

28

Molecular Basis of Inheritance

TOPIC 1

The Genetic Material- DNA and RNA

01 Which one of the following statements about histones is wrong? [NEET 2021]

- (a) Histones are organised to form a unit of 8 molecules.
- (b) The pH of histones is slightly acidic
- (c) Histones are rich in amino acids lysine and arginine
- (d) Histones carry positive charge in the side chain

Ans. (b)

Statement in option (a), (c) and (d) are correct. Histone proteins are composed of basic amino acid. These proteins attach to the DNA to form the nucleosome. Histones are organised to form a unit of eight molecules called as histone octamer.

Histones are rich in basic amino acid residues lysine and arginine. It carries positive charges in their side chains and negatively charge DNA wrap around it. Statement in option (b) is incorrect and can be corrected as

The pH of histones is slightly basic.

02 Which is the "only enzyme" that has "capability" to catalyse initiation, elongation and termination in the process of transcription in prokaryotes? [NEET 2021]

- (a) DNA-dependent DNA polymerase
- (b) DNA-dependent RNA polymerase
- (c) DNA ligase
- (d) DNase

Ans. (b)

Prokaryotes utilize one RNA polymerase for transcription of all types of RNA. The enzyme RNA polymerase is needed for RNA formation from DNA, i.e. DNA dependent RNA polymerase. It occurs in the cytoplasm of prokaryotic cells. RNA polymerase is the only enzyme which, has the capability to catalyse all initiation, elongation and termination in prokaryotes.

03 Which of the following RNAs is not required for the synthesis of protein? [NEET 2021]

- (a) mRNA
- (b) tRNA
- (c) rRNA
- (d) siRNA

Ans. (d)

siRNA mainly protect the cell from exogenous mRNA attacks. It degrades the growing mRNA and stop gene expression. It is highly specific and reduces the synthesis of particular proteins by reducing the translation of specific messenger RNAs. Hence, siRNA is not required for protein synthesis but is used to reduce its synthesis. Whereas rRNA, mRNA and tRNA are required for synthesis of protein.

04 If adenine makes 30% of the DNA molecule, what will be the percentage of thymine, guanine and cytosine in it? [NEET 2021]

- (a) T : 20, G : 30, C : 20
- (b) T : 20, G : 20, C : 30
- (c) T : 30, G : 20, C : 20
- (d) T : 20, G : 25, C : 25

Ans. (c)

Chargaff rule - In DNA there is always equality in quantity between the bases A and T and between the bases G and C.

According to Chargaff rule

$$(A)+(G)+(C)+(T)=100\%$$

A=30% therefore T is also 30%

Therefore G+C = 100% - 60% = 40%

Hence, G = 20% and C = 20%

05 Complete the flow chart on central dogma [NEET 2021]

- (a) (a)-Replication; (b)-Transcription; (c)-Transduction; (d)-Protein
- (b) (a)-Translation; (b)-Replication; (c)-Transcription; (d)-Transduction
- (c) (a)-Replication; (b)-Transcription; (c)-Translation (d)-Protein
- (d) (a)-Transduction; (b)-Translation (c)-Replication; (d)-Protein

Ans. (c)

Central dogma of molecular biology was proposed by Francis Crick which states that the genetic information flows from DNA → RNA → Protein.

Here, a, b, c and d are

a-Replication, b-Transcription, c-Translation, d-Protein

06 *E. coli* has only 4.6×10^6 base pairs and completes the process of replication within 18 minutes, then the average rate of polymerisation is approximately [NEET (Oct.) 2020]

- (a) 2000 bp/s
- (b) 3000 bp/s
- (c) 4000 bp/s
- (d) 1000 bp/s

Ans. (c)

E. coli has 4.6×10^6 base pairs.

It completes replication process in 18 minutes i.e. 18×60 seconds.

$$\begin{aligned} \text{Rate of polymerisation} &= \frac{4.6 \times 10^6 \text{ bp}}{18 \times 60 \text{ s}} \\ &= \frac{4.6 \times 10^5}{18 \times 6} = \frac{46 \times 10^4}{108} \\ &= \frac{460000}{108} = 42591 \text{ bp/s} \end{aligned}$$

or approximately 4000 bp/sec
Thus, the correct option is (c).

07 Name the enzyme that facilitates opening of DNA helix during transcription. [NEET (Sep.) 2020]

- (a) DNA helicase
- (b) DNA polymerase
- (c) RNA polymerase
- (d) DNA ligase

Ans. (c)

The correct option is (c) because RNA polymerase facilitates opening of DNA helix during transcription. RNA polymerase is the main transcription enzyme. Transcription begins when RNA polymerase binds to a promoter sequence near the beginning of a gene. DNA helicases function in other cellular processes where double-stranded DNA must be separated, including DNA repair and transcription.

DNA ligase helps in joining breaks in the phosphodiester backbone of DNA that occur during replication. DNA polymerase does not function during transcription.

08 Who coined the term 'Kinetin'? [NEET (Oct.) 2020]

- (a) Skoog and Miller
- (b) Darwin
- (c) Went
- (d) Kurosawa

Ans. (a)

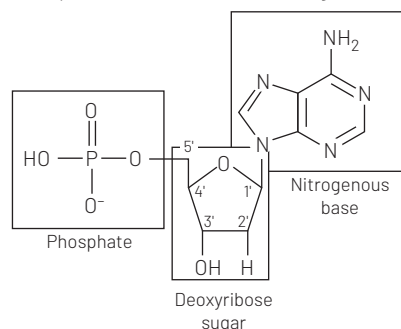
The term kinetin was coined by Skoog and Miller in 1955. Chemically kinetin is 6-furfuryl aminopurine. It was the first cytokinin to be discovered from the degraded auto claved herring sperm DNA. Kinetin does not occur naturally.

09 In the polynucleotide chain of DNA, a nitrogenous base is linked to the -OH of [NEET (Oct.) 2020]

- (a) 2' C pentose sugar
- (b) 3' C pentose sugar
- (c) 5' C pentose sugar
- (d) 1' C pentose sugar

Ans. (d)

In a DNA polynucleotide chain, a nitrogenous base is linked to the hydroxy (-OH) of 1' C pentose sugar. It is represented in the structure given below



10 The term 'Nuclein' for the genetic material was used by [NEET (Oct.) 2020]

- (a) Franklin
- (b) Meischer
- (c) Chargaff
- (d) Mendel

Ans. (b)

The nucleic acid was first reported by Friedrich Miescher in 1869 from the nuclei of pus cells and was named nuclein.

11 Which of the following statements is correct? [NEET (Sep.) 2020]

- (a) Adenine pairs with thymine through one H-bond
- (b) Adenine pairs with thymine through three H-bonds
- (c) Adenine does not pair with thymine
- (d) Adenine pairs with thymine through two H-bonds

Ans. (d)

The statement in option (d) is correct because

Adenine pairs with thymine through two H-bonds, i.e. A = T and the cytosine pairs with guanine by three hydrogen bonds. Between the G-C base pairs there are 3 hydrogen bonds which makes this bond pair stronger than the A-T base pair.

12 If the distance between two consecutive base pairs is 0.34 nm and the total number of base pairs of a DNA double helix in a typical mammalian cell is 6.6×10^9 bp, then the length of the DNA is approximately [NEET (Sep.) 2020]

- (a) 2.5 meters
- (b) 2.2 meters
- (c) 2.7 meters
- (d) 2.0 meters

Ans. (b)

The distance between two consecutive base pairs is 0.34 nm (0.34×10^{-9} m). The length of DNA double helix in a typical mammalian cell can be calculated by multiplying the total number of bp with distance between the two consecutive bp, i.e. $6.6 \times 10^9 \text{ bp} \times 0.34 \times 10^{-9} \text{ m/bp} = 2.2$ metres (the length of DNA). Thus, option (b) is correct.

13 In RNAi, the genes are silenced using [NEET (Odisha) 2019]

- (a) dsRNA
- (b) ssDNA
- (c) ssRNA
- (d) dsDNA

Ans. (a)

In RNAi, the genes are silenced using dsRNA. RNA interference (RNAi) takes place in all eukaryotic organisms as a method of cellular defence. This method involves silencing of a specific mRNA due to a complementary dsRNA molecule that binds to and prevents translation of the mRNA (silencing).

14 What initiation and termination factors are involved in transcription in eukaryotes? [NEET (Odisha) 2019]

- (a) σ and ρ , respectively
- (b) α and β , respectively
- (c) β and γ , respectively
- (d) α and σ , respectively

Ans. (a)

This question is not correct because out of the given initiation and termination factors, none is involved in transcription in eukaryotes. Only option (a) gives initiation and termination factors which are involved in transcription. These factors (σ and ρ) initiate and terminate transcription in prokaryotes (not in eukaryotes). Initiation and termination factors involved in transcription in eukaryotes are General Transcription Factors (TF IIA - TF IIF) and Transcription Termination Factor-1 (TTF-1), respectively.

15 Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? [NEET (Odisha) 2019]

- (a) Beadle and Tatum
- (b) Meselson and Stahl
- (c) Hershey and Chase
- (d) Jacob and Monod

Ans. (c)

Alfred Hershey and Martha Chase (1952) experimentally proved that DNA is the sole genetic material in bacteriophage.

On the other hand, Beadle and Tatum (1940s) experimentally showed one gene-one enzyme hypothesis using *Neurospora*. Meselson and Stahl first showed that DNA replicates semiconservatively through experiments on *E. coli*. Jacob and Monod were first to explain *lac* operon.

