes.
Reason : It employs the principle of polymorphism in DNA sequences as the polymorphisms are inheritable from parent to children.

MATCHING TYPE QUESTIONS

54. Match the enzymes (given in column I) with their function (given in column II) and choose the correct combination from the given options.

	Column - I		**Column - II**
A.	Helicase	I.	Joining of nucleotides
B.	Gyrase	II.	Opening of DNA
C.	Primase	III.	Unwinding of DNA
D.	DNA polymerase III	IV.	RNA priming

(a) A – II; B – I; C – III; D – IV
(b) A – II; B – I; C – IV; D – III
(c) A – IV; B – III; C – I; D – II
(d) A – II; B – III; C – IV; D – I

55. Match the following and choose the correct combination from the given options.

	Column - I		**Column - II**
A.	Splicing	I.	*Lac* operon
B.	Okazaki fragments	II.	Lagging strands
C.	Jacob and Monad	III.	Lactose
D.	Inducer	IV.	Removal of intron

(a) A – IV; B – II; C – I; D – III
(b) A – II; B – I; C – IV; D – III
(c) A – IV; B – III; C – I; D – II
(d) A – II; B – III; C – I; D – IV

56. Match the column-I with column-II and choose the correct combination from the given options.

	Column - I		**Column - II**
A.	Operator site	I.	Binding site for RNA polymerase
B.	Promoter site	II.	Binding site for repressor molecule
C.	Structural gene	III.	Codes for enzyme protein
D.	Regulator gene	IV.	Codes for repressor molecules

(a) A – II; B – I; C – III; D – IV
(b) A – II; B – I; C – IV; D – III
(c) A – IV; B – III; C – I; D – II
(d) A – II; B – III; C – I; D – IV

57. Match the steps of protein by synthesis given in column-I with their feature given in column-II and select the correct combination from the given options.

	Column - I		**Column - II**
A.	Termination	I.	Aminoacyl tRNA synthetase
B.	Translation	II.	Okazaki fragments
C.	Transcription	III.	GTP dependent release factor
D.	DNA replication	IV.	RNA polymerase

(a) A – II; B – I; C – III; D – IV
(b) A – III; B – I; C – IV; D – II
(c) A – IV; B – III; C – I; D – II
(d) A – II; B – III; C – I; D – IV

58. Match the column-I with column-II and select the correct combination from the given options.

	Column - I		**Column - II**
A.	Griffith	I.	Nucleoid
B.	Hershey and Chase	II.	Active chromatin
C.	Prokaryotic DNA	III.	Transduction
D.	Euchromatin	IV.	Transformation

(a) A – II; B – I; C – III; D – IV
(b) A – III; B – I; C – IV; D – II
(c) A – IV; B – III; C – I; D – II
(d) A – II; B – III; C – I; D – IV

59. Match the codons given column I with their respective amino acids given in column II and choose the correct answer.

Column -I (Codons)		**Column -II (Amino acids)**	
A	UUU	I.	Serine
B	GGG	II.	Methionine
C	UCU	III.	Phenylalanine
D	CCC	IV.	Glycine
E	AUG	V.	Proline

(a) A – III; B – IV; C – I; D – V; E – II
(b) A – III; B – I; C – IV; D – V; E – II
(c) A – III; B – IV; C – V; D – I; E – II
(d) A – II; B – IV; C – I; D – V; E – III

60. Match the enzymes given in column -I with its function given in column -II and select the correct option.

Column - I		**Column - II**	
A	β-galactosidase	I.	Joining of DNA fragments
B	Permease	II.	Peptide bond formation
C	Ligase	III.	Hydrolysis of lactose
D	Ribozyme	IV.	Increase permeability of -galactosidase

(a) A – II; B – I; C – IV; D – III
(b) A – III; B – IV; C – I; D – II
(c) A – II; B – IV; C – I; D – III
(d) A – I; B – II; C – IV; D – III

61. Match the scientists given in column-I with their work given in column-II and select the correct option.

	Column-I		**Column-II**
A.	F. Meischer	I.	DNA double helix
B.	Griffith	II.	Nuclein
C.	Hershey and	III.	*S. pneumoniae* Chase
D.	Watson and Crick	IV.	Bacteriophages
E.	Wilkins and	V.	X-ray diffraction studies Franklin

(a) A – II; B – III; C –IV; D – I; E – V
(b) A – V; B – IV; C –III; D – I; E – II
(c) A – I; B – III; C –IV; D – II; E – V
(d) A – I; B – IV; C –III; D – II; E – V

62. Match column-I with column-II and select the correct combination from the given options.

	Column-I		**Column-II**
A.	Sigma factor	I.	5' – 3'
B.	Capping	II.	Initiation
C.	Tailing	III.	Termination
D.	Coding strand	IV.	5' end
		V.	3' end

(a) A – III; B – V; C – IV; D – II
(b) A – II; B – IV; C – V; D – I
(c) A – II; B – IV; C – V; D – III
(d) A – III; B – V; C – IV; D – I

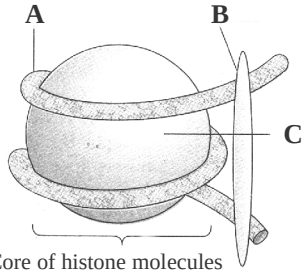
63. Match column-I (Scientists) with column-II (Discoveries) and select the correct options.

