CHAPTER
6

Molecular Basis of Inheritance

CASE STUDY / PASSAGE BASED QUESTIONS

1

Read the following and answer any four questions from 1(i) to 1(v) given below:
Deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) are the two types of nucleic acids found in the living systems. DNA acts as the genetic material in most of the organisms. Although RNA also acts as a genetic material in some organisms.

(i) In which of the following organisms, RNA acts as a genetic material?
(a) *Escherichia coli* (b) Qβ Bacteriophage
(c) Tobacco Mosaic viruses (d) Both (b) and (c)

(ii) What is the reason for the additional stability of DNA in comparison to RNA?
(a) Presence of thymine (b) Presence of uracil
(c) Presence of OH group (d) Presence of deoxyribose sugar

(iii) Which of the following criteria a molecule must fulfill to act as a genetic material?
(a) It should be able to generate its replica.
(b) It should be stable chemically and structurally.
(c) It should be able to express itself in the form of Mendelian character.
(d) All of these

(iv) **Assertion :** RNA is liable and easily degradable.
Reason : The 2′–OH group present at every nucleotide in RNA is a reactive group.
(a) Both assertion and reason are true and reason is the correct explanation of assertion.
(b) Both assertion and reason are true but reason is not the correct explanation of assertion.
(c) Assertion is true but reason is false.
(d) Both assertion and reason are false.

(v) Read the given statement and select the option that correctly fill in the blanks.
Pyrimidines present in DNA are _(i)_ and _(ii)_ while pyrimidines present in RNA are _(iii)_ and _(iv)_.
(a) (i)-Adenine, (ii)-Guanine, (iii)-Cytosine, (iv)-Thymine
(b) (i)-Cytosine, (ii)-Thymine, (iii)-Cytosine, (iv)-Uracil
(c) (i)-Cytosine, (ii)-Uracil, (iii)-Adenine, (iv)-Guanine
(d) (i)-Cytosine, (ii)-Uracil, (iii)-Cytosine, (iv)-Thymine

Syllabus
Search for genetic material and DNA as genetic material; Structure of DNA and RNA; DNA packaging; DNA replication; Central Dogma; transcription, genetic code, translation; gene expression and regulation - lac operon; Genome, Human and rice genome projects; DNA fingerprinting.

2

Read the following and answer any four questions from 2(i) to 2(v) given below:

In prokaryotes, DNA is circular and present in the cytoplasm but in eukaryotes, DNA is linear and mainly confined to the nucleus. DNA or deoxyribonucleic acid is a long polymer of nucleotides. In 1953, the first correct double helical structure of DNA was worked out by Watson and Crick. Based on the X-ray diffraction data produced by Maurice Wilkins and Rosalind Franklin. It is composed of three components, *i.e.*, A phosphate group, a deoxyribose sugar and a nitrogenous base. Different forms of DNA are B-DNA, Z-DNA, A-DNA, C-DNA and D-DNA.

(i) Name the linkage present between the nitrogen base and pentose sugar in DNA.

(a) Phosphodiester bond (b) Glycosidic bond (c) Hydrogen bond (d) None of these

(ii) The double helix structure of DNA was proposed by

(a) James Watson and Francis Crick (b) Earwin Chargaff

(c) Federick Griffith (d) Hershey and Chase.

(iii) The double chain of B-DNA is coiled in a helical fashion. The spiral twisting of B-DNA duplex produces

(a) right and left part (b) major and minor grooves

(c) upper and lower sides (d) linear and circular part.

(iv) **Assertion :** The two strands of DNA helix have uniform distance between them.
Reason : A large sized purine always paired opposite to a small sized pyrimidine.

(a) Both assertion and reason are true and reason is the correct explanation of assertion.

(b) Both assertion and reason are true but reason is not the correct explanation of assertion.

(c) Assertion is true but reason is false.

(d) Both assertion and reason are false.

(v) Which of the following describes the structure of B-DNA?

	Polynucleotide chains	**Number of base pairs per complete turn of helix**
(a)	Parallel	5
(b)	Anti-parallel	10
(c)	Parallel	15
(d)	Anti-parallel	20

3

Read the following and answer any four questions from 3(i) to 3(v) given below:

DNA replication is a complex multistep process that requires enzymes, protein factors and metal ions. DNA replication in eukaryotes occurs in the nucleus during the S-phase of the cell cycle. It is semidiscontinuous in eukaryotes. In prokaryotes, replication takes place in the cytoplasm. DNA replication in bacteria occurs prior to fission. Nucleoid or viral chromosome is a single molecule of nucleic acid, it may be linear of circular. Nucleic acid in a virus is either DNA or RNA but never both.

(i) In viral DNA, how many origin of replication are present?

(a) Single (b) Twice (c) Multiple (d) None

(ii) Select the main enzyme involved in DNA replication.