16 What will be the sequence of mRNA produced by the following stretch of DNA?

3'ATGCATGCATGCATG5'
TEMPLATE STRAND

5'TACGTACGTACGTAC3' CODING STRAND [NEET (Odisha) 2019]

- (a) 3'-AUGCAUGCAUGCAUG 5'
- (b) 5'-UACGUACGUACGUAC 3'
- (c) 3'-UACGUACGUACGUAC 5'
- (d) 5'-AUGCAUGCAUGCAUG 3'

Ans. (b)

The mRNA will be complementary to the DNA strand, but in RNA, uracil will be present in place of thymine. If the template strand is 3'-ATGCATGCATGCATG-5' then the base sequence of mRNA for the given DNA strand will be 5'-UACGUACGUACGUAC-3'.

17 Which of the following nucleic acids is present in an organism having 70S ribosomes only? [NEET (Odisha) 2019]

- (a) Single-stranded DNA with protein coat
- (b) Double-stranded circular naked DNA
- (c) Double-stranded DNA enclosed in nuclear membrane
- (d) Double-stranded circular DNA with histone proteins

Ans. (b)

Double-stranded circular naked DNA type of nucleic acid is present in an organism having 70S ribosomes. These are present in prokaryotic organisms or cells. All prokaryotic cells have a single double-stranded (double helix), circular DNA molecule for their genetic material. This DNA is attached to the inner cell membrane where the DNA replicating machinery is located. The DNA is "naked", it does not have proteins associated with it as eukaryotic DNA does.

18 Purines found both in DNA and RNA are [NEET (National) 2019]

- (a) adenine and guanine
- (b) guanine and cytosine
- (c) cytosine and thymine
- (d) adenine and thymine

Ans. (a)

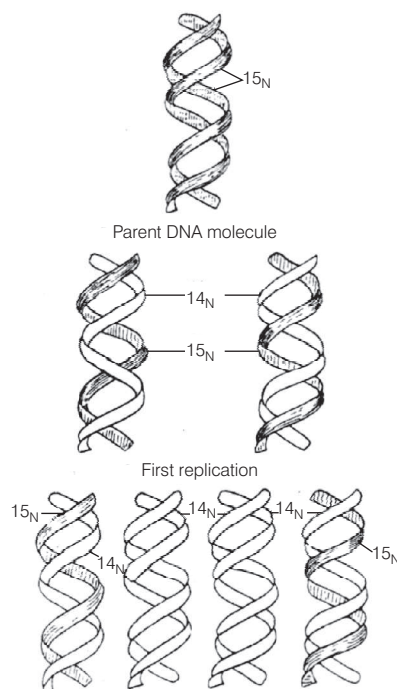
Adenine and guanine are the purines which are found both in DNA and RNA. Cytosine and thymine are the pyrimidines which are found in DNA. In case of RNA, thymine is replaced by uracil.

19 The experimental proof for semiconservative replication of DNA was first shown in a [NEET 2018]

- (a) plant
- (b) bacterium
- (c) fungus
- (d) virus

Ans. (b)

The experimental proof for semiconservative replication of DNA was first shown in a bacterium, *Escherichia coli*. It was discovered by Meselson and Stahl (1958).



Interpretation of results of experiment of Meselson and Stahl (1958) to prove semi-conservative replication of DNA. In this mode of replication, one strand of parent DNA is conserved in the progeny while the second is freshly synthesised. Meselson and Stahl proved this by using heavy isotope of Nitrogen (N^{15}).

20 The final proof for DNA as the genetic material came from the experiments of [NEET 2017]

- (a) Griffith
- (b) Hershey and Chase
- (c) Avery, MacLeod and McCarty
- (d) Hargobind Khorana

Ans. (b)

The final proof that DNA is the genetic material came from the experiments of Alfred Hershey and Martha Chase (1952). Griffith's experiment proved the existence of genetic material while Avery, MacLeod and McCarty worked to determine the biochemical nature of transforming principle.

Concept Enhancer Hershey and Chase during their experiment, grew viruses in two mediums, one containing ^{32}P and other ^{35}S , when these were allowed to infect bacteria, they observed that viruses containing ^{32}P DNA were radioactive while those with ^{35}S protein were not radioactive. Hence, DNA not protein coat entered bacterial cells from viruses.

21 The association of histone H1 with a nucleosome indicates [NEET 2017]

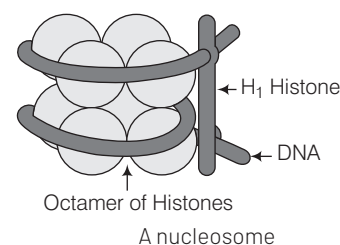
- (a) transcription is occurring
- (b) DNA replication is occurring
- (c) the DNA is condensed into chromatin fibre
- (d) the DNA double helix is exposed

Ans. (c)

The association of H_1 histone with nucleosome indicates that DNA remains in its condensed form.

Concept Enhancer In eukaryotes, DNA packaging is carried out with the help of histone proteins. Nucleosome is the unit of compaction. Its core consists of four pairs of histones (H_2A , H_2B , H_3 and H_4). The linker DNA, consisting of H_1 histone connects two adjacent nucleosomes.

They together constitute chromatosome. It gives rise to a chromatin fibre after further condensation.



22 Spliceosomes are not found in cells of [NEET 2017]

- (a) plants
- (b) fungi
- (c) animals
- (d) bacteria

Ans. (d)

Spliceosome is a large molecular complex found in nucleus of eukaryotic cells of plants, animals and fungi, etc. It is assembled from snRNAs and protein complexes that plays an important role in splicing of introns. Spliceosome is absent in cells of bacteria.

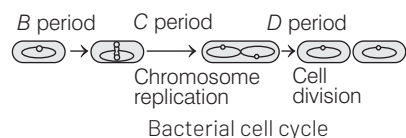
23 DNA replication in bacteria occurs [NEET 2017]

- (a) during S-phase
- (b) within nucleolus
- (c) prior to fission
- (d) just before transcription

Ans. (c)

Bacteria lack a cell nucleus. Due to their primitive nature they lack a well marked S-phase. In bacteria DNA replication occurs before fission.

Concept Enhancer: Bacterial cell cycle is divided into the B, C and D periods. The B period extends from the end of cell division to the beginning of DNA replication. DNA replication occurs during the C period. The D period refers to the stage between the end of DNA replication and the division of bacterial cell into two daughter cells.



24 Which of the following RNAs should be most abundant in animals cell? [NEET 2017]

- (a) rRNA
- (b) tRNA
- (c) mRNA
- (d) miRNA

Ans. (a)

There are three main types of RNA, i.e. rRNA, tRNA and mRNA. rRNA is the most abundant form of RNA; because it is responsible for coding and protein synthesis in the cell and associated with ribosomes. mRNA provides the template for translation. tRNA brings amino acids and reads the genetic code.

25 A complex of ribosomes attached to a single strand of RNA is known as [NEET 2016, Phase I]

- (a) polymer
- (b) polypeptide
- (c) okazaki fragment
- (d) polysome

Ans. (d)

In prokaryotes, several ribosomes may attach to single mRNA and form a chain called polyribosomes or polysomes.

26 DNA-dependent RNA polymerase catalyses transcription on one strand of the DNA which is called the [NEET 2016, Phase II]

- (a) template strand
- (b) coding strand
- (c) alpha strand
- (d) anti strand

Ans. (a)

DNA dependent RNA polymerase catalyses transcription on one strand of the DNA called a template strand. A template can be considered as one of those strands of DNA which decodes its information directly through RNA polymerase.

This information is then restored within the RNA molecule and transferred outside the nucleus for protein synthesis within the cytoplasm.

27 A molecule that can act as a genetic material must fulfill the traits given below, except [NEET 2016, Phase II]

- (a) it should be able to express itself in the form of 'Mendelian characters'
- (b) it should be able to generate its replica
- (c) it should be unstable structurally and chemically
- (d) it should provide the scope for slow changes that are required for evolution

Ans. (c)

A molecule that can act as a genetic material must be unstable structurally and chemically.

The criteria that a molecule must fulfil to act as a genetic material are as following

- (i) It should be able to replicate.
- (ii) It should be chemically and structurally stable.
- (iii) It should provide the scope for slow changes, i.e. mutations which are required for evolution.

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

28 Which of the following rRNAs act as structural RNA as well as ribozyme in bacteria? [NEET 2016, Phase II]

- (a) 5 srRNA
- (b) 18 srRNA
- (c) 23 srRNA
- (d) 5-8 srRNA

Ans. (c)

Bacterial cells use their 23 srRNA as an enzyme during protein synthesis. This is the only non-proteinaceous enzyme known so far.

29 Taylor conducted the experiments to prove semiconservative mode of chromosome replication on [NEET 2016, Phase II]

- (a) *Vinca rosea*
- (b) *Vicia faba*
- (c) *Drosophila melanogaster*
- (d) *E. coli*

Ans. (b)

The use of radioactive thymidine to detect the semiconservative mode of replication of newly synthesised DNA in the chromosomes was performed on *Vicia faba* by Taylor and colleagues in 1958. This experiment proved that the DNA in chromosomes replicates semiconservatively. Hence, the option (b) is correct.

30 The equivalent of a structural gene is [NEET 2016, Phase II]

- (a) muton
- (b) cistron
- (c) operon
- (d) recon

Ans. (b)

Cistron is the segment of DNA which determines the synthesis of complete polypeptide. Thus, it is considered as equivalent to a structural gene. Therefore, option (b) is correct and others are incorrect.

Concept Enhancer Eukaryotic structural gene is monocistronic whereas prokaryotic structural gene is polycistronic.

Muton Smallest unit of DNA in which mutation occurs.

Operon Functional unit of genomic DNA containing a cluster of genes under control of single promoter.

Recon Smallest unit of DNA for recombination.