	Column-I (Scientists)		**Column-II (Discoveries)**
A.	Alec Jeffreys	I.	*Lac* operon
B.	F. Sanger	II.	Automated DNA sequences
C.	Jacob and Monod	III.	DNA finger printing
D.	Avery, Mc Leod and McCarty	IV.	Transforming principle

(a) A – II; B – III; C – IV; D – I
(b) A – III; B – II; C – I; D – IV
(c) A – III; B – II; C – IV; D – I
(d) A – I; B – II; C – III; D – IV

DIAGRAM TYPE QUESTIONS

64. The given figure shows the structure of nucleosome with their parts labelled as A, B & C. Identify A, B and C.



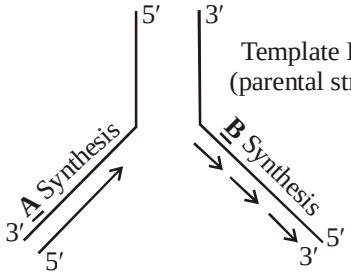
(a) A – DNA; B – H_1 histone; C – Histone octamer

(b) A – H_1 histone; B – DNA; C – Histone octamer

(c) A – Histone octamer; B – RNA; C – H_1 histone

(d) A – RNA; B – H_1 histone; C – Histone octamer

65. Name the types of synthesis A and B occurring in the replication fork of DNA as shown below.



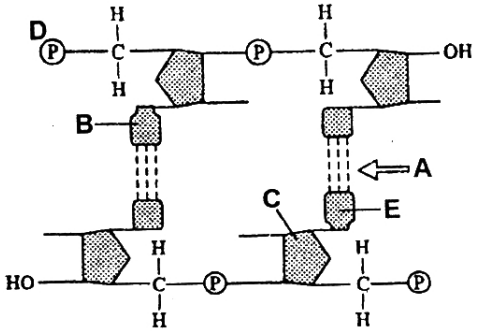
(a) A - Continuous synthesis (synthesis of leading strand); B - Discontinuous synthesis (synthesis of lagging strand).

(b) A - Discontinuous synthesis (synthesis of leading strand); B - Continuous synthesis (synthesis of lagging strand).

(c) A- Continuous synthesis (synthesis of lagging strand); B - Discontinuous synthesis (synthesis of leading strand).

(d) A - Discontinuous synthesis (synthesis of lagging strand); B - Continuous synthesis (synthesis of leading strand).

66. The given figure represents the double stranded poly-nucteotide chain. Some parts are labelled as A, B, C, D and E. Identify the correct labelling of A, B, C, D & E.



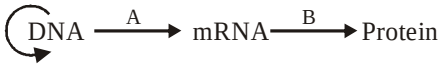
(a) A–Hydrogen bonds, B–Pyrimidine, C–Hexose (deoxyribose) sugar, D–5' end, E–Purine base

(b) A–Hydrogen bonds, B–Purine base, C–Hexose (deoxyribose) sugar, D–5' end, E–Pyrimidine

(c) A–Hydrogen bonds, B–Pyrimidine, C–Pentose (deoxyribose) sugar, D–5' end, E–Purine base

(d) A–Hydrogen bonds, B–Purine base, C–Pentose (deoxyribose) sugar, D– 5' end, E– Pyrimidine

67. The diagram given below shows an important concept (proposed by C) in the genetic implication of DNA. The process occuring in that concept are marked as A and B. Identify A, B and C.



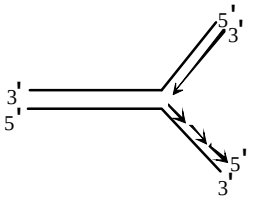
(a) A-Translation, B - Transcription, C-Erwin Chargaff

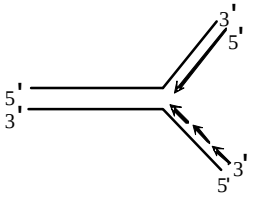
(b) A-Transcription, B - Translation, C-Francis Crick

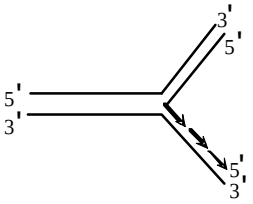
(c) A-Translation, B - Extension, C-Rosalind Franklin

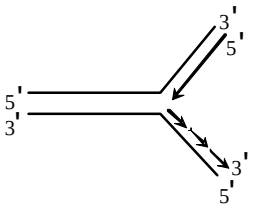
(d) A-Transcription, B - Replication, C-James Watson

68. Which one of the following correctly represents the manner of replication of DNA ?

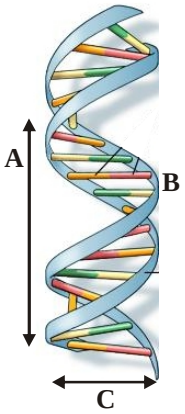
(a)


(b)


(c)


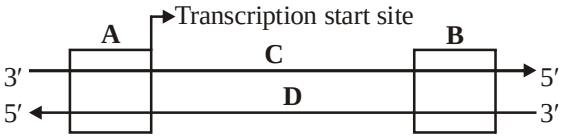
(d)


69. Given figure represent the DNA double helix model, proposed by Watson and Crick (1953). Select the option that shows correct measurement of A, B and C marked in the figure.



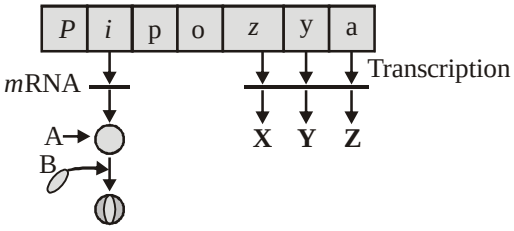
(a) A – 3.4 nm, B – 0.34 nm, C – 2 nm
(b) A – 34 nm, B – 3.4 nm, C – 20 nm
(c) A – 3.4 Å, B – 0.34 Å, C – 20 Å
(d) A – 34 Å, B – 3.4 Å, C – 2 Å

70. Given diagram represents the schematic structure of a transcription unit with some parts labelled as A, B, C and D. Select the option which shows its correct labelling.



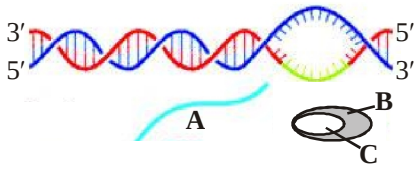
	A	B	C	D
(a)	Terminator	Promoter	Template strand	Coding strand
(b)	Promoter	Terminator	Coding strand	emplate strand
(c)	Promoter	Terminator	Template strand	Coding strand
(d)	Terminator	Promoter	Coding strand	emplate strand

71. The given figure shows *lac* operon model and its functioning. Select the option which correctly labels A, B, X, Y and Z marked in the figure and also identify the label (L) which is primarily responsible for the hydrolysis of the disaccharide, lactose, into galactose & glucose.