(a) DNA ligase (b) DNA dependent DNA polymerase

(c) Topoisomerase (d) Helicase

(iii) Read the given statement and select the option that correctly fill in the blanks.

Enzyme __(i)__ acts over the *Ori* site and unwinds the two strands of DNA by destroying __(ii)__ bonds.

(a) (i)-Helicase, (ii) Glycosidic (b) (i)-Helicase, (ii)-Hydrogen

(c) (i)-Unwindase, (ii)-Phosphodiester (d) (i)-Unwindase, (ii)-Glycosidic

(iv) DNA strand, built up of Okazaki fragments is called

(a) lagging strand (b) leading strand

(c) complementary strand (d) parental strand.

(v) Select the incorrect statement about DNA polymerase in eukaryotes.

(a) Polymerase α is required for initiation of replication.

(b) When the RNA primer gets removed the gap is filled by DNA polymerase β in eukaryotes.

(c) Polymerase ε helps in elongation of lagging strand.

(d) Polymerase δ is largest and main enzyme for DNA replication in eukaryotes.

4

Read the following and answer any four questions from 4(i) to 4(v) given below:

The process of copying genetic information from template strand of DNA into RNA is called transcription. It is mediated by RNA polymerase. Transcription takes place in the nucleus of eukaryotic cells. In transcription, only a segment of DNA and only one of the strands is copied into RNA.

(i) What are regions of transcription unit in a DNA molecule?

(a) Promoter (b) Structural gene (c) Terminator (d) All of these

(ii) Monocistronic structural genes are found in which organisms?

(a) Prokaryotes (b) Bacteria (c) Viruses (d) Eukaryotes

(iii) Which enzyme helps in tailing or polyadenylation?

(a) Poly-A polymerase (b) Exonucleases (c) RNA polymerase I (d) RNA polymerase II

(iv) **Assertion :** A single RNA polymerase in prokaryotes synthesis all types of RNAs.

Reason : Prokaryotic RNA polymerase has sigma (σ) factor.

(a) Both assertion and reason are true and reason is the correct explanation of assertion.

(b) Both assertion and reason are true but reason is not the correct explanation of assertion.

(c) Assertion is true but reason is false.

(d) Both assertion and reason are false.

(v) Read the given list of materials.

1. RNA polymerase enzyme
2. DNA template
3. RNA primers
4. Okazaki segments
5. Four types of ribonucleotides triphosphates
6. Divalent metal ions Mg^{2+} as a cofactor.

Which of the above given materials are required for transcription?

(a) (1), (2), (3) and (4) (b) (1), (2), (3), (5) and (6)

(c) (1), (2), (5) and (6) (d) All of these

5

Read the following and answer any four questions from 5(i) to 5(v) given below:

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 bases in the *m*RNA. The amino acids are joined by a bond called peptide bond. Ribosome is the site of protein synthesis.

(i) Which ion is essential for association of both units of ribosome at the time of protein formation?

(a) Mg^{2+} (b) Mn^{2+} (c) Cl^{-} (d) Ca^{2+}

(ii) During translation, how many initiation factors are required in eukaryotes for initiation reactions?

(a) 3 (b) 6 (c) 7 (d) 9

(iii) Which part of *m*RNA contains untranslated regions (UTR)?

(a) 3′ end
(b) 5′ end
(c) Either 3′ or 5′ end
(d) Both 5′ end and 3′ end

(iv) Name the enzyme that helps in combining amino acid to its particular *t*RNA.

(a) Activating enzyme
(b) Amino-acyl *t*RNA-synthetase
(c) Peptidyl transferase
(d) Both (a) and (b)

(v) From the given list, select the translation machinery.

1. *m*RNA
2. Ribosomes
3. Amino acids
4. *t*RNAs
5. Peptidyl transferase
6. Amino acyl *t*RNA synthetase
7. Pyrophosphatase

(a) (1), (2), (3), (4) and (6)
(b) (1), (2), (3), (4) and (5)
(c) (1), (2), (3), (4), (5) and (6)
(d) (1), (2), (3), (4), (5), (6) and (7)

6

Read the following and answer any four questions from 6(i) to 6(v) given below:

The process of translation requires transfer of genetic information from a polymer of nucleotides to synthesise a polymer of amino acids. The relationship between the sequence of amino acids in a polypeptide and nucleotide sequence of DNA or *m*RNA is called genetic code. George Gamow suggested that in order to code for all the 20 amino acids, code should be made up of three nucleotides.

(i) What is a codon?

(a) A length of DNA which codes for a particular protein.
(b) A part of the *t*RNA molecule to which a specific amino acid is attached.
(c) A part of the *t*RNA molecule which recognises the triplet code on the messenger RNA.
(d) A part of the messenger RNA molecule that has a sequence of bases coding for an amino acid.