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

Ans. (d)

Chargaff's rule is not applicable to RNA. He is the generalisations formulated about DNA structure. The rule states that DNA from any cell of all organisms should have a 1 : 1 ratio (base pair rule) of pyrimidine and purine bases, i.e. the amount of guanine is equal to cytosine and the amount of adenine is equal to thymine. Further complementary base pairing is sometimes, visible in RNA as well (in doubled stranded RNAs of viruses) hence option (a) is not taken into consideration.

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

Ans. (c)

The correct order of organisation of genetic material from largest to smallest is as follows

Genome, chromosome, gene, nucleotide.

Genome It is the total genetic material of an individual.

Chromosome It is a packed and organised structure containing most of the DNA of a living organism.

Gene It is a segment of DNA that encodes for a protein.

Nucleotide It is one of the structural components, or building blocks, of DNA and RNA.

- 33** Transformation was discovered by
[CBSE AIPMT 2014]
- (a) Meselson and Stahl
 - (b) Hershey and Chase
 - (c) Griffith
 - (d) Watson and Crick

Ans. (c)

Transformation was discovered by F Griffith [1928]. He isolated the DNA as genetic material that inherit the genetic information between two generations by using two strain of *Pneumococcus* bacteria which infect mice. i.e. a type III S(smooth) and type II R(rough) strain.

- 34** Removal of RNA polymerase-III from nucleoplasm will affect the synthesis of
[CBSE AIPMT 2012]
- (a) tRNA
 - (b) hnRNA
 - (c) mRNA
 - (d) rRNA

Ans. (a)

RNA polymerase III transcribes tRNA, therefore tRNA synthesis will be affected. RNA polymerase-II synthesises mRNA while, RNA polymerase-I synthesis rRNA in eukaryotes.

- 35** Which one of the following is not a part of a transcription unit in DNA?
[CBSE AIPMT 2012]
- (a) The inducer
 - (b) A terminator
 - (c) A promoter
 - (d) The structural gene

Ans. (a)

Transcription unit consists of promoter, structural gene and terminator. The inducer (lactose/allolactose) is not a component of transcription unit.

- 36** Ribosomal RNA is actively synthesised in
[CBSE AIPMT 2012]
- (a) lysosomes
 - (b) nucleolus
 - (c) nucleoplasm
 - (d) ribosomes

Ans. (b)

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

- 37** Removal of introns and joining of exons in a defined order during transcription is called
[CBSE AIPMT 2012]
- (a) looping
 - (b) inducing
 - (c) slicing
 - (d) splicing

Ans. (d)

The primary transcript from a typical eukaryotic gene contains introns as well as exons. During RNA splicing, introns are removed and exons are joined in a defined order, to produce functional RNA.

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

Ans. (c)

Nucleosome appear as "beads-on-string" in the chromosomes. Nucleosome is sub-microscopic sub-unit of chromatin which is formed by wrapping of DNA over a core of histone proteins. The term was coined by Oudet, et. al [1975]. It is oblate structure with a length of 10 nm and a thickness of 5-5.7 nm. Its core is called nu-body. The latter is formed of four pairs of histone molecules—H₂A, H₂B, H₃ and H₄. DNA makes 1.75 turns over the octamer to form a nucleosome.

Two adjacent nucleosomes are connected by a short segment of unbound DNA called linker DNA. A fifth type of histone called H₁ is attached over the linker DNA.

- 39** Whose experiments cracked the DNA and discovered unequivocally that a genetic code is a triplet?
[CBSE AIPMT 2009]
- (a) Nirenberg and Matthaei
 - (b) Hershey and Chase
 - (c) Morgan and Sturtevant
 - (d) Beadle and Tatum

Ans. (a)

The existence of triplet code was simply an assumption till 1961, when Nirenberg and Matthaei proved its existence by experiments. They were able to synthesise artificial mRNA, which contained only one nitrogenous base, i.e. uracil. This synthetic poly U sequence was then placed in a cell free system containing protein synthesising enzymes (extracted from bacterium *E. coli*) and 20 amino acids together with necessary ATP. During the process, a small polypeptide molecule was produced, which was formed by the linking of phenylalanine.

This suggested that UUU is the code for phenyl alanine. Nirenberg got Nobel Prize for his contributions.

40 Polysome is formed by
[CBSE AIPMT 2008]

- (a) several ribosomes attached to a single mRNA
- (b) many ribosomes attached to a strand of endoplasmic reticulum
- (c) a ribosome with several subunits
- (d) ribosomes attached to each other in a linear arrangement

Ans. (a)

The group of ribosomes together with the single mRNA molecules, they are translating is called polysome. They are formed by several ribosomes attached to a single mRNA.

In eukaryotic cells the ribosomes are attached to rough endoplasmic reticulum by ribophorin protein. Electron microscopy reveals that membranes of homogenised endoplasmic reticulum disrupt to form closed vesicles called microsomes. Microsomes derived from rough endoplasmic reticulum are studied with ribosomes and are called rough ribosomes.

41 The Okazaki fragments in DNA chain growth [CBSE AIPMT 2007]

- (a) result in transcription
- (b) polymerise in the 3' to 5' direction and forms replication fork
- (c) prove semi-conservative nature of DNA replication
- (d) polymerise in the 5' to 3' direction and explain 3' to 5' DNA replication

Ans. (a)

The Okazaki fragments in DNA chain growth polymerise in the 5' to 3' direction. The replicated DNA results in transcription.

42 The length of DNA molecule greatly exceeds the dimensions of the nucleus in eukaryotic cells. How is this DNA accommodated?
[CBSE AIPMT 2007]

- (a) Deletion of non-essential genes
- (b) Super-coiling in nucleosomes
- (c) DNase digestion
- (d) Through elimination of repetitive DNA

Ans. (b)

In eukaryotic cells, DNA is accommodated by super-coiling in nucleosomes.

43 Molecular basis of organ differentiation depends on the modulation in transcription by
[CBSE AIPMT 2007]

- (a) RNA polymerase
- (b) ribosome
- (c) transcription factor
- (d) anticodon

Ans. (c)

Transcription factor is molecular basis of organ differentiation.

44 Telomere repetitive DNA sequences control the function of eukaryotic chromosomes because they [CBSE AIPMT 2007]

- (a) act as replicons
- (b) are RNA transcription initiator
- (c) help chromosome pairing
- (d) prevent chromosome loss

Ans. (d)

Telomeres, i.e. the ends of chromosome, have repetitive DNA sequences and are stable and resistant to exonuclease digestion hence, prevent chromosome loss.

45 Which one of the following makes use of RNA as a template to synthesise DNA?
[CBSE AIPMT 2005]

- (a) Reverse transcriptase
- (b) DNA dependant RNA polymerase
- (c) DNA polymerase
- (d) RNA polymerase

Ans. (a)

In 1970 H Temin and D Baltimore independently discovered the enzyme reverse transcriptase. This enzyme uses RNA as template for the synthesis of cDNA (complementary DNA).

46 Which one of the following hydrolyses internal phosphodiester bonds in a polynucleotide chain?
[CBSE AIPMT 2005]

- (a) Lipase
- (b) Exonuclease
- (c) Endonuclease
- (d) Protease

Ans. (c)

Endonuclease hydrolyses internal phosphodiester bonds in a polynucleotide chain.

47 During transcription holoenzyme RNA polymerase binds to a DNA sequence and the DNA assumes a

saddle like structure at that point. What is that sequence called?

[CBSE AIPMT 2005]

- (a) CAAT box
- (b) GGTT box
- (c) AAAT box
- (d) TATA box

Ans. (d)

TATA box is present in eukaryotic promoter region. It has a resemblance with Pribnow box of prokaryotes. TATA box was identified by Dr. Hogness and so, it is also called as Hogness box. It is a 7 bp long region located 20 bp upstream to the start point.

During the process of transcription the RNA polymerase (a holoenzyme which has a core unit and a sigma factor for proper initiation of transcription) binds to TATA box due to which DNA assumes a saddle like structure at this place.

48 Telomerase is an enzyme which is a [CBSE AIPMT 2005]

- (a) repetitive DNA
- (b) RNA
- (c) simple protein
- (d) ribonucleoprotein

Ans. (d)

Ends of an eukaryotic chromosome are known as telomeres.

Telomerase, which is a special ribonucleoprotein molecule (enzymatic in nature) is responsible for the synthesis of these telomeres.

49 During replication of a bacterial chromosome DNA synthesis starts from a replication origin site and [CBSE AIPMT 2004]

- (a) RNA primers are involved
- (b) is facilitated by telomerase
- (c) moves in one direction of the site
- (d) moves in bi-directional way

Ans. (a)

The events for initiation of DNA replication in prokaryotes may be classified into (a) pre-priming (occurring only at the origin); (b) priming (recurring with the initiation of each Okazaki fragment during elongation phase. Unwinding of DNA is followed by the synthesis of RNA primers by RNA primase.

50 The telomeres of eukaryotic chromosomes consist of short sequences of [CBSE AIPMT 2004]

- (a) thymine rich repeats
- (b) cytosine rich repeats
- (c) adenine rich repeats
- (d) guanine rich repeats

Ans. (d)

Telomeres have been shown to have unique structures that include short nucleotide sequences present as tandemly repeated units. In eukaryotes the telomeres terminate with a single-stranded DNA [12-16 nucleotides long) rich in guanine.

- 51** During transcription, the nucleotide sequence of the DNA strand that is being coded is ATACG, then the nucleotide sequence in the mRNA would be [CBSE AIPMT 2004]

(a) TATGC (b) TCTGG
(c) UAUGC (d) UATGG

Ans. (c)

If DNA has **ATACG** nucleotide sequence then the mRNA would contain UAUGC sequence. The formation of mRNA from DNA is termed as transcription. This process takes place in the nucleus (eukaryotes) or in the cytoplasm (prokaryotes).

The base sequence of mRNA is complementary copy of the template DNA strand.