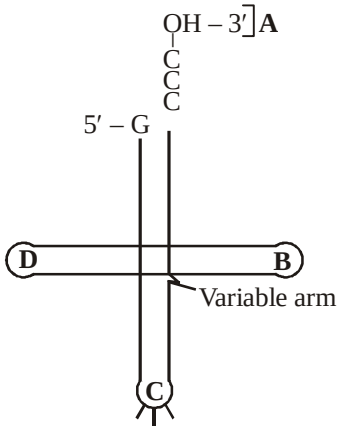
	A	B	X	Y	Z	L
(a)	Repressor	Inducer	β-Galacto-sidase	Permease	Trans-acetylase	X
(b)	Repressor	Inducer	Permease	β-Galacto-sidase	Trans-acetylase	Y
(c)	Inducer	Repressor	β-Galacto-sidase	Permease	Trans-acetylase	Z
(d)	Inducer	Repressor	β-Galacto-sidase	Trans-acetylase	Permease	B

72. The given figure represent one of the step in the process of transcription in bacteria. Identify the step and label A, B & C marked in the figure.



(a) Initiation; A – DNA, B – RNA, C – Promoter
(b) Termination; A – RNA, B – RNA polymerase, C – Rho factor
(c) Elongation; A – RNA, B – RNA polymerase, C – Sigma factor
(d) Elongation; A – DNA, B – DNA polymerase, C – RNA

73. Identify the labels A, B, C and D in the given structure of tRNA and select the correct option.



	A	B	C	D
(a)	Anticodon	TψC loop	AA binding site	DHU loop
(b)	AA binding site	TψC loop	Anticodon loop	DHU loop
(c)	AA binding	DHU loop site	Anticodon	TψC loop loop
(d)	AA binding site	DHU loop	TψC loop loop	Anticodon loop

CRITICAL THINKING TYPE QUESTIONS

74. In tertiary structure of DNA, what is a histone octamer ?
(a) A complex consisting of eight positively charged histone proteins (two of each H_2A, H_2B, H_3 and H_4) that aid in the packaging of DNA.
(b) A complex consisting of eight negatively charged histone proteins (two of each H_2A, H_2B, H_3 and H_4) that aid in the packaging of DNA.
(c) A complex consisting of nine positively charged histone proteins (H_1 and two of each H_2A, H_2B, H_3 and H_4) that aid in the packaging DNA.
(d) A complex consisting of nine negatively charged histone proteins (H_1 and two of each H_2A, H_2B, H_3 and H_4) that aid in the packaging of DNA.

75. RNA polymerases used for the transcription of genes require a _____ template.
(a) *r*RNA (b) DNA
(c) RNA (d) *m*RNA

76. The most abundant type of RNA in the cell is
(a) *r* RNA (b) *m* RNA
(c) *t* RNA (d) *hn* RNA

77. In terms of DNA and RNA structure, what is a nucleotide ?
(a) A nucleotide is a heterocyclic base.
(b) A nucleotide is a sugar molecule covalently bonded to a heterocyclic base.
(c) A nucleotide is a sugar molecule bonded to phosphate group and a heterocyclic base.
(d) A nucleotide is a heterocyclic base bonded to phosphate group.

78. DNA exists in a double-stranded form whereas RNA is mainly a single stranded molecule. What is the likely reason for DNA being double stranded ?
(a) RNA strands cannot form base pairs.
(b) Double stranded DNA is a more stable structure.
(c) DNA cannot exist in the single stranded form.
(d) It is easier to replicate double stranded DNA than single stranded RNA.

79. *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 with their parent DNA.
(b) different density but resemble with their parent DNA.
(c) same density and resemble with their parent DNA.
(d) same density but do not resemble with their parent DNA.

80. Which step of translation does not consume high energy phosphate bond?
(a) Translocation
(b) Peptidyl transferase reaction
(c) Amino acid activation
(d) Aminoacyl tRNA binding to A-site

81. During elongation of polypeptide chain, sigma factor is
(a) functionless.
(b) retained for specific function.
(c) released for re-use.
(d) required during closing of chain.

82. Determination of one amino acid by more than one codon is due to
(a) redundancy of genetic code.
(b) continuous nature of genetic code.
(c) punctuation in genetic code.
(d) universal nature of genetic code.

83. Operon is a
(a) sequence of three nitrogen bases determining a single amino acid.
(b) set of closely placed genes regulating a metabolic pathway in prokaryotes.
(c) segment of DNA specifying a polypeptide.
(d) gene responsible for switching on and switching off other genes.

84. Clover leaf secondary structure of *t*RNA has a loop for
(a) three nucleotides of a codon.
(b) three nucleotides of an anticodon.
(c) no nucleotides.
(d) both (a) and (b)

85. DNA replication is semi-conservative as
(a) only non-parent strand acts as template.
(b) both strands of new molecule are synthesized *de novo*.
(c) one of the strand in each new molecule is parental and the other is new.
(d) daughter strands are dispersive.

86. Mutations which alter nucleotide sequence within a gene are called
(a) frame shift mutations
(b) base pair substitutions
(c) both (a) and (b)
(d) none of these

87. Which one of the following pair is a purine pair?
(a) Uracil, Guanine
(b) Cytosine, Thymine
(c) Adenine, Guanine
(d) Adenine, Thymine

88. Which one of the following group of codons is called as degenerate codons?
(a) UAA, UAG and UGA
(b) GUA, GUG, GCA, GCG and GAA
(c) UUC, UUG, CCU, CAA and CUG
(d) UUA, UUG, CUU, CUC, CUA and CUG

89. The two strands of a double helix model of DNA are held together by hydrogen bonds between
(a) sugar and phosphate groups.
(b) sugar and nitrogenous bases.
(c) phosphate groups and nitrogenous bases.
(d) nitrogenous bases.

90. Transcription
(a) starts at initiator region and ends at stop region.
(b) starts at operator region and ends at telomeric end.
(c) starts at promoter region and ends at terminator region.
(d) starts at CAAT box and ends at TATA box.