(ii) Three consecutive bases in the DNA molecule provide the code for each amino acid in a protein molecule. What is the maximum number of different triplets that could occurs?

(a) 16 (b) 20 (c) 24 (d) 64

(iii) Listed below are some amino acids and their corresponding *m*RNA triplets.

Amino acid	*m*RNA triplet
Phenylalanine	UUU
Lysine	AAG
Arginine	CGA
Alanine	GCA

Which DNA sequence would be needed to produce the following polypeptide sequence?

Alanine-Arginine-Lysine-Phenylalanine

(a) CGT GCT TTC AAA
(b) CGT GCT TTC TTT
(c) CGU GCU UUC AAA
(d) CGU GCU UUC TTT

(iv) Identify the non-sense codons among the following.

(a) AUG (b) GUG (c) UAA (d) UGG

(v) A polypeptide is made using synthetic *m*RNA molecules as shown.

Synthetic *m*RNA used	Polypeptide produced
UUUAAAUUUAAA	Phenylalanine-lysine-phenylalanine-lysine

What are the DNA codes for the amino acids phenylalanine and lysine?

	Phenylalanine	**Lysine**
(a)	AAA	TTT
(b)	AAA	UUU
(c)	GGG	CCC
(d)	TTT	GGG

7

Read the following and answer any four questions from 7(i) to 7(v) given below:

Mutation explains the relationship between gene and DNA. The effects of large deletions and rearrangement in a segment of DNA results in loss or gain of gene and its function. Insertion or deletion of one or two bases changes the reading frame from the point of insertion or deletion. A classical example of point mutation is a change of single base pair in the gene for beta globin chain that results in change of amino acid residue glutamate to valine and results into a diseased condition called sickle cell anaemia.

(i) A mutation is a change produced by an alteration in the genetic mechanism and

(a) may arise spontaneously (b) is always induced by the environment
(c) is never advantageous (d) is not inherited.

(ii) The DNA code for glutamic acid is CTC or CTT. The code for valine is CAA or CAT. In sickle cell haemoglobin, valine is present instead of glutamic acid.
Assuming a single base pair substitution has occurred, what is the *m*RNA code in the affected mutant?

(a) CUU (b) GAA (c) GAG (d) GUA

(iii) A mutation involving the substitution of one nitrogenous base for another has altered the base sequence of a DNA molecule, coding for four amino acids, as shown below.

Normal A-G-C-A-T-G-G-A-T-C-C-T

Mutant A-G-C-A-T-G-C-A-T-C-C-T

The table shows six codons and the corresponding amino acids into which each is translated.

mRNA codon	Amino acid
AAG	Lysine
CUA	Leucine
GGA	Glycine
GUA	Valine
UAC	Tyrosine
UCG	Serine

The mutation has changed the amino acid

(a) leucine to valine
(b) lysine to glycine
(c) serine to leucine
(d) tyrosine to lysine.

(iv) **Assertion :** Insertion or deletion of three or its multiple bases, insert or delete one or multiple codons and so one or multiple amino acids.

Reason : Reading frame remains unaltered with insertion or deletion of three or its multiple bases.

(a) Both assertion and reason are true and reason is the correct explanation of assertion.
(b) Both assertion and reason are true but reason is not the correct explanation of assertion.
(c) Assertion is true but reason is false.
(d) Both assertion and reason are false.

(v) Part of the amino acid sequences in normal and sickle cell haemoglobin are shown.

Normal haemoglobin	Sickle cell haemoglobin
Thr-Pro-Glu-Glu	Thr-Pro-Val-Glu

*m*RNA codons for these amino acids are

Glutamine (Glu)	GAA	GAG
Proline (Pro)	CCU	CCC
Threonine (Thr)	ACU	ACC
Valine (Val)	GUA	GUG

Which transfer RNA molecule is involved in the formation of this part of the sickle cell haemoglobin?

(a) 

(b) 

(c) 

(d) 

8

Read the following and answer any four questions from 8(i) to 8(v) given below:

Gene regulation is the mechanism of switching off and switching on of the genes depending upon the requirement of cells and the state of development. Gene regulation is of two types : negative and positive. In negative gene

regulation the genes continue expressing their effect till their activity is suppressed. Positive gene regulation is the one in which the genes remain non-expressed unless and until they are induced to do it.
Operon model is a co-ordinated group of genes such as structural gene, operator gene, promoter gene, regulator gene which function together and regulate a metabolic pathway as a unit, *e.g.*, *lac* operon, *trp* operon, *ara* operon, etc.

(i) Regulation of gene expression occurs at the level of
(a) transcription (b) processing/splicing (c) translation (d) all of these.