- 52** Which form of RNA has a structure resembling clover leaf? [CBSE AIPMT 2004]

(a) rRNA (b) hnRNA
(c) mRNA (d) tRNA

Ans. (d)

The basic plan of the structure of tRNA assumes the pattern of a clover leaf. The structures of different tRNAs for almost all amino acids are now available and all of these fit the clover leaf model. The tRNA structure can be decomposed into its primary structure and its secondary structure (usually seen as clover leaf structure) and tertiary structure.

- 53** During transcription, the DNA site at which RNA polymerase binds is called [CBSE AIPMT 2003]

(a) receptor (b) enhancer
(c) promoter (d) regulator

Ans. (c)

Promoter is the nucleotide sequence to which RNA polymerase binds and initiates transcription. Formation of a single stranded linear chain of complementary RNA (mRNA) on the template strand of DNA in nucleus (eukaryotes) or in cytoplasm (prokaryotes) is known as transcription.

- 54** Chromosomes in a bacterial cell can be 1-3 in number and [CBSE AIPMT 2003]

(a) can be either circular or linear, but never both within the same cell
(b) can be circular as well as linear within the same cell
(c) are always circular
(d) are always linear

Ans. (c)

Bacterial chromosomes are circular DNA molecules.

- 55** Exon part of mRNAs have code for [CBSE AIPMT 2002]

(a) protein (b) lipid
(c) carbohydrate (d) phospholipid

Ans. (a)

Exon part of mRNA consists of codons for protein synthesis. Exon is the stretch of bases which codes for amino acids, while the non-coding stretches of bases are called intron.

- 56** Which of the following reunites the exon segments after RNA splicing? [CBSE AIPMT 2002]

(a) RNA polymerase (b) RNA primase
(c) RNA ligase (d) RNA protease

Ans. (c)

RNA ligase reunites the exon segments after RNA splicing.

- 57** Which statements is correct for bacterial transduction? [CBSE AIPMT 2002]

(a) Transfer of some genes from one bacteria to another bacteria through virus
(b) Transfer of genes from one bacteria to another bacteria by conjugation
(c) Bacteria obtained its DNA directly
(d) Bacteria obtained DNA from other external source

Ans. (a)

Transduction involves the picking up of DNA by bacteriophage from one bacterial cell and carrying it to another where, the DNA fragment may get incorporated into the bacterial host's genome.

- 58** In a DNA percentage of thymine is 20. What is the percentage of guanine? [CBSE AIPMT 2002]

(a) 20% (b) 40%
(c) 30% (d) 60%

Ans. (c)

Total DNA [100] = A + T + C + G

A = 20% (given)

A = T (base pairing rule)

100 = 20 + 20 + C + G

C + G = 100 - 40 = 60

C = G = 30 (C = G)

- 59** Sequence of which of the following is used to know the phylogeny? [CBSE AIPMT 2002]

(a) mRNA (b) rRNA
(c) tRNA (d) DNA

Ans. (b)

The genes for rRNAs tend to be highly conserved and, are therefore, often employed for phylogenetic studies.

- 60** In which direction mRNA is synthesised on DNA template? [CBSE AIPMT 2001]

(a) 5' → 3' (b) 3' → 5'
(c) Both (a) and (b) (d) Any of above

Ans. (a)

5' → 3' is the direction of synthesis of mRNA on DNA template.

- 61** Gene and cistron words are sometimes used synonymously because [CBSE AIPMT 2001]

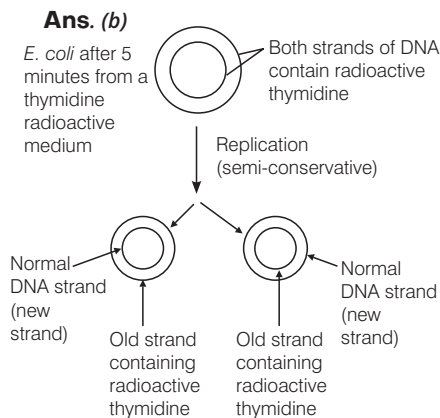
(a) one cistron contains many genes
(b) one gene contains many cistrons
(c) one gene contains one cistron
(d) one gene contains no cistron

Ans. (c)

Cistron is generally accepted as a synonym for gene. Gene (Gr. *genos* = birth, race) is the basic unit of heredity. It is a sequence of nucleotides on a chromosome that encodes a polypeptide or RNA molecule and so, determines the nature of individual's inherited traits. Cistron is a segment of DNA that codes for one polypeptide.

- 62** *E. coli* about to replicate was placed in a medium containing radioactive thymidine for five minutes. Then it was made to replicate in a normal medium. Which of the following observation shall be correct? [CBSE AIPMT 2001]

(a) Both the strands of DNA will be radioactive
(b) One strand radioactive
(c) Each strand half radioactive
(d) None is radioactive



Since, DNA replication is semiconservative, the newly synthesised strand of DNA would be normal while the strand obtained from parent molecule would be radioactive. In the given experiment

63 Due to discovery of which of the following in 1980's the evolution was termed as RNA world?
[CBSE AIPMT 2001]

- (a) mRNA, tRNA, rRNA synthesise proteins
- (b) In some viruses, RNA is genetic material
- (c) Some RNAs have enzymatic property
- (d) RNA is not found in all cells

Ans. (c)

Ribozymes are catalytically active RNA molecules discovered in 1980's. These are self-splicing introns indicating their possible role as intermediates in the evolution of biological systems from abiotic substances.

64 During replication of DNA, its two strands separate. Each of these serves as a template for the formation of new strands. Such type of replication is called
[CBSE AIPMT 2000]

- (a) non-conservative
- (b) semi-conservative
- (c) flexible
- (d) conservative

Ans. (b)

Since, each daughter DNA molecule contains one strand of the parent DNA double helix (only one strand synthesised afresh) the process of replication is called semi-conservative. Mathew Meselson and Franklin Stahl in 1958 proved experimentally that DNA replication is semi-conservative.

65 One of the similarities between DNA and RNA is that both
[CBSE AIPMT 2000]

- (a) are polymers of nucleotides
- (b) are capable of replicating
- (c) have similar sugars
- (d) have similar pyrimidine bases

Ans. (a)

DNA Composition	RNA Composition
Deoxyribose sugar.	Ribose sugar.
Adenine, guanine (both purine) and cytosine, thymine (both pyrimidine), nitrogenous bases.	Adenine, guanine (both purine) and uracil, cytosine (both pyrimidine) nitrogenous bases.
Phosphate molecules.	Phosphate molecules.
It is polymer of nucleotides.	It is also polymer of nucleotides.
It is capable to replicate in all cases because it functions as heredity material.	It is formed from DNA by the process of transcription only in few cases (RNA viruses) it functions as heredity material.

66 The *Pneumococcus* experiment proves that
[CBSE AIPMT 1999]

- (a) DNA is the genetic material
- (b) RNA sometime controls the production of DNA and proteins
- (c) bacteria undergo binary fission
- (d) bacteria do not reproduce sexually

Ans. (a)

The *Pneumococcus* experiment proves that DNA is the genetic material as Frederick Griffith (1928) found that 'something' passed from heat-killed encapsulated forms of *Pneumococcus* to live non-encapsulated forms which caused them to develop capsules and become virulent. Avery *et al.*, (1944) found this transforming agent (hence, genetic material) to be DNA.

67 DNA elements, which can switch their position, are called
[CBSE AIPMT 1998]

- (a) exons
- (b) introns
- (c) cistrons
- (d) transposons

Ans. (d)

Transposons are genetic elements varying from 750 base pairs to 40 kilo base pairs in length and can move from a site in one genome to another site in the same or in a different genome.

68 Genes are packaged into a bacterial chromosome by
[CBSE AIPMT 1997]

- (a) histones
- (b) basic protein
- (c) acidic protein
- (d) actin

Ans. (b)

Bacteria are prokaryotic organisms. Polyamines (basic proteins) like spermidine and cadaverine (instead of histones) are associated with DNA packaging in bacteria.

69 The hereditary material present in the bacterium *E. coli* is
[CBSE AIPMT 1997]

- (a) single stranded RNA
- (b) double stranded RNA
- (c) single stranded DNA
- (d) double stranded DNA

Ans. (d)

Bacterial chromosome is single, circular double stranded DNA molecule.

70 An enzyme that joins the ends of two strands of nucleic acid is a
[CBSE AIPMT 1996, 2002]

- (a) polymerase
- (b) synthetase
- (c) helicase
- (d) ligase

Ans. (d)

Ligase enzyme joins the ends of two strands of nucleic acid.

71 Okazaki fragments are seen during
[CBSE AIPMT 1996]

- (a) transcription
- (b) translation
- (c) replication
- (d) transduction

Ans. (c)

During DNA replication in lagging strand DNA fragments are formed in small pieces these are called Okazaki fragments.

72 In split genes, the coding sequence are called
[CBSE AIPMT 1995]

- (a) introns
- (b) operons
- (c) exons
- (d) cistrons

Ans. (c)

In split genes coding region is called exons. In higher organisms (eukaryotes) gene is not continuous, within a single gene there may be four or five silent regions. These regions are called introns (which do not transcribe mRNA). The remaining part is called as exons (transcribe mRNA).

73 Protein helping in opening of DNA double helix in front of replications fork is

- (a) DNA gyrase
- (b) DNA polymerase-I
- (c) DNA ligase
- (d) topoisomeras

Ans. (a)

DNA gyrase helps in opening of DNA double helix in front of replication fork.

74 Reverse transcriptase is
[CBSE AIPMT 1994]

- (a) RNA dependent RNA polymerase
- (b) DNA dependent RNA polymerase
- (c) DNA dependent DNA polymerase
- (d) RNA dependent DNA polymerase

Ans. (d)

Reverse transcriptase is RNA dependent DNA polymerase. H Temin and D Baltimore discovered reverse transcription. Reverse transcriptase has modified central dogma of molecular biology as RNA → DNA → RNA → Protein.