91. Consider the process that a cell uses to replicate its double-strand DNA to make copies for daughter cells. Which statement describes the DNA in daughter cells ?
(a) The double helix in one daughter cell consists of two strands that were originally in the parent cell, while the double helix in the other daughter cell consists of two newly made strands.
(b) The two strands of the double helices in both daughter cells consist of segments of new and parental DNA.
(c) The double helices in each daughter cell consists of one parental strand and one newly made strand.
(d) None of the above.

92. Nucleotides are linked by
(a) hydrogen bonds. (b) phosphodiester bonds.
(c) peptic bonds. (d) ionic bonds.

93. A geneticist isolates a gene for a specific traits under study, she also isolate the corresponding mRNA. Upon comparison, the mRNA is found to contain 1,000 fewer bases than the DNA sequence. Did the geneticist isolate the wrong DNA ?
(a) Yes, mRNA is made from a DNA template and should be the same length as the gene sequence.
(b) Yes, the mRNA should contain more bases than the DNA sequence because bases flanking the gene are also transcribed.
(c) No, the final mRNA contains only exons, the introns were removed.
(d) No, the mRNA was partially degraded after it was transcribed.

94. A DNA strand with the sequence AACGTAACG is transcribed. What is the sequence of the mRNA molecule synthesized ?
(a) AACGTAACG (b) UUGCAUUGC
(c) AACGUAACG (d) TTGCATTGC

95. During translation, proteins are synthesized by
(a) ribosomes using the information on DNA.
(b) lysosome using the information on DNA.
(c) ribosome using the information on mRNA.
(d) lysosome using the information on mRNA.

96. What role does messenger RNA play in the synthesis of proteins ?
(a) It catalysis the process.
(b) It translates the genetic code to a specific amino acid.
(c) It provides the genetic blue print for the protein.
(d) It modifies messenger RNA molecules prior to protein synthesis.

97. What is the main function of tRNA in relation to protein synthesis ?
(a) Initiates transcription
(b) Inhibits protein synthesis.
(c) Identifies amino acids and transport them to ribosomes.
(d) proof reading.

98. Which of the following molecule contains the genetic code?
(a) DNA (b) mRNA
(c) tRNA (d) rRNA

99. What sequence on the template strand of DNA corresponds to the first amino acid inserted into a protein ?
(a) TAC (b) UAC
(c) UAG (d) AUG

100. Which of the following would you expect to find in an inducible system ?
(a) A repressor protein, which is bound to DNA in absence of any other factor.
(b) A repressor protein, which is bound to DNA in the presence of a co-repressor.
(c) An activator protein, which is bound to DNA in the absence of any other factor.
(d) An activator protein, which is bound to DNA only in the absence of air inhibitor.

101. What effect would you expect if gene expression of the *lac* operon were completely repressed ?
(a) The cell would be more efficient without 'wasting' the energy required for the low level of *Lac* Z, *Lac*Y, and *Lac* A gene expression.
(b) Allolactose would accumulate within the cell and become toxic.
(c) Lactose would not be converted into the inducer and the operon could not be induced.
(d) All of the above

102. Which of the following is **Not** a goal of the human genome project ?
(a) To sequence the genomes of selected model organisms.
(b) To eliminate all diseases.
(c) To consider social, ethical and legal aspects of genetic information.
(d) To develop computational tools for analyzing sequence information.

103. In addition to the human genome sequence, draft or finished genome sequences existed for eight model organisms by 2002. Which of the following organisms are not the part of that group of eight model organisms ?
(a) *Saccharomyces cerevisiae*
(b) *Drosophila melanogaster*
(c) *Oryza sativa*
(d) *Quercus rubra*

104. Each individual has a unique DNA fingerprint as individuals differ in
(a) number of minisatellites on chromosome.
(b) location of minisatellites on chromosome.
(c) size of minisatellites on chromosome.
(d) All of the above

105. DNA fingerprinting using Variable Number Tandem Repeats (VNTRs) is based on the observation that
(a) every individual has unique alleles at each VNTR locus.
(b) the DNA of VNTR loci is more stable than that of loci which code for proteins.
(c) VNTR sequences show little variability.
(d) VNTR loci are highly polymorphic.

106. The okazaki fragments in DNA chain
(a) result in transcription.
(b) polymerize in the 3' to 5' direction and forms replication form.
(c) prove semi-conservative nature of DNA replication.
(d) polymerize in the 5' to 3' direction and explain 3' to 5' DNA replication.

Hints & Solutions

Chapter 28 : Molecular Basis of Inheritance

1. (c) In DNA, the two chains are held together by hydrogen bonds between pairs of bases which help to stabilize the interaction.

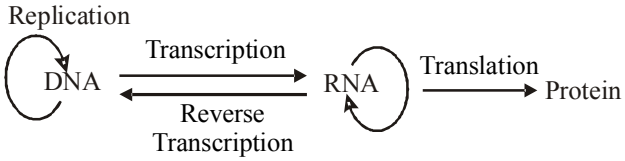
2. (a) X-ray crystallography is the study of molecular structure by examining diffraction patterns made by x-rays beamed through a crystalline form of the molecules. It is widely used in biochemistry to examine the molecular structure of molecules such as proteins and DNA.

3. (d) Chargaff's rule are applicable to double stranded DNA because according to the Chargaff's rule, percentage of adenine is equal to the percentage of thymine and percentage of guanine is equal to the percentage of cytosine.

4. (d) There are about 10 base pairs in each turn of DNA double helix.

5. (a) According to Watson and Crick model of DNA, it is a double helical molecule with 10 base pairs and 3.4 Å distance for every turn.

6. (d) Central dogma term was proposed by Crick (1958). It proposes unidirectional or one way flow of information from DNA to RNA and then to protein (polypeptide).



7. (c) Nucleosome is the structural unit of a eukaryotic chromosome, and thought to be present only during interphase of cell cycle. It consists of DNA wrapped around histone octamer.