(ii) Inducible operon system usually occurs in A pathways. Nutrient molecules serve as B to stimulate production of the enzymes necessary for their breakdown. Genes for inducible operon are usually switched C and the repressor is synthesised in an D form.

	A	B	C	D
(a)	anabolic	corepressor	on	inactive
(b)	anabolic	inducer	off	active
(c)	catabolic	inducer	off	active
(d)	catabolic	corepressor	on	inactive

(iii) An *m*RNA molecule transcribed from the *lac* operon contains nucleotide sequences complementary to
(a) structural genes coding for the enzymes (b) the operator region
(c) the promotor region (d) the repressor gene.

(iv) Which statement correctly describes the control of transcription of the genes involved in the breakdown of lactose in *Escherichia coli*?
(a) A repressor protein binds to the operator and the genes are switched on.
(b) A repressor protein binds to the operator and the genes are switched off.
(c) A transcription factor binds to the promoter and the genes are switched on.
(d) A transcription factor binds to the promoter and the genes are switched off.

(v) Function of catabolic activator protein in lac operon is
(a) to form *m*RNA (b) help to bind RNA polymerase
(c) code for repressor (d) to activates *lac* gene when glucose is absent.

9

Read the following and answer any four questions from 9(i) to 9(v) given below:
DNA fingerprinting is a technique of determining nucleotide sequences of certain areas of DNA which are unique to each individual. Each person has a unique DNA fingerprint. Each fingerprint is the same for every cell, tissue and organ of a person. DNA fingerprinting is the basis of paternity testing in case of disputes.

(i) The technique developed to identify a person with the help of DNA restriction analysis is known as
(a) DNA profiling (b) DNA fingerprinting (c) RFLP (d) both (a) and (b).

(ii) For DNA fingerprinting, DNA is obtained from
(a) blood (b) hair root cells (c) semen (d) all of these.

(iii) During DNA fingerprinting, the radioactive probes
(a) hybridise with DNA sample to form double stranded structure
(b) degrade the DNA
(c) create positive charge on DNA
(d) cut the DNA sample at various sites.

(iv) In India, DNA fingerprinting technique was developed by

(a) Dr. Lalji Singh (b) Alec Jeffreys (c) Dr. Khorana (d) none of these.

(v) Which of the following is true about DNA fingerprinting?

(a) VNTR is used as probe.

(b) DNA samples are loaded on agarose gel electrophoresis.

(c) It is based on identification of nucleotide sequence present on the DNA molecule.

(d) All of these

10

Read the following and answer any four questions from 10(i) to 10(v) given below:

RNA or ribonucleic acid is a single chain polyribonucleotide which functions as carrier of coded genetic or hereditary information from DNA to cytoplasm for taking part in protein and enzyme synthesis. Six types of RNAs are ribosomal, transfer, messenger, genomic, small nuclear and small cytoplasmic RNA. Out of these, *r*RNA, *m*RNA and *t*RNA are major classes of RNAs that are involved in gene expression.

(i) Which one is referred to a soluble RNA?

(a) *m*RNA (b) *t*RNA (c) *r*RNA (d) hnRNA

(ii) The RNA that picks up specific amino acid from amino acid pool in the cytoplasm to ribosome during protein synthesis is

(a) *r*RNA (b) hnRNA (c) *m*RNA (d) *t*RNA.

(iii) Which of the following is found in both DNA and messenger RNA?

(a) Double helix structure (b) Ribose

(c) Sugar-phosphate chain (d) Thymine

(iv) Which of the following statements regarding RNA is correct?

(a) Messenger RNAs carries coded information for synthesis of polypeptide.

(b) Ribosomal RNAs bind with *t*RNA to catalyse the formation of phosphodiester bonds.

(c) Genomic RNA is always single stranded.

(d) Synthesis of *r*RNA occurs in cytoplasm by RNA polymerase III.

(v) In studying a virus, you find the following proportions of nitrogenous bases present : adenine 23%, guanine 37%, cytosine 23% uracil 17%. Which of the following statement(s) regarding this virus is/are correct?

I. It probably uses RNA as its genetic material.

II. The genetic material of this virus is probably single stranded.

III. Base pairing rules in virus in this virus include adenine : cytosine.

(a) I only (b) I and II only (c) II and III only (d) All of these.

ASSERTION & REASON

For question numbers 11-30, two statements are given-one labelled Assertion and the other labelled Reason. Select the correct answer to these questions from the codes (a), (b), (c) and (d) as given below.

(a) Both assertion and reason are true and reason is the correct explanation of assertion.

(b) Both assertion and reason are true but reason is not the correct explanation of assertion.

(c) Assertion is true but reason is false.

(d) Both assertion and reason are false.

11. **Assertion :** The uptake of DNA during transformation is an active, energy requiring process.
Reason : Transformation occurs in only those bacteria, which possess the enzymatic machinery involved in the active uptake and recombination.