75 Nucleosome core is made of
[CBSE AIPMT 1993]

- (a) H1, H2A, H2B and H3
- (b) H1, H2A, H2B and H4
- (c) H1, H2A, H2B, H3 and H4
- (d) H2A, H2B, H3 and H4

Ans. (d)

A nucleosome is an octamer of histone proteins and has a core of 8 molecules of histone proteins (two each of H2A, H2B, H3 and H4) wrapped by two turns of DNA.

76 A DNA with unequal nitrogen bases would most probably be
[CBSE AIPMT 1993]

- (a) single stranded
- (b) double stranded
- (c) triple stranded
- (d) four stranded

Ans. (a)

A single stranded DNA do not possess its complementary base pairs so it would have unequal nitrogen bases.

77 During DNA replication, the strands separate by
[CBSE AIPMT 1993]

- (a) DNA polymerase
- (b) topoisomerase
- (c) unwindase/helicase
- (d) gyrase

Ans. (c)

Unwinding of DNA helix is caused by enzyme helicase.

78 Who proved that DNA is basic genetic material?
[CBSE AIPMT 1993]

- (a) Griffith
- (b) Watson
- (c) Boveri and Sutton
- (d) Hershey and Chase

Ans. (d)

Hershey and Chase [1952] proved that DNA is basic genetic material.

79 Nucleotide arrangement in DNA can be seen by
[CBSE AIPMT 1993]

- (a) X-ray crystallography
- (b) electron microscope
- (c) ultracentrifuge
- (d) light microscope

Ans. (a)

Astbury by his X-ray diffraction studies suggested 3-D configuration for DNA molecules which was confirmed by Wilkins and Franklin in 1952 and then in 1953 Watson and Crick designed the model of DNA molecule.

80 The transforming principle of *Pneumococcus* as found out by Avery, MacLeod and McCarty was
[CBSE AIPMT 1993]

- (a) mRNA
- (b) DNA
- (c) protein
- (d) polysaccharide

Ans. (b)

Avery, MacLeod and McCarty [1944] showed the significance of DNA in hereditary transmission in bacteria *Pneumococcus*. They discovered the biochemical nature of gene.

81 Experimental material in the study of DNA replication has been
[CBSE AIPMT 1992]

- (a) *Escherichia coli*
- (b) *Neurospora crassa*
- (c) *Pneumococcus*
- (d) *Drosophila melanogaster*

Ans. (a)

Meselson and Stahl [1958] proved experimentally that in *E. coli* DNA is replicated by semi-conservative manner.

82 *Escherichia coli* fully labelled with N^{15} is allowed to grow in N^{14} medium. The two strands of DNA molecule of the first generation bacteria have [CBSE AIPMT 1992]

- (a) different density and do not resemble parent DNA
- (b) different density but resemble parent DNA
- (c) same density and resemble parent DNA
- (d) same density but do not resemble parent DNA

Ans. (b)

When *E. coli* fully labelled with N^{15} is allowed to grow in N^{14} medium, then after first generation of replication one of the two strands would have N^{15} and the other strand would have N^{14} . The resulting molecule would have a density which is intermediate between N^{15} DNA and N^{14} DNA.

These two molecules of DNA will be similar but not same in density.

83 In RNA, thymine is replaced by
[CBSE AIPMT 1992]

- (a) adenine
- (b) guanine
- (c) cytosine
- (d) Uracil

Ans. (d)

DNA consists of nitrogenous bases, adenine, guanine, cytosine and thymine, whereas in RNA thymine is replaced by uracil. The other nitrogenous bases, i.e. adenine, guanine, cytosine are present both in RNA and DNA.

84 A nucleotide is formed of
[CBSE AIPMT 1991]

- (a) purine, pyrimidine and phosphate
- (b) purine, sugar and phosphate
- (c) nitrogen base, sugar and phosphate
- (d) pyrimidine, sugar and phosphate

Ans. (c)

Nucleotide is the basic unit of nucleic acids (DNA and RNA). It is composed of nucleoside (nitrogenous base + pentose sugar) and phosphate group.

85 The process of transfer of genetic information from DNA to RNA/formation of RNA from DNA is
[CBSE AIPMT 1991]

- (a) transversion
- (b) transcription
- (c) translation
- (d) translocation

Ans. (b)

The transfer of genetic information from DNA to RNA (mRNA) is known as transcription. Both the strands of DNA do not transcribe RNA but only one of them does it which is called as template strand.

86 Which is not consistent with double helical structure of DNA?

[CBSE AIPMT 1990]

- (a) $A=T, C=G$
- (b) Density of DNA decreases on heating
- (c) $A + T/C + G$ is not constant
- (d) Both (a) and (b)

Ans. (c)

According to Erwin Chargaff, the base ratio $A + T/G + C$ may vary from one species to another, but is constant for a given species. It is rarely equal to one and varies from 0.4 and 1.9.

87 DNA replication is

[CBSE AIPMT 1989]

- (a) conservative and discontinuous
- (b) semi-conservative and semidiscontinuous
- (c) semi-conservative and discontinuous
- (d) conservative

Ans. (b)

DNA replication is semi-conservative that means DNA formed after replication contains one strand of its parent DNA and this was proved by Meselson and Stahl [1958].

During replication the strand formed in leading strand is continuous, while the strand formed in lagging strand is discontinuous in the small pieces (Okazaki fragments).

88 Which one contains four pyrimidine bases?

[CBSE AIPMT 1994]

- (a) GATCAATGC
- (b) GCUAGACAA
- (c) UAGCGGUAA
- (d) TGCCTAACG

Ans. (a)

Pyrimidines are 6-membered nitrogen bases that contain nitrogen at 1 and 3 positions, e.g. cytosine (C), thymine (T), uracil (U).

89 A segment of DNA has 120 adenine and 120 cytosine bases. The total number of nucleotides present in the segment is

[CBSE AIPMT 1991]

- (a) 120
- (b) 240
- (c) 60
- (d) 480

Ans. (d)

According to Chargaff's rule, molar amount of adenine is equal to that of thymine and cytosine equals to guanine, $A + G = T + C$. So, a segment of DNA with 120 adenine base and 120 cytosine base will have same number of each thymine and guanine base (as, $A = T$ and $C = G$), i.e. 120 thymine bases, 120 guanine bases, thus a total of 480 nucleotides.

TOPIC 2

Genetic Code and Gene Expression

90 Statement I The codon 'AUG' codes for methionine and phenylalanine.

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

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

[NEET 2021]

- (a) Both statement I and statement II are true
- (b) Both statement I and statement II are false
- (c) Statement I is true, but statement II is false
- (d) Statement I is false, but statement II is true

Ans. (d)

Statement I is false, but statement II is true and can be corrected as The codon AUG only codes for methionine. As the codons are universal. From bacteria to mammals AUG only codes for methionine.

Some amino acids are coded by more than one codon, hence the code is degenerate. AAA and AAG both codons code for the amino acid lysine.

91 Identify the correct statement.

[NEET 2021]

- (a) In capping, methyl guanosine triphosphate is added to the 3' end of hnRNA
- (b) RNA polymerase binds with Rho factor to terminate the process of transcription in bacteria
- (c) The coding strand in a transcription unit is copied to an mRNA
- (d) Split gene arrangement is characteristic of prokaryotes

Ans. (b)

Statement in option (b) is correct and other statements can be corrected as A heterogeneous nuclear RNA or hnRNA is a primary mRNA transcript that is localised in the nucleus. Capping is a process in which at the 5' end of hnRNA, a cap of 7-methyl guanosine is added.

The template strand is a transcription unit is copied to a mRNA.

Split gene arrangement is characteristic of eukaryotes.

92 What is the role of RNA polymerase-III in the process of transcription in eukaryotes?

[NEET 2021]

- (a) Transcribes rRNAs (28S, 18S and 5.8S)
- (b) Transcribes tRNA (5s rRNA and snRNA)
- (c) Transcribes precursor of mRNA
- (d) Transcribes only snRNAs

Ans. (b)

In eukaryotes, at least three classes of RNA polymerases (Pol I-III) are required for the cellular RNA synthesis. In eukaryote cells, RNA polymerase III (also called Pol III) transcribes DNA to synthesise ribosomal 5S rRNA, tRNA and other small RNAs. The genes transcribed by RNA Pol III fall in the category of "housekeeping" genes whose expression is required in all cell types and most environmental conditions.

93 Identify the statement which is incorrect.

[NEET (Oct.) 2020]

- (a) Sulphur is an integral part of cysteine
- (b) Glycine is an example of lipids
- (c) Lecithin contains phosphorus atom in its structure
- (d) Tyrosine possesses aromatic ring in its structure

Ans. (b)

Statement (b) is incorrect. It can be corrected as Glycine is an example of amino acid. It is a neutral amino acid that contains only one amino group and one carboxylic group with non-cyclic hydrocarbon chain.

94 The first phase of translation is

[NEET (Sep.) 2020]

- (a) recognition of DNA molecule
- (b) aminoacylation of tRNA
- (c) recognition of an anti-codon
- (d) binding of mRNA to ribosome

Ans. (b)

The first phase of translation is aminoacylation of tRNA, i.e. activation of amino acids and the formation of AA-tRNA complex. In the presence of an enzyme tRNA synthetase, the amino acid (AA) molecule is activated and then each amino acid is attached to the specific tRNA molecule at 3' / CCA end to form aminoacyl- tRNA complex. The reaction needs ATP. This process is thus called charging of tRNA or aminoacylation of tRNA.