8. (c) Nucleotide is an organic molecule consisting of a nucleoside (nitrogenous base and pentose sugar) connected to a phosphate group. It forms the basic structural unit of nucleic acids (such as DNA or RNA) which carry the genetic information.

9. (b) Histones are positively charged, basic proteins, enriched in the amino acids arginine and lysine. Thus, being basic, histones bind tightly to DNA which is an acid H_4.

10. (d) In Meselson and Stahl's experiments, heavy DNA was distinguished from normal DNA by centrifugation in CsCl gradient. When DNA is mixed with caesium chloride it will settle down at a particular height in centrifugation and heavier one higher up.

11. (a) Griffith (1928) described the phenonmenon of bacterial transformation. He experimented with the smooth and rough strains of *Streptococcus pneumoniae*. Smooth strains of bacteria were virulent or pathogenic & cause pneumonia.

12. (c) The scientists involved in the discovery of DNA as chemical basis of heredity were Avery, Mac Leod and McCarty. They expanded the work of Griffith on the process of transformation.

13. (d) The experiment conducted by Hershey and Chase proved that DNA is the genetic material and that during infection of *E. coli* cells by bacteriophage T2, only nucleic acids (DNA or RNA) enter the cell. Nucleic acids from the head pass through the hollow tail and enter the bacterial cell. The remainder of the phage remains on the outside of the bacterium as "ghost".

14. (c) The purines and pyrimidines are always in equal amounts as per chargaff's rule. So, if cytosine is 20%, the thymine will be 30% and thymine is equal to adenine. Then the percentage of adenine will be 30%.

15. (d) RNA and DNA both are genetic material and carry genetic information from one generation to other. A virus is a small parasite that cannot reproduce by itself. Most viruses have either RNA or DNA as their genetic material. Once a virus infects a susceptible cell, it can direct the cell machinery to produce more viruses.

16. (b) Few bacteriophages were grown in bacteria containing ^{35}S which was incorporated into the cysteine and methionine amino acids of proteins and thus these amino acids with ^{35}S formed the proteins of phage.

17. (a) Leading strand during DNA replication is formed continuously in 5' - 3' direction by continuous polymerization at the 3' growing tip.

18. (c) DNA replication is the process in which a double-stranded DNA molecule is copied to produce two identical DNA molecules. In DNA replication each new strand is half the original parent strand (hence called semiconservative) and one strand is synthesized continuously and other discontinuous (hence called discontinuous).

19. (c) In capping, unusual nucleotide (methyl guanosine triphosphate) is added to 5' end of hn-RNA and forms cap. CCA segment is also added to t-RNA as terminal addition for specific function.

20. (c) Genetic code is the depiction of codon by which the information in RNA is decoded in a polypeptide

chain. The information is transferred in the form of triplet of bases coding for one amino acid. It is triplet, universal, non-ambiguous and degenerate in nature.

21. (a) In RNA splicing, intron sequences are removed by process (known as splicing) and ligates the ends of exon sequences together.

22. (a) Frame shift mutation are those mutation in which the reading of the frame of the base sequence shifts laterally either in forward direction due to addition of one or more nucleotides or in backward direction due to deletion of one or more nucleotides.

23. (d) AUG is the initiation codon of protein synthesis in eukaryotes. AUG always codes for methionine in eukaryotes.

24. (b) In eukaryotes, RNA polymerase are of 3 types:
(i) RNA polymerase I : Transcribes rRNA (285S, 18S, 5.8S). It is found in nucleolus.
(ii) RNA polymerase II : Transcribes mRNA (hnRNA-heterogenous RNA). It is found in nucleoplasm.
(iii) RNA polymerase III : Transcribes tRNA, 5S rRNA and SnRNA (small nuclear RNAs). It is found in nucleoplasm.

25. (b) Lactose operon (model proposed by Jacob and Monad) produces three enzymes - β- galactosidase (*z*), permease (*y*), transacetylase (*a*). β- Galactosidase (*z*) is responsible for the splitting of lactose into glucose and galactose. Permease (*y*) is required in entry of the lactose/galactose. Transacetylase (*a*) transfers an acetyl CoA to β- Galactosides.

26. (a) The inducer for *Lac* operon of *Escherichia coli* is lactose (actually allolactose or metabolite of Lactose). This *lac* operon normally remains inactive. When *lac* operon contacts with lactose, the lactose acts as an inducer and combines with the repressor, and the repressor is detached from operator gene. Thus RNA polymerase enzyme gets its passage and reaches to the structural genes and starts the transcription.

27. (d) Hershey & Chase (1962) discovered that DNA is the genetic material of bacteriophage. They experimented with T_2 phage which attacks the bacterium *E. coli*. Some virus made to grow on culture containing radioactive sulphur and some on radioactive phosphorus. Findings indicated that protein did not enter the bacteria from the viruses but DNA from the virus particle enters bacteria as genetic material.

28. (c) Lac operon is an inducible operon. Inducible operon system regulates genetic material which remains switched off normally but becomes operational in the presence of inducer.

29. (d) Satellite DNA is a portion of DNA consisting of short, repeating sequences of nucleotide pairs near the region of the centromere. Normally it does not code for any protein but shows polymorphisms. It is classified in many categories like micro- or minisatellites based on the composition, length of segments and number of repetitive units.

30. (a) Polymerase chain reaction (PCR) is a process used for the amplification (copy - small segments) of DNA. It is a technique for enzymatically replicating DNA without using living organisms, such as *E. coli* or yeast. It is commonly used in the medical and biological research labs for a variety of tasks, like detection of hereditary diseases, the identification of genetic fingerprints, diagnosis of infectious diseases, cloning of genes, paternity testing etc.

31. (d) Polymorphism in DNA sequence is a variation at genetic level. It arises due to mutation and is the basis of genetic mapping of human genome as well as of DNA fingerprinting.

32. (a) In human genome, there are about 200,000 satellite loci. These simple tandem repeats of short sequences are called 'Variable Number Tandem Repeats' (VNTRs). These repeats are inherited from the parents, and are used as genetic markers in a personal identity test.