12. **Assertion :** R-type of *Pneumococcus* is non-virulent.
Reason : R-type of *Pneumococcus* can be virulent by having transformation with S - type of *Pneumococcus*.

13. **Assertion :** Adenine and guanine are double - ring bases.
Reason : Adenine and guanine are pyrimidines.

14. **Assertion :** B-DNA has a constant diameter of 20 Å.
Reason : A pyrimidine always pairs with a purine.

15. **Assertion :** Sequences of bases in one polynucleotide chain of DNA can determine the sequence of bases in the other chain.
Reason : In a DNA, amount of adenine equals that of thymine and amount of guanine equals that of cytosine, *i.e.,* A = T and C = G.

16. **Assertion :** Z-DNA follows a zig-zag course.
Reason : Z-DNA is left handed.

17. **Assertion :** The concept of one gene-one enzyme was changed to one gene-one polypeptide.
Reason : Each enzyme may consist of two or more different polypeptides.

18. **Assertion :** Core enzyme catalyses chain elongation of RNA.
Reason : The presence of sigma factor is required for initiation of transcription.

19. **Assertion :** *t*RNA acts as an adapter molecule.
Reason : *t*RNA recognizes codon sequence of *m*RNA during translation.

20. **Assertion :** The genetic code is degenerate.
Reason : For a particular amino acid more than one codons can be used.

21. **Assertion :** Same *t*RNA can recognise more than one codons differing only at the third position.
Reason : The specificity of a codon is particularly determined by the first two bases.

22. **Assertion :** The subunits of ribosomes come together only at the time of protein formation.
Reason : Mg^{2+} causes their association or dissociation.

23. **Assertion :** Initiation step of protein synthesis in prokaryotes and eukaryotes has several differences.
Reason : They both form *m*RNA - *t*RNA complex with smaller subunit of ribosome.

24. **Assertion :** UAA, UAG and UGA terminate protein synthesis.
Reason : They are not recognised by *t*RNA.

25. **Assertion :** Ribosomes attached to endoplasmic reticulum release proteins into lumen of ER.
Reason : Such proteins are used for formation of hydrolytic enzymes or are modified.

26. **Assertion :** Constitutive genes are continuously being expressed.
Reason : Constitutive genes are frequently needed for various metabolic functions.

27. **Assertion :** Synthesis of tryptophan is self regulatory.
Reason : Tryptophan works both as co-repressor and through feedback inhibition.

28. **Assertion :** No *lac* *m*RNA is made in the presence of glucose.
Reason : In the presence of glucose and lactose activity of *lac* operon is not needed.

29. **Assertion :** Lactose in *lac* operon is promoter gene.
Reason : Lactose inactivates the repressor gene.

30. **Assertion :** Regulator and operator genes are not associated with constitutive genes.
Reason : Constitutive genes need not be repressed.

1. **(i) (d):** DNA is the genetic material in *E. coli*. RNA is the genetic material in Tobacco Mosaic virus and Qβ bacteriophage.

(ii) (a): The presence of thymine in DNA at the place of uracil which is present in RNA provides additional stability to DNA.

(iii) (d)

(iv) (a)

(v) (b): Purines present in DNA and RNA are adenine and guanine, while pyrimidines present in DNA are cytosine and thymine and pyrimidines present in RNA are cytosine and uracil.

2. **(i) (b):** In DNA the nitrogenous base and a pentose sugar joins to form nucleoside with the help of bond called glycosidic bond or N-glycosidic linkage.

(ii) (a): The correct structure of DNA was first worked out by James Watson and Francis Crick in 1953. Their double-helix model of DNA structure was based on two major investigations, *i.e.*, Chargaff's rules of base pairing and study of X-ray diffraction pattern of DNA produced by Maurice Wilkins and Rosalind Franklin which helped Watson and Crick to design the 3-dimensional structure of DNA.

(iii) (b): Due to spiral twisting, the B-DNA duplex comes to have two types of alternate grooves, *i.e.*, major (length 22 Å) and minor (length 12 Å).

(iv) (a)

(v) (b): The double helical chains of B-DNA are bound to each other *via* hydrogen bonds in an antiparallel fashion, *i.e.*, 5′-3′ in one and 3′-5′ in other. The pitch of helix per turn is 3.4 nm with 10 base pairs in each turn.

3. **(i) (a):** Replication begins at a particular spot called origin of replication or *ori*. Bacterial and viral DNA has a single origin of replication. It functions as a single replicating unit or replicon.

(ii) (b): A large number of enzymes are required for DNA replication. DNA-dependent DNA polymerase is the main enzyme which takes part in combining deoxyribose nucleotides to form new DNA strands.

(iii) (b)

(iv) (a): Lagging strand is a replicated strand of DNA which is formed in short segments called Okazaki fragments. Its growth is discontinuous.