95 The specific palindromic sequence which is recognised by EcoRI is

[NEET (Sep.) 2020]

- (a) 5'- GGAACC - 3'
- (b) 5' - CTTAAG - 3' 3' - CCTTGG - 5'
3' - GAATTC - 5'
- (c) 5' - GGATCC - 3'
- (d) 5' - GAATTC - 3' 3' - CCTAGG - 5'
3' - CTTAAG - 5'

Ans. (d)

The correct option is (d) because the specific palindromic sequence which is recognised by EcoRI is 5'-GAATTC-3' 3'-CTTAAG-5'.

A palindromic sequence is a sequence made up of nucleic acids within double helix of DNA or RNA that is the same when read from 5' to 3' on one strand and 3' to 5' on the other, complementary strand.

96 The sequence that controls the copy number of the linked DNA in the vector, is termed

- (a) Ori site
- (b) palindromic sequence
- (c) recognition site
- (d) selectable marker

Ans. (a)

The sequence that controls the copy number of linked DNA in the vector is called as Ori site. Origin of replication is a sequence from where replication starts and any foreign DNA is linked to this region.

Ori site is also responsible for controlling copy number of linked DNA.

Therefore, if any person wants to produce many copies of the target DNA he/she should clone in a vector whose Ori site supports high copy number.

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

[NEET (Odisha) 2019]

- (a) Universal, Non-ambiguous, Overlapping
- (b) Degenerate, Overlapping, Commaless

- (c) Universal, Ambiguous, Degenerate
- (d) Degenerate, Non-overlapping, Non-ambiguous

Ans. (d)

The correct combination of salient features of Genetic code is degenerate, Non-overlapping, Non-ambiguous. These are explained as one codon codes for only one amino acid, hence genetic code is unambiguous and specific. Some amino acids are coded by more than one codon, hence the code is degenerate. The codon is read in mRNA in a contiguous fashion. There are no punctuations and overlapping.

98 Which of the following features of genetic code does allow bacteria to produce human insulin by recombinant DNA technology?

[NEET (National) 2019]

- (a) Genetic code is redundant
- (b) Genetic code is nearly universal
- (c) Genetic code is specific
- (d) Genetic code is not ambiguous

Ans. (b)

Bacteria is able to produce human insulin because genetic code is nearly universal in all organisms. For example, the codon AGG specifies amino acid Arginine in bacteria, animals and plants. But there are also some exceptions to it, e.g. in mitochondria, stop codon UGA specifies amino acid tryptophan.

99 Match the following RNA polymerases with their transcribed products

1. RNA polymerase I	i. tRNA
2. RNA polymerase II	ii. rRNA
3. RNA polymerase III	iii. hnRNA

Select the correct option from the following [NEET (Odisha) 2019]

- 1 2 3
- (a) (i) (iii) (ii)
- (b) (i) (ii) (iii)
- (c) (ii) (iii) (i)
- (d) (iii) (ii) (i)

Ans. (c)

The correct matches are

1. RNA polymerase I transcribes	(ii) rRNAs (28S, 18S and 5.8S)
2. RNA polymerase II	(iii) hnRNA
3. RNA polymerase III	(i) tRNA

100 Expressed Sequence Tags (ESTs) refers to [NEET (National) 2019]

- (a) polypeptide expression
- (b) DNA polymorphism
- (c) novel DNA sequences
- (d) genes expressed as RNA

Ans. (d)

Expressed Sequence Tags (EST) refers to the genes expressed as RNA. These are the DNA sequences that are expressed as mRNA for protein synthesis.

101 AGGTATCGCAT is a sequence from the coding strand of a gene. What will be the corresponding sequence of the transcribed mRNA?

[NEET 2018]

- (a) ACCUAUGCGAU
- (b) AGGTUTCGCAT
- (c) AGGUAUCGCAU
- (d) UCCAUAGCGUA

Ans. (c)

Coding strand is the one that codes for mRNA. It has same nucleotide sequence as that of mRNA except thymine (T) is replaced by uracil (U) in mRNA. Hence, the corresponding sequence of transcribed mRNA by template or non-coding strand (complementary to RNA) is AGGUAUCGCAU.

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

[NEET 2017]

- (a) 1
- (b) 11
- (c) 33
- (d) 333

Ans. (c)

33 codons will be altered if the 901st base is deleted and RNA has only 998 bases instead of 999 bases.

Total bases present in RNA = 999

Bases left after deletion of 901st base in RNA

$$= 999 - 901 \\ = 98$$

Number of codon present in 98 = 33

(Approximately as three codons code for one amino acid).

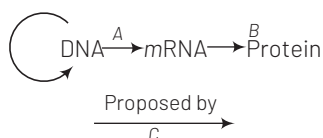
103 Which one of the following is the starter codon? [NEET 2016, Phase I]

- (a) UGA (b) UAA
(c) UAG (d) AUG

Ans. (d)

AUG is the start codon. It also codes for amino acid called methionine which is the first amino acid in a polypeptide chain. UAA, UAG and UGA are stop codons and are meant for termination of polypeptide chain during protein synthesis.

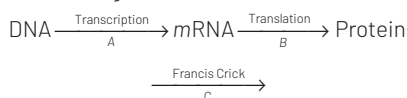
104 The diagram shows an important concept in the genetic implication of DNA. Fill in the blanks A to C. [NEET 2013]



- (a) A-transcription, B-replication, C-James Watson
(b) A-translation, B-transcription, C-Erwin Chargaff
(c) A-transcription, B-translation, C-Francis Crick
(d) A-translation, B-extension, C-Rosalind Franklin

Ans. (c)

Central dogma is



105 If one strand of DNA has the nitrogenous base sequence as ATCTG, what would be the complementary RNA strand sequence? [CBSE AIPMT 2012]

- (a) TTAGU (b) UAGAC
(c) AACTG (d) ATCGU

Ans. (b)

If one strand of DNA has the nitrogenous base sequence as ATCTG, the complementary sequence of mRNA will be UAGAC.

106 What is not true for genetic code? [CBSE AIPMT 2009]

- (a) A codon in mRNA is read in a non-contiguous fashion
(b) It is nearly universal
(c) It is degenerate
(d) It is unambiguous

Ans. (a)

The general features of genetic code are

- (i) The genetic code is written in linear form, using the ribonucleotide bases that compose mRNA molecule as letters.
(ii) Each word of codon consists of three letters, i.e., the codon is triplet.
(iii) The genetic code inside the cell medium is said to be non-ambiguous.
(iv) The code is degenerate, i.e. a given amino acid can be specified by more than one codons.
(v) The codon contains 'start' and 'stop' signals.
(vi) The code is said to be commaless.
(vii) The code is non-overlapping.

107 Which one of the following pairs of codons is correctly matched with their function or the signal for the particular amino acid? [CBSE AIPMT 2008]

- (a) GUU, GCU — Alanine
(b) UAG, UGA — Stop
(c) AUG, ACG — Start/methionine
(d) UUA, UCA — Leucine

Ans. (b)

The group of nucleotides that specifies one amino acid is a code word or codon. The nucleotides of mRNA are arranged as a linear sequence of codons, each codon consisting of three successive nitrogenous bases.

Three codons UAG, UAA and UGA are the termination codons. They do not code for any of the amino acids.

In most organisms AUG codon is the start or initiation codon, i.e. the polypeptide chain starts either with methionine or N-formylmethionine.

Leucine — UUA, UUG, CUU, CUC, CUA, CUG.

Alanine — GUC, GCC, GCA, GCG.

GUU — Valine

UCA — Serine.

108 One gene-one enzyme relationship was established for the first time in [CBSE AIPMT 2007]

- (a) *Neurospora crassa*
(b) *Salmonella typhimurium*
(c) *Escherichia coli*
(d) *Diplococcus pneumoniae*

Ans. (a)

One gene-one enzyme relationship was initially proposed by Beadle and Tatum

based on their experiments conducted on *Neurospora crassa*. They were awarded by Nobel Prize in 1958.

109 A sequential expression of a set of human genes occurs when a steroid molecule binds to the [CBSE AIPMT 2007]

- (a) transfer RNA (b) messenger RNA
(c) DNA sequence (d) ribosome

Ans. (c)

The steroid hormone receptor protein complex activate transcription of target gene by binding to sepecific DNA sequence.

110 One gene-one enzyme hypothesis was postulated by [CBSE AIPMT 2006]

- (a) R Franklin
(b) Hershey and Chase
(c) A Garrod
(d) Beadle and Tatum

Ans. (d)

'One gene-one enzyme' hypothesis was given by Beadle and Tatum [1948] which states that particular gene controls the synthesis of specific enzyme. Later, it was modified to 'one gene-one polypeptide hypothesis' by Yanofsky, et. al, [1965].

111 Amino acid sequence, in protein synthesis is decided by the sequence of [CBSE AIPMT 2006]

- (a) tRNA (b) mRNA
(c) cDNA (d) rRNA

Ans. (b)

In the process of protein synthesis, the messenger RNA (mRNA) is responsible for carrying the genetic code transcribed from DNA to specialised sites within the cell (called ribosomes) where the information is translated into protein. The sequence of amino acids in a particular protein is determined by the sequence of nucleotides in mRNA. Sequence of tRNA, cDNA or rRNA do not decide the amino acid sequence in protein synthesis.

112 After a mutation at genetic locus the character of an organism changes due to the change in [CBSE AIPMT 2004]

- (a) protein structure
(b) DNA replication
(c) protein synthesis pattern
(d) RNA transcription pattern

Ans. (a)

Normally, genetic information flows from DNA → mRNA → protein. Hence, any change in nucleotides due to the mutation, would result in change in the structure of protein/enzyme which might result in some change in the organism.

113 The following ratio is generally constant for a given species

[CBSE AIPMT 2004]

- (a) A + G/C + T
- (b) T + C/G + A
- (c) G + C/A + T
- (d) A + C/T + G

Ans. (c)

The base ratio A + T / G + C may vary from one species to another, but is constant for a given species. It is rarely equal to one and varies between 0.4 and 1.9.