33. (c) Single nucleotide polymorphism(SNP) is the most common type of genetic variation among people. Each SNP represents a difference in a single DNA building block, called a nucleotide. For example, a SNP may replace the nucleotide cytosine (C) with the nucleotide thymine (T) in a certain stretch of DNA.

34. (b) Human Genome Project (HGP) is closely associated with the rapid development of a new area in biology called bioinformatics which is used for storage and analysis of enormous amount of data.

35. (b) DNA polymerase is an enzyme which is involved in the replication and repair of DNA. It synthesizes new DNA strands using a DNA template in the 5' - 3' direction.

36. (b) DNA fingerprinting is a test to identify and evaluate the genetic information called DNA (deoxyribonucleic acid) in a person's cells. DNA fingerprinting is a form of identification based on sequencing specific non-coding portions of DNA that are known to have a high degree of variability from person to person. These sections are known as tandem repeats. The test is used to determine whether a family relationship exists between two people, to identify organisms causing a disease, and to solve criminal cases.

37. (a) Peptidase catalyses the breaking of peptide bond. The UTRs are present at both 5′-end (before start codon) and 3'-end (after stop codon). At the end of translation release factor binds to the stop codon, terminating translation and releasing the complete polypeptide from the ribosome.

38. (d) DNA fingerprinting involves identifying differences in repetitive DNA. Since the DNA from every tissue of an individual show the same degree of polymorphism, they become very useful identification tool in forensic application.

39. (d) RNA used to act as a genetic material as well as a catalyst (in some important biochemical reactions). But, RNA being a catalyst is reactive and unstable.

40. (d) Introns or intervening sequences do not appear in mature or processed RNA.

41. (a) Repetitive sequences are stretches of DNA sequences that are repeated many times sometimes hundred to thousand times. They are thought to have no direct coding functions, but they shed light on chromosome structure, dynamics and evolution.

42. (d) The process involved in the RNA formation on the DNA template is called transcription.

43. (c) Jacob and Monod proposed the *lac* operon of *E. coli*. The *lac* operon contains a promoter, an operator, and three structural genes called Z, Y, and A, coding for the enzyme, β galactosidase, permease and transacetylase respectively. The *lac* regulator gene, designated as *i* gene, codes for repressor. In the absence of the inducer, the repressor binds to the *lac* operator, preventing RNA polymerase from binding to the promoter and thus transcribing the structural gene.

44. (a) Statement (i) and (iv) are correct.
Regulation of *lac* operon by repressor is referred to as negative regulation. In negative regulation, a repressor molecule binds to the operator of an operon and terminates transcription. In positive regulation, an activator interacts with the RNA polymerase in the promoter region to initiate transcription.
Human genome contains some 20,000 - 25,000 genes billion bases.

45. (d) mRNA provides the template for synthesis of proteins. A segment of DNA coding for polypeptide is called exon.

46. (d) RNA pol I transcribes rRNAs, whereas the RNA pol III is responsible for transcription of tRNA, 5srRNA and snRNAs. RNA pol II transcribes hnRNA.

47. (a) 3 codons do not code for any amino acid. Such codons are called non-sense codons or terminator codon. Eg UAG, UAA & UGA.

48. (c) Two nucleotides are linked through 3' – 5' phosphodiester linkage to form a dinucleotide. The chromatin that is more densely packed and stains dark is called heterochromatin.

49. (a) Adenine pairs with thymine and cytosine pairs with guanine due to the perfect match of hydrogen donor and acceptor sites.

50. (a) A single mRNA strand is capable of forming different polypetide chains because it has different reading frame (the way through which reading of mRNA by tRNA)

51. (a) Phenomenon in which more than one codon encodes a single amino-acid is called degeneracy of genetic code.

52. (a) In eukaryotes the replication and transcription takes place in the nucleus. mRNA came out from the nucleus through the nuclear pore. In cytoplasm translation occurs. In prokaryote there is no nuclear membrane, so replication, transcription and translation all occur in the cytoplasm.

53. (b)

54. (d) Helicase is an enzyme which unwinds the DNA strand by breaking the H - Bonding present between the nucleotide pairs. Gyrase catalyzes the breaking and rejoining of bonds linking adjacent nucleotides in circular DNA to generate supercoiled DNA helices. The synthesis of RNA primer is done by primase enzyme. DNA polymerase III is involved in the synthesis of DNA from its deoxyribonucleoside triphosphate precursors.

55. (a) Splicing is a process in which introns and intervening sequences of non - essential nature are removed by nuclease. Okazaki fragments are newly synthesized DNA fragments that is associated with the lagging or discontinuous strand. Jacob and Monad were the first to elucidate a transcriptionally regulated system. They proposed lac (lactose) operon. The lac operon is an operon which is required for the transport and metabolism of lactose in *Escherichia coli* bacteria and some other enteric bacteria. It has three adjacent structural genes, lacZ, lacY, and lacA. Inducer is a molecule that regulates gene expression. It attaches to repressor and changes the shape of operator binding site so that repressor no more remains attached to the operator. In the lac operon, allolactose is the actual inducer while lactose is the apparent inducer.

56. (a) Operator site gives passages to RNA polymerase moving from the promoter to structural gene. Promoter site is the initiation point for transcription and the site for binding of RNA polymerase. Structural gene determines the amino acid sequence on the segment of DNA molecule. Regulator gene controls the activity of operator gene by producing repressor molecules.

57. (b) GTP dependent release factor is involved in the termination. Termination requires the activities of three release factors R1, R2, R3. A release factor

allows for the termination of translation by recognizing the termination codon or stop codon in an mRNA sequence. Amino acyl tRNA synthetase is an enzyme which plays an important role in translation during protein synthesis. This enzyme is responsible for the specific amino acylation of tRNA. Transcription is the process of transferring the information stored in DNA into a new molecule of mRNA through the synthesis of RNA over the DNA template. Transcription is carried out with the help of an RNA polymerase enzyme and a number of accessory proteins (called transcription factors). RNA polymerase enzyme is responsible for copying a DNA sequence into an RNA sequence. DNA replication is the process in which a double-stranded DNA molecule is copied to produce two identical DNA molecules. Okazaki fragments are short, newly synthesized DNA fragments that are formed on the lagging (or discontinuous) template strand during DNA replication.