(v) (d): DNA Polymerase α is the largest and main enzyme for replication in eukaryotes.

4. **(i) (d)**

(ii) (d): Monocistronic structural gene carries information for synthesis of one polypeptide chain. They are mostly found in eukaryotes.

(iii) (a): Tailing or polyadenylation is addition of a poly-A tail at 3′ end of hn *m*RNA with the help of poly-A polymerase. The poly-A tail contains adenate residues (about 200-300 residues). Polyadenylation is thought to protect the 3′ end from degradation by exonucleases.

(iv) (b)

(v) (c): RNA primer and Okazaki segments are not needed in transcription.

5. **(i) (a):** The two subunits of ribosomes come together at the time of protein formation. This phenomenon is called association. Mg^{2+} is essential for it.

(ii) (d): Eukaryotes have nine initiation factors- elf2, elf3, elf1, elf4A, elf4B, elf4C, elf4D, elf5,elf6.

(iii) (d): An *m*RNA molecule has some additional sequences that are not translated and are called untranslated regions (UTR). The UTRs are present at both 5′ end (before start codon) and at 3′-end (after stop codon). They are required for efficient translation process.

(iv) (d): Amino-acyl *t*RNA-synthetase is also called aa-activating enzyme.

(v) (a): Enzyme peptidyl transferase is component of larger subunit of ribosome. It catalyses two principal chemical reaction - peptide bond formation and peptide release. Enzyme pyrophosphatase hydrolyses pyrophosphate and provides energy for driving the initial reaction of activating amino acids.

6. **(i) (d):** Codon is complementary to a triplet of templet strand. It is found in *m*RNA. Anticodon is complementary to a codon it occurs in *t*RNA.

(ii) (d) : The triplet code consists of three of the four nucleotide bases - A, C, G or T. Thus the maximum number of codon is $4^3 = 64$.

(iii) (b): The complementary bases of GCA-CGA-AAG-UUU are CGT-GCT-TTC-AAA on the DNA strand.

(iv) (c): AUG and GUG are initiation codon which codes for methionine and valine respectively. UGG codes for tryptophan. UAA (ochre) is a termination codon.

(v) (a): The triplet codon of phenylalanine (UUU) will base pair with AAA in the DNA molecule and that of lysine (AAA) will base pair with TTT.

7. (i) (a): A mutation is a change in the DNA that changes the physiological effect of the DNA on the cell. Such phenomenon may be caused by radiation, chemical carcinogens or may occur spontaneously.

(ii) (d): Since a single base pair substitution has caused this mutation, the original codon for glutamic acid must have been CTT, and the mutant codon is CAT. The *m*RNA code for this mutant is hence GUA, *i.e.*, complementary to CAT.

(iii) (a): The segment coding for GAT on the normal DNA molecule has been transcribed into CUA in the *m*RNA molecule, therefore the mutant DNA strand CAT will be transcribed into GUA on the *m*RNA molecule. This implies a change from the amino acid leucine to valine.

(iv) (b)

(v) (b): CAU in *t*RNA is the only one that can compliment the valine in the sickle cell haemoglobin.

8. (i) (d) : Regulation of gene expression can be exerted at four levels : transcriptional level during formation of primary transcript, processing like splicing, terminal additions or modifications, transport of *m*RNAs from nucleus to the cytoplasm and translational level.

(ii) (c)

(iii) (a): Only the structural genes of an operon are transcribed into *m*RNA molecule. Structural gene is a region of DNA that codes for a protein or RNA molecule that forms part of a structure or has an enzymatic function. In the case of *lac* operon, the structural genes are *lac Z*, *lac Y*, *lac A* which codes for β-galactosidase, lac permease and β-galactoside transacetylase respectively.

(iv) (b): The lac operon consists of :
Promoter : binding site of RNA polymerase
Operator : binding site of the lac repressor protein
CAP Binding Site : binding site of catabolite activator protein.
3 structural genes : *lac Z*, *lac Y* and *lac A*.
When lac repressor protein is synthesised in its active conformation, it binds to the operator and the operon is switched off, so there is no transcription.

(v) (d)

9. (i) (d)

(ii) (d): For DNA fingerprinting, DNA is obtained from blood, semen, hair roots, tissue samples, nuclei of white blood cells or of spermatozoa, body secretions, etc.

(iii) (a): In DNA fingerprinting, during hybridisation the bands are flooded with single stranded radioactive DNA probe. This single stranded DNA probe and sample DNA hybridise to form double stranded structure due to natural affinity.

(iv) (a): In India, DNA fingerprinting technique was developed by Dr. Lalji Singh.

(v) (d)

10. (i) (b): *t*RNA is also referred to as soluble RNA (*s*RNA) because it cannot be easily separated even by ultra centrifugation technique.