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

[CBSE AIPMT 2003]

- (a) 61
- (b) 60
- (c) 20
- (d) 64

Ans. (a)

Out of 64 codons three (UAA, UAG, UGA) are chain terminating codons the translating mechanism is not able to read these codons and 61 codons are used to code all the 20 essential amino acids.

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

[CBSE AIPMT 2003]

- (a) A polypeptide of 49 amino acids will be formed
- (b) A polypeptide of 25 amino acids will be formed
- (c) A polypeptide of 24 amino acids will be formed
- (d) Two polypeptides of 24 and 25 amino acids will be formed

Ans. (c)

UAA is the 'stop' codon hence, polypeptide chain will not grow after 24th amino acid. In the absence of new initiating codon rest of codons will not be able to translate.

116 Degeneration of a genetic code is attributed to the

[CBSE AIPMT 2003]

- (a) entire codon
- (b) third member of a codon
- (c) first member of a codon
- (d) second member of a codon

Ans. (b)

It has been seen variously that one tRNA molecule codes for more than one amino acid molecules. This is possible due to the improper pairing of third codon with the first anticodon of tRNA.

117 During translation initiation in prokaryotes, a GTP molecule is needed in

[CBSE AIPMT 2003]

- (a) association of 30S, mRNA with formyl met tRNA
- (b) association of 50S subunit of ribosome with initiation complex
- (c) formation of formyl met tRNA
- (d) binding of 30S subunit of ribosome with mRNA

Ans. (a)

During the process of translation an initial complex is formed between mRNA, 30S ribosomal sub-unit and methionyl tRNA. This complex is formed due to the association of IF_1 , IF_2 , IF_3 initiation factors and GTP molecule.

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

[CBSE AIPMT 2003]

- (a) UGU—Leucine
- (b) UAC—Tyrosine
- (c) UCG—Start
- (d) UUU—Stop

Ans. (b)

UGU	→	Cystine
UAC	→	Tyrosine
UCG	→	Serine
UUU	→	Phenylalanine
UAG, UGA, UAA	→	Stop codons
UAG	→	Start codon.

119 'Signal hypothesis' for the biosynthesis of secretory type of proteins was proposed by

[CBSE AIPMT 2000]

- (a) Camillo Golgi
- (b) Blobel and Sabatini
- (c) Baltimore
- (d) Sheeler and Bianchi

Ans. (b)

A variety of proteins are synthesised on ribosomes. However, these have different destinations. David Sabatini and G. Blobel proposed 'signal sequence' hypothesis according to which a short amino acid sequence at the amino terminus of a newly synthesised polypeptide directs a protein to its appropriate sequence.

120 The transfer RNA molecule in 3D appears

[CBSE AIPMT 2000]

- (a) L-shaped
- (b) E-shaped
- (c) Y-shaped
- (d) S-shaped

Ans. (a)

Kim *et al.*, (1973) suggested L shaped model of tRNA by X-ray diffraction while studying phenyl alanine tRNA of yeast. L shape structure of tRNA is a 3-dimensional (3D) structure of 20 Å thickness.

121 Which is not involved in protein synthesis?

[CBSE AIPMT 1994]

- (a) Transcription
- (b) Initiation
- (c) Elongation
- (d) Termination

Ans. (a)

Transcription is the synthesis of RNA on DNA template. It is not involved in protein synthesis (translation).

122 In DNA when AGCT occurs, their association is as per which of the following pair?

[CBSE AIPMT 1999]

- (a) ACGT
- (b) AGCT
- (c) ATGC
- (d) All of these

Ans. (c)

In DNA AGCT is associated with pair ATGC because in a DNA molecule, the purine adenine in either chain is associated with the pyrimidine thymidine on the other. Similarly, purine guanine in either chain is associated with pyrimidine cytosine on the other.

123 Protein synthesis in an animal cell takes place

[CBSE AIPMT 1997]

- (a) only in the cytoplasm
- (b) in the nucleolus as well as in the cytoplasm
- (c) in the cytoplasm as well as in mitochondria
- (d) only on ribosomes attached to a nucleus

Ans. (c)

Protein synthesis is a complex process it essentially involves DNA for the synthesis of mRNA (transcription) which contains information for the synthesis of proteins (translation). The process of translation takes place on ribosomes which are found in cytoplasm (in attached form on ER) and in mitochondria (in the free form).

124 The RNA that picks up specific amino acid from amino acid pool in the cytoplasm to ribosome during protein synthesis is called

[CBSE AIPMT 1997]

- (a) mRNA (b) tRNA
(c) rRNA (d) RNA

Ans. (b)

tRNA (soluble RNA = sRNA) is a 70-75 nucleotide long molecule. 80% of this RNA is double helical, one end of this molecule has G and other C-C-A sequences.

The clover leaf model [2D] of tRNA was given by R Holley [1968] and Kim *et al.*, [1973] suggested 'L' shaped model (3D) of tRNA by X-ray diffraction while studying phenyl alanine tRNA of yeast.

Each amino acid had its own specific tRNA molecule which transfers it from cytoplasm to the ribosome.

125 The codons causing chain termination are [CBSE AIPMT 1997]

- (a) TAG, TAA, TGA (b) GAT, AAT, AGT
(c) AGT, TAG, UGA (d) UAA, UAG, UGA

Ans. (d)

UAA, UAG and UGA act as stop codons (terminator codons) because these are not translated into amino acid. UAA is called ochre, UAG as amber and UGA as opal.

126 The translation termination triplet is [CBSE AIPMT 1996]

- (a) UAU (b) UAA
(c) UAC (d) UGC

Ans. (b)

Termination codons are three in number they are UAA (ochre) UAG (amber) and UGA (opal).

127 If the sequence of bases in DNA is ATTCGATG, then the sequence of bases in its transcript will be [CBSE AIPMT 1995]

- (a) CAUCGAAU (b) UAAGCUAC
(c) GUAGCUUA (d) AUUCGAUG

Ans. (b)

Transcription is the process of synthesis of mRNA on DNA template by the complementary bases. As thymine is replaced by uracil in RNA so, the sequence of bases will be UAAGCUAC.

128 Anticodon is an unpaired triplet of bases in an exposed position of [CBSE AIPMT 1995]

- (a) mRNA (b) rRNA
(c) tRNA (d) sRNA

Ans. (c)

tRNA possess anticodon stem which includes five paired bases. The anticodon loop consists of 7 unpaired bases. The third, fourth and fifth of which form anticodon. This anticodon permits temporary complementary pairing with three bases on mRNA.

129 DNA template sequence of CTGATAGC is transcribed over mRNA as [CBSE AIPMT 1994]

- (a) GUCTUTCG
(b) GACUAUCG
(c) GAUTATUG
(d) UACTATCU

Ans. (b)

During transcription complementary mRNA is formed on DNA template in which T is replaced by U. So, the sequence will be GACUAUCG.

130 The number of base substitution possible in amino acid codons is [CBSE AIPMT 1994]

- (a) 261 (b) 264
(c) 535 (d) 549

Ans. (d)

There are 64 codons out of which 61 codes for amino acid. Each codon possess 3 bases which can undergo transition and transversion, so the number of base substitution possible in amino acid codons is $61 \times 3^2 = 549$.

131 Initiation codon of protein synthesis (in eukaryotes) is [CBSE AIPMT 1993, 94, 99, 2000]

- (a) GUA (b) GCA
(c) CCA (d) AUG

Ans. (d)

At 5' end of mRNA where protein synthesis starts codon AUG is present. So, AUG is called as initiating or starting codon or start signal.

132 The process of translation is [CBSE AIPMT 1993]

- (a) ribosome synthesis
(b) protein synthesis
(c) DNA synthesis
(d) RNA synthesis

Ans. (b)

Translation is the process of protein synthesis in which the triplet base sequences of mRNA molecules is converted into a specific sequences of amino acids in a polypeptide chain, this occurs on ribosomes.

133 Because most of the amino acids are represented by more than one codon, the genetic code is [CBSE AIPMT 1993, 2002]

- (a) overlapping (b) wobbling
(c) degenerate (d) generate

Ans. (c)

Degeneracy means lack of specificity. Presence of more than one meaningful codons for an amino acid is called degeneracy, e.g. methionine and tryptophan has single code for each. The maximum number of codons for an amino acid is six, e.g. serine, arginine and leucine. Degeneracy provides a protection against mutation.

134 Khorana first deciphered the triplet codons of [CBSE AIPMT 1992]

- (a) serine and isoleucine
(b) threonine and histidine
(c) tyrosine and tryptophan
(d) phenylalanine and methionine

Ans. (b)

Dr. Hargobind Khorana deciphered first triplet codon of threonine and histidine.

135 In the genetic dictionary, there are 64 codons as [CBSE AIPMT 1990]

- (a) 64 amino acids are to be coded
(b) 64 types of tRNAs are present
(c) there are 44 non-sense codons and 20 sense codons
(d) genetic code is triplet

Ans. (d)

It has been found that a sequence of 3 consecutive bases in a DNA molecule codes for one specific amino acid. So, genetic code is a triplet code and there are 64 triplets which are called codons ($4 \times 4 \times 4 = 64$) of nitrogen bases for protein synthesis.