58. (c) Griffith described the phenomenon of bacterial transformation. Hershey and Chase discovered that RNA is the genetic material of bacteriophage. Prokaryotic DNA is also called nucleoid. Nucleoid is an irregularly-shaped region within the cell of a prokaryote (unicellular organisms) that contains all or most of the genetic material. Euchromatin is a chromosome material and comprises the most active portion of the genome within the cell nucleus. It does not stain strongly except during cell division and represents the major genes and is involved in transcription.

59. (a) A-III, B-IV, C-I, D-V, E-II

UUU	–	Phenylalanine
GGG	–	Glycine
UCU	–	Serine
CCC	–	Proline
AUG	–	Methionine

60. (b) A-III, B-IV, C-I, D-II

β-galactosidase	–	Hydrolysis of lactose
Permease	–	Increases permeability to β-galactosidase
Ligase	–	Joining of DNA fragments
Ribozyme	–	Peptide bond formation

61. (a) F. Meischer discovered nuclein as an acidic substance present in nucleus. Griffith experimented with the smooth(S) and rough (R) strains of *S. pneumoniae*. Smooth strains of bacteria were virulent or pathogenic and cause pneumonia. Rough strains were non-pathogenic or avirulent. Hershey and Chase discovered that RNA is the genetic material of bacteriophage (virus which infects bacteria). Watson and Crick proposed the three dimensional structure of DNA based on X ray diffraction photographs of DNA taken by Rosalind Franklin and M H F Wilkins.

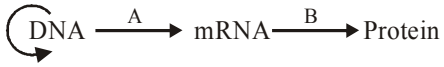
62. (b) Sigma factor is associated with the initiation of transcription. Sigma factor conferrs the specificity of RNA synthesis at the promoter region. Capping involves the addition of unusual nucleotide at the 5' end of hn RNA. Tailing involves the addition of adenylate residues at 3' end in a template independently. Coding strand (also called leading strand) is a strand synthesized by an enzyme in continuous piece in 5' - 3' direction.

63. (b) Alec Jeffreys developed techniques for DNA fingerprinting and DNA profiling. These techniques are now used worldwide in forensic science. F. Sanger worked on protein sequencing and DNA sequencing and got Noble prize for the same. Jacob and Monad proposed the lac (lactose) operon. Avery, McLeod and McCarty expanded the work of Griffith on the process of transformation.

64. (a) Nucleosome is a structural unit of a eukaryotic chromosome which consists of a length of DNA coiled around a core of histones and are thought to be present only during interphase of cell cycle. In the given figure of nucleosome structure, the parts marked as A, B and C are respectively DNA, H1 histones and histone octamer.

65. (a) Replication fork is a site on a DNA molecule at which both unwinding of the helices and synthesis of daughter molecules occurs. In the given figure of replication fork of DNA, the A and B synthesis are respectively called continuous (the template with polarity 3' - 5') and discontinuous (the template with polarity 5' - 3') synthesis.

66. (d)

67. (b) 

The given figure shows the concept of central dogma of molecular biology. In this question A is transcription, B - translation C - Francis Crick. It is unidirectional flow of information DNA to mRNA (transcription) and then decoding the information present in mRNA in the formation of polypeptide chain or protein (translation).

68. (d) The given figure represents the figure of replication fork of DNA. The new strands of DNA are formed in the $5' \rightarrow 3'$ direction from the $3' \rightarrow 5'$ template DNA by the addition of deoxyribonucleotides to the 3' end of primer RNA.

69. (a) A, B and C represent the pitch (a complete turn) of helix, distance between a base pair in a helix and distance between two strand of DNA molecule respectively.

70. **(c)**

71. **(a)** In the given figure of lac operon model (proposed by Jacob and Monad), the labels A, B, X, Y and Z are respectively repressor, inducer, β- galactosidase (*z*), permease (*y*), transacetylase (*a*). *z*, *y* and a are three structural genes which produces three enzymes for the degradation of lactose to glucose and galactose. Label X (β- galactosidase) is primarily responsible for the hydrolysis of disaccharide lactose into galactose and glucose.

72. **(b)** In the given figure, the step shown is termination of transcription in bacteria. The label A, B and C are respectively RNA, RNA polymerase and rho factor. RNA polymerase is an enzyme that synthesizes the formation of RNA from a DNA template during transcription. Rho factor is a termination factor which releases RNA from the DNA template.

73. **(b)** tRNA or transfer RNA is a single stranded molecule and takes the shape of a clover leaf. In the process of transcription tRNA brings amino acid and reads the genetic code and acts as an adapter molecule. In the given structure of tRNA, the labels A, B, C and D are respectively AA binding site (amino acid binding site), TψC loop, anticodon loop (codon recognition site) and DHU loop (amino acid recognition site).

74. **(a)** A histone octamer is a complex of eight positively charged histone proteins (two of each H_2A, H_2B, H_3 and H_4) that aid in the packaging of DNA. Negatively charged DNA wraps around these histone octamers to form the nucleosome. The DNA is held there by ionic bonds. Linker histone H1 binds to each nucleosome where the DNA enters and exits and this draws a string of nucleosomes closer together to form the 10 nm fibre. The nucleosomes in chromatin are seen as beads-on string structure when viewed under electron microscope.

75. **(b)**

76. **(a)** Ribosomal RNA or rRNA is the most abundant types of RNA (about 80%) in the cell. It is found to be a catalytic element for protein synthesis.

77. **(c)** A nucleoside is made up of a sugar molecules and a heterocyclic base while a nucleotide is made up of a sugar molecule, phosphate group and a heterocyclic base.

78. **(b)** Double stranded DNA is much more stable than single stranded RNA and this helps to protect our genetic code. Having a second copy of our genetic code means that there is a reference for repair in the event of a mutation or damage.

79. **(a)** Messelson and Stahl (1958) cultured (*Escherichia coli*) bacteria in a culture medium containing ^{15}N. After these had been replicated for a few generations in the medium both the strands of their DNA contained ^{15}N as constituents of purines and pyrimidines. When these bacteria with ^{15}N were transferred in cultural medium containing ^{14}N, it was found that DNA separated from fresh generation of bacteria possesses one strand heavier than the other. The heavier strand represents the parental strand and lighter one is the new one synthesized from the culture indicating semi conservative mode of DNA replication.

80. **(b)**

81. **(a)** The function of sigma factor is to confer the specificity of RNA synthesis at the promoter site. But during elongation of polypeptide chain, sigma factor is functionless.

82. **(a)** Degeneracy of codons is the redundancy of the genetic code. A single amino acid may be specified by many codon *i.e.*, called degeneracy. Degeneracy is due to the last base in codon (which is known as wobble base). Thus, first two codon are more important to determine the amino acid and third one differ without affecting the coding *i.e.*, known wobble hypothesis, proposed by Crick which establishes an economy of tRNA molecule.

83. **(b)** Operons are segments of genetic material (DNA) which functions as regulated unit or units that can be switched on or switched off. It is a sequence of closely placed genes regulating a metabolic pathway in prokaryotes.

84. **(b)** Clover leaf secondary structure of *t*RNA has a loop for three unpaired bases (triplet of base) whose sequence is complementary with a codon in mRNA.

85. **(c)** Replication is the formation of exact carbon copy or replica. According to semi -conservative method of DNA replication, the two strands of DNA molecule separate and the complementary strand is synthesized from the medium. After the completion of replication, each DNA molecule would have one parental and one newly synthesized strand.

86. **(c)** In frame shift mutation the reading of the frame of the base sequence shifts laterally either in forward direction due to addition of one or more nucleotides or in backward direction due to deletion of one or more nucleotides. Whereas in base pair substitution a base pair is replaced by another base which results in change of nucleotide sequence.

87. **(c)** DNA (deoxyribose nucleic acid) consists of 3 different molecules-phosphate, 5-carbon deoxyribose sugar and nitrogenous base. The nitrogenous base may be a 9-membered, double purine, *i.e.*, adenine (A) or guanine (G), or a 6-membered, single -ringed pyrimidine, *i.e.*, thymine (T) or cytosine (C).

88. **(a)** Degenerate codons (also called as non - sense codons or terminator codons) do not code for any amino

acids. Three types of degenerate codons are UAG (amber), UAA (ochre) and UGA (opal).

89. (d) The two strands of a double helix model of DNA are held together by hydrogen bonds between nitrogenous bases which help to stabilize the interaction. Adenine - thymine pair has two hydrogen bonds while guanine - cytosine pair has three hydrogen bonds.

90. (c) Formation of mRNA from DNA is called as transcription. The segment of DNA involved in transcriptions is cistron, which have a promoter region where initiation is started and terminator region where transcription ends. Enzyme involved in transcription is RNA polymerase-II.

91. (c)

92. (b) Nucleotides have three components - a nitrogenous base, pentose sugar and a phosphate group. The phosphate group of one nucleotide is linked by phosphodiester bonds with the pentose sugar of the other nucleotide.

93. (c) The mRNA formed after transcription of a gene is shorter than the DNA because the intervening sequences called introns are removed through splicing.

94. (b) When a DNA strand with the sequence AACGTAACG is transcribed, the resultant sequence of the mRNA molecule synthesized is UUGCAUUGC. This is based on the paring of nitrogenous bases - adenine pairs with thymine (in DNA) and uracil (in RNA) and guanine with cytosine.

95. (c) Translation is the process of decoding of the messages from mRNA to protein with the help of tRNA, ribosome and enzyme.

96. (c) The process of protein synthesis is catalyzed by ribosomal RNA. Messenger RNA provides the genetic blueprint for the protein. Transfer RNA is responsible for translating the triplet code into a specific amino acid. Messenger RNA molecules are modified prior to protein synthesis by small nuclear RNA.

97. (c) tRNA (or transfer RNA) is a single stranded RNA molecule which brings amino acid and reads the genetic code in the process of transcription. It helps decode a messenger RNA (mRNA) sequence into a protein. It functions at specific sites in the ribosome during translation, which is a process that synthesizes a protein from a mRNA molecule.

98. (b) mRNA carries the coded information for synthesis of one (monocistronic) or more polypeptides (polycistronic). Its codons are recognized by tRNAs.

99. (a) The first mRNA codon to specify an amino acid is always AUG. A DNA strand with the sequence TAC will corresponds to the first amino acid *i.e.*, AUG. On DNA strand A always pairs with T while on RNA strand A always pairs with U.

100. (a) Inducible system includes a repressor protein which is bound to DNA in the absence of any other factor.

101. (c) A low level of *Lac* Z expression is required for conversion of lactose to the inducer, allolactose.

102. (b) Human genome project was launched in the year 1990. It is an international scientific research project having the goal to determine the sequence of base pairs which make up human DNA, and to identify and map all of the genes of the human genome.

103. (d) Many non-human model organisms such as bacteria, *Saccharomyces cerevisiae* (yeast), *Caenorhabditis elegans* (a free living non-pathogenic nematode) *Drosophila* (the fruit fly), plants (*Oryza sativa* and *Ararbidopsis thalliana*), etc. have also been sequences.

104. (d) Minisatellites are inherently unstable and susceptible to mutation at a higher rate than other sequences of DNA. Thus, due to difference in number, location and size of minisatellites on chromosomes, each individual has a unique DNA fingerprint.

105. (d) The technique of DNA fingerprinting was initially developed by Alec Jeffrey's. He used a satellite DNA as probe that shows high degree of polymorphisms. DNA fingerprinting using variable number tandem repeats is based on the observation that VNTR loci are highly polymorphic.

106. (d) On template strand which has 5' $\rightarrow$ 3' orientation, DNA polymerase synthesizes short pairs on new DNA (about 1000 nucleotide long) in 5' $\rightarrow$ 3' direction and then joins these piece together. These small framments are called **okazaki fragments** and new DNA strand made in this discontinuous manner is called **lagging strand**. Okazaki fragments are joined by means of DNA ligase.