(ii) (d) : *t*RNA carries specific type of amino acid at CCA end to the ribosome during protein synthesis. It places the required amino acid properly in the sequence and translates the coded message of *m*RNA in terms of amino acids.

(iii) (c): The double helix structure is only found in DNA. Ribose is only found in *m*RNA, DNA has deoxyribose sugar instead. Thymine is found only in DNA, uracil replaces thymine in *m*RNA. Only the sugar-phosphate backbone is found common in both.

(iv) (a): Ribosomal RNA is made in the nucleus. Ribosomal RNA binds with proteins to form large and small ribosomal subunits which combine to form ribosomes in the cytoplasm. Genomic RNA may be single stranded or double stranded. It is fragmented in influenza virus. Synthesis of *r*RNA occur in nucleolus.

(v) (b): Uracil is present in this virus. So, RNA is the genetic material. The genetic material is not double stranded as the percentage of guanine and cytosine are not equal. Bases do not pair in single stranded viruses.

11. (b): Transformation does not involve passive entry of DNA molecules through permeable cell walls and membranes. It does not occur 'naturally' in all

species of bacteria, only in those species possessing the enzymatic machinery involved in the active uptake and recombination processes. Even in these species, all cells in a given population are not capable of active uptake of DNA. Only competent cells, which possess a so - called competence factor are capable of serving as recipients in transformation.

12. **(b):** Transformation is the change in the genetic constitution of an organism by picking up genes present in the environment. *Pneumococcus* has two strains - virulent (*S*) and non-virulent (*R*). The virulent strain causes pneumonia. *R*-type bacteria form irregular or rough colonies and did not produce any disease while the *S*-type bacteria cause pneumonia and then death in the mice. Griffith injected a combination of live *R*-type and heat killed *S*-type bacteria into mice. While some mice survived, others developed the disease of pneumonia and died. Autopsy of the dead mice showed that they possessed both the types of bacteria in living state though the mice had been injected with dead virulent and living non-virulent bacteria. The occurrence of living *S*-type virulent bacteria is possible only by their formation from *R*-type non-virulent bacteria which pick up the trait of virulence from dead bacteria. The phenomenon is called transformation.

13. **(c):** The bases of nucleic acids are of two types (*i*) pyrimidines and (*ii*) purines. Adenine and guanine are double-ring bases called purines; cytosine, thymine and uracil are single - ring bases called pyrimidines.

14. **(a):** B-DNA is a helical structure with diameter of 20 Å. If pairing occurs between two purines, it would need too much space and if pairing occurs between two pyrimidines, it would occupy too little space. The constancy of DNA diameter is maintained only when a pyrimidine always pairs with a purine.

15. **(b):** Although A = T and C = G, there is no any restriction or sequence of bases in one polynucleotide chain. Since A is always linked to T and C to G as determined from the above evidences, sequence of bases in one of polynucleotide should determine the sequence of bases in the other polynucleotide of the double helix.

16. **(b):** Z-DNA is left-handed double helix with zig-zag back - bone, alternate purine and pyrimidine bases, single turn of 45 Å length with 12 base pairs and a single groove. Due to a different arrangement of molecules within Z - DNA polymer, phosphate backbone follows a zig-zag course, while in B - DNA it is regular. In Z - DNA, sugar residues have alternating orientation so that the repeating unit is a dinucleotide.

17. **(a):** In 1948, Beadle and Tatum proposed that a gene controls the synthesis of one enzyme. But, many enzymes as well as the haemoglobins were shown to consist of two or more different polypeptide chains and each polypeptide was found to be the product of a separate gene. Tryptophan synthetase of *E. coli*, for example, contains an α - polypeptide, the product of the *trp A* gene and a β - polypeptide, the product of the β gene. It was necessary, therefore, to change the concept of one gene-one enzyme to one gene-one polypeptide.

18. **(b):** The "core' enzyme which catalyses covalent chain extension, consists of two α - polypeptides (each of molecular weight about 41,000), one β - polypeptide (molecular weight about 155,000) one β'-polypeptide (molecular weight about 165,000) and one ω-polypeptide (molecular weight about 12,000). The "holoenzyme" contains in addition, α -polypeptide (molecular weight about 95,000). The presence of the sigma factor is required for initiation at the proper transcription initiation (or promoter) sites. After each RNA chain - initiation event, sigma is released and the core enzyme catalyses chain elongation.

19. **(b):** *t*-RNA is an adaptor molecule because it adapts amino acid to bring it to protein synthesis site in activated form and not because it recognises the codon on *m*RNA.

20. **(a):** For a particular amino acid, more than one codons can be used. This phenomenon is described by saying that the code is degenerate. A non - degenerate code would be one where there is one to one relationship between amino acids and the codons, so that 44 codons out of 64, will be useless or nonsense codons. However, there are no nonsense codons. The codons which were earlier called nonsense codons are also known to mean stop signals.