136 Genetic code consists of
[CBSE AIPMT 1988]

- (a) adenine and guanine
- (b) cytosine and uracil
- (c) cytosine and guanine
- (d) All of the above

Ans. (d)

The sequence of nitrogen bases on the mRNA which store information for linking the amino acids in a definite sequence during synthesis of proteins is called **genetic code**. These nitrogen bases include adenine, guanine, cytosine and uracil

TOPIC 3

Regulation of Gene Expression

137 In the process of transcription in eukaryotes, the RNA polymerase I transcribes [NEET (Odisha) 2019]

- (a) mRNA with additional processing, capping and tailing
- (b) tRNA, 5 srRNA and snRNAs
- (c) rRNAs-28 S, 18 S and 5.8 S
- (d) precursor of mRNA, hnRNA

Ans. (c)

In the process of transcription (i.e. copying of genetic information from one strand of the DNA into RNA) in eukaryotes, the RNA polymerase I transcribes rRNA - 28S, 18S and 5.8S. On the other hand, tRNA, 5srRNA and snRNAs are transcribed by RNA polymerase III. RNA polymerase II transcribes precursor of mRNA, hnRNA.

138 Match the following genes of the Lac operon with their respective products [NEET (National) 2019]

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

Select the correct option.

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

Ans. (b)

(A)-(iii), (B)-(i), (C)-(iv), (D)-(ii)

In a Lac operon, *i* gene is a regulator gene which produces a repressor that

binds to operator gene and stops its functioning. *z*, *y* and *a* are the three structural genes in the lac operon of *E. coli*. *z* gene produces β -galactosidase for hydrolysing galactoside. *y* gene produces permease for allowing the entry of lactose from outside.

A gene produces transacetylase which helps to transfer an acetyl group from acetyl Co-A to beta-galactoside.

139 Select the correct match.
[NEET 2018]

- (a) Matthew Meselson : *Pisum sativum* and F. Stahl
- (b) Alfred Hershey and : TMV Martha Chase
- (c) Alec Jeffreys : *Streptococcus pneumoniae*
- (d) Francois Jacob : Lac operon and Jacques Monod

Ans. (d)

Jacob and Monod (1916) discovered the **lac operon**. An operon is a part of genetic material or DNA which acts as a single regulated unit. It possesses one or more structural genes, an operator gene, a promoter gene, a regulator gene, a repressor gene and an inducer or corepressor.

Matthew Meselson and F Stahl discovered the semi-conservative mode of DNA replication in *E. coli*. **Alfred Hershey and Martha Chase** use T_2 Bacteriophage in their experiments to infect *E. coli* and proved that DNA is the genetic material. **Alec Jeffreys** (1984) invented the DNA fingerprinting technique. This technique determines nucleotide sequences of certain areas of DNA which are unique to each individual.

140 All of the following are parts of an operon except [NEET 2018]

- (a) an enhancer
- (b) structural genes
- (c) an operator
- (d) a promoter

Ans. (a)

Except enhancer, all the given components are parts of an operon. Enhancer sequences are present in eukaryotes that, when bound by specific proteins or transcription factors, enhance the transcription of an associated gene.

On the other hand, operon is a regulatory unit of DNA containing a cluster of genes in prokaryotes.

141 Which of the following is required as inducer(s) for the expression of lac operon? [NEET 2016, Phase I]

- (a) galactose
- (b) lactose
- (c) lactose and galactose
- (d) glucose

Ans. (b)

Lac operon is an inducible operon. Lactose is the substrate for the enzyme β -galactosidase and it also regulates switching on and off of the operon. Hence, it is termed as inducer.

142 Which one of the following is wrongly matched? [CBSE AIPMT 2014]

- (a) Transcription - Writing information from DNA to tRNA
- (b) Translation - Using information in mRNA to make protein
- (c) Repressor protein - Binds to operator to stop enzyme synthesis
- (d) Operon - Structural genes, operator and promoter

Ans. (a)

Statement (a) is wrongly matched because transcription is a process of mRNA synthesis from a DNA template. It involves three main events, i.e. initiation (binding of RNA polymerase to as DNA), elongation (development of a short stretch of DNA) and termination (recognition of the transcription termination sequence and the release of RNA polymerase).

143 Which enzyme/s will be produced in a cell in which there is a non-sense mutation in the lac Y-gene? [NEET 2013]

- (a) β -galactosidase
- (b) Lactose permease
- (c) Transacetylase
- (d) Lactose permease and transacetylase

Ans. (a)

β -galactosidase is a structural gene, which carry codes for the synthesis of protein. Mutation in the lac Y gene of *E. coli* needs residues of cytoplasmic enzyme β -galactosidase. Lactose permease is a membrane protein, which is a major facilitator superfamily. Transacetylase is an enzyme transferring acetyl groups from one compound to another.

144 Select the two statements out of the four (I-IV) given below about *lac* operon.

- I. Glucose or galactose may bind with the repressor and inactivate it.
- II. In the absence of lactose, the repressor binds with the operator region.
- III. The *z*-gene codes for permease.
- IV. This was elucidated by Francois Jacob and Jacques Monod.

The correct statements are
[CBSE AIPMT 2010]

- (a) I and III (b) I and III
(c) II and IV (d) I and II

Ans. (c)

Statement II and IV are true about *lac* operon. In prokaryotes, a hypothesis was given in 1961 to explain the protein synthesis regulation. This hypothesis was given by F Jacob and J Monod and for this they were awarded Nobel Prize in 1965, the hypothesis was known by the name of Operon Model.

The operator gene is the segment of DNA, which exercise a control over transcriptions. In the absence of lactose, the repressor binds with the operator gene.

145 Differentiation of organs and tissues in a developing organism is associated with [CBSE AIPMT 2007]

- (a) developmental mutations
(b) differential expression of genes
(c) lethal mutations
(d) deletion of genes

Ans. (b)

Differentiation of organs and tissues in a developing organism is associated with differential expression of genes. In regulation of gene expression the chromosomal proteins play important role.

The chromosomal proteins are of two types, histones and non-histones. The regulation of gene expression involves an interaction between histones and non-histones.

146 What does '*lac*' refer to in what we call the *lac* operon?
[CBSE AIPMT 2003]

- (a) Lac insect
(b) The number, 1,00,000
(c) Lactose
(d) Lactase

Ans. (c)

Lac operon refers to the DNA sequence in the genome of the bacterium *E. coli* encoding enzymes involved in lactose uptake and metabolism.

147 In *E. coli*, during lactose metabolism repressor binds to
[CBSE AIPMT 2002]

- (a) regulator gene (b) operator gene
(c) structural gene (d) promoter gene

Ans. (b)

In *Lac* operon, the repressor protein combines with the operator gene to express its functioning.

148 Jacob and Monod studied lactose metabolism in *E. coli* and proposed Operon concept. Operon concept applicable for [CBSE AIPMT 2002]

- (a) all prokaryotes
(b) all prokaryotes and some eukaryotes
(c) all prokaryotes and all eukaryotes
(d) all prokaryotes and some protozoans

Ans. (b)

Jacob and Monod's operon concept is basically a theory of gene expression in prokaryotes— though it is of some value in the explanation of eukaryotic gene expression.

149 In negative operon
[CBSE AIPMT 2001]

- (a) co-repressor binds with repressor
(b) co-repressor does not bind with repressor
(c) co-repressor binds with inducer
(d) cAMP has negative effect on *lac* operon

Ans. (a)

In negative operon co-repressor binds with repressor to form repressor co-repressor complex which further binds with operator. Since, the product of the regulator (the repressor) acts by shutting off the transcription of structural genes, it is referred to as a negative control system.

150 Genes that are involved in turning on or off the transcription of a set of structural genes are called
[CBSE AIPMT 1998]

- (a) polymorphic genes
(b) operator genes
(c) reductant genes
(d) regulatory genes

Ans. (d)

The switching on and off of an operator is controlled by repressor protein which is coded by the regulator gene R.

151 The wild type *E. coli* cells are growing in normal medium with glucose. They are transferred to a medium containing only lactose as sugar. Which of the following changes takes place?
[CBSE AIPMT 1995]

- (a) The *lac* operon is repressed
(b) All operons are induced
(c) The *lac* operon is induced
(d) *E. coli* cells stop dividing

Ans. (c)

Inducible genes are the genes which remain inactive or repressed in a cell and can be activated when a certain substrate is to be metabolised. It has been seen when lactose is added to the medium of *E. coli* the operon is induced and synthesis of enzymes required for degradation of lactose to glucose and galactose starts.

152 In *Escherichia coli lac* Operon is induced by [CBSE AIPMT 1994]

- (a) lactose
(b) promoter gene
(c) β -galactosidase
(d) I-gene

Ans. (a)

In *E. coli lac* operon is induced by adding lactose sugar to the culture.

153 Binding of specific protein on regulatory DNA sequence can be studied by means of
[CBSE AIPMT 1993]

- (a) ultra centrifugation
(b) electron microscope
(c) light microscope
(d) X-rays crystallography

Ans. (d)

X-ray crystallography is an important technique in molecular biology to analyse the structure and orientation of molecules. It is used to find out 3-D positions of atoms in the molecules of DNA, RNA and proteins, binding of specific protein on regulatory DNA sequences, 3-D structure of haemoglobin, insulin, DNA, proteins, collagen fibre, muscle and actin protein.

TOPIC 4

Human Genome Project and DNA Fingerprinting

154 DNA fingerprinting involves identifying differences in some specific regions in DNA sequence, called as [NEET 2021]

- (a) satellite DNA
- (b) repetitive DNA
- (c) single nucleotides
- (d) polymorphic DNA

Ans. (b)

Repetitive DNA are DNA sequences that are repeated in the genome. These sequences do not code for protein. One class termed highly repetitive DNA consists of short sequences, 5-100 nucleotides, repeated thousands of times in a single stretch and includes satellite DNA.

Other options can be explained as:

The density of DNA is a function of its base and sequence, and satellite DNA with its highly repetitive DNA has a reduced or a characteristic density compared to the rest of the genome.

Single nucleotide polymorphisms, frequently called SNPs (pronounced 'snips'), are the most common type of genetic variation among people. Each SNP represents a difference in a single DNA building block, called a