21. **(a):** It has been shown, for instance that the same *t*RNA can recognise more than one codons differing only at the third position. This pairing is not very stable and is allowed due to wobbling in base pairing at this third position. This kind of wobbling allows economy of the number of *t*RNA molecules, since several codons meant for same amino acid are recognised by same *t*RNA. For instance, anticodon CGC can recognise codons GCU, GCC and GCA.

22. **(b):** During protein synthesis, two subunits of ribosomes associate. Mg^{2+} is essential for it. Soon after the completion of protein synthesis, the subunits separate. The phenomenon is called dissociation.

23. **(b):** The differences between initiation step of protein synthesis in eukaryotes and prokaryotes are :
(*i*) In prokaryotes initiation factors are three - IF1, IF2 and IF3. Eukaryotes have at least ten initiation factors - eIF1, eIF2, eIF3, eIF4A, eIF4B, eIF4C, eIF4D, eIF4F, eIF5 and eIF6.
(*ii*) In eukaryotes, formylation of methionine does not take place. In prokaryotes *t*RNA is charged with formylated methionine.
(*iii*) The larger subunit of ribosome combines with 40 S - *m*RNA–*t*RNAMet (in case of prokaryotes, 30 S) complex to form intact ribosome. It requires initiation factor IF1 in prokaryotes and factors eIF1, eIF4 (A, B, C) in eukaryotes.

24. **(a):** Synthesis of polypeptide terminates when a nonsense codon of *m*RNA reaches the *A* - site. There are three nonsense codons - UAA, UAG and UGA. These codons are not recognised by any of the *t*RNAs. Therefore, no more aminoacyl *t*RNA reaches the *A* - site. The *P* - site *t*RNA is hydrolysed and the completed polypeptide is released in the presence of release factor. Thus termination occurs.

25. **(b):** Polyribosomes attached to membranes of endoplasmic reticulum produce proteins which either pass into their lumen or become integrated into the membranes. The proteins released into the lumen generally reach Golgi apparatus for modifications like formation of hydrolytic enzymes and glycosylation (addition of sugar residues). The modified proteins are packed in vesicles for export or formation of lysosomes, cell wall enzymes, plasma membrane, etc.

26. **(a):** Certain gene-products, such as *t*RNA molecules, *r*RNA molecules, ribosomal proteins, RNA polymerase components (polypeptides) and other enzymes catalysing metabolic processes that are frequently referred to as cellular "housekeeping" functions, are essential components of almost all living cells. Genes that specify products of this type are continually being expressed in most cells. Such genes are said to be expressed constitutively and are frequently referred to as constitutive genes.

27. **(a):** Tryptophan regulates its own active synthesis by regulating the expression of its gene *via* feedback mechanism and also by acting as co-repressor which attaches with repressor proteins produced by regulator gene and blocking the promotor gene site thus blocking *m*-RNA synthesis and further steps.
It is thus obvious that the synthesis of tryptophan is self regulatory, since it, when present in plenty, work firstly by feedback inhibition, and secondly through co-repression to stop further synthesis of tryptophan.

28. **(a):** The function of β-galactosidase enzyme in lactose metabolism is to form glucose by cleaving lactose. Thus if both glucose and lactose are present in the growth medium, activity of *lac* operon is not needed, and indeed, no β-galactosidase is formed until virtually all of the glucose in the culture medium is consumed. The lack of synthesis of β-galactosidase is a result of lack of synthesis of *lac* *m*RNA. No *lac* *m*RNA is made in the presence of glucose, because in addition of an inducer to inactivate the *lac i* repressor, another element (*c*AMP-CAP) is needed for initiating *lac* *m*RNA synthesis, the activity of this element is regulated by the concentration of glucose. However, the inhibitory effect of glucose on expression of lac operon is quite indirect.

29. **(d):** Lactose is not a promotor gene but an inducer of *lac* operon as it combines with repressor protein formed by repressor or regulatory gene and not the gene itself. The inducer joins the repressor, forming a repressor-inducer complex. This complex prevents the repressor from binding with the operator gene of the operon. This frees the operator gene so that the RNA polymerase can move from the promoter to the structural genes.
The structural genes are then transcribed, forming a piece of polycistronic *m*RNA. The latter is transcribed by *t*RNA and ribosomes into enzymes.

30. **(a):** Regulator gene controls the operator gene in cooperation with a chemical compound called inducer present in the cytoplasm. The regulation gene codes for and produce a protein substance called repressor. The repressor substance combines with the operator gene to repress its function. Therefore it is called regulator gene.
The constitutive genes keep on functioning all the time. They need not be repressed. Therefore, the regulator and operator genes are not associated with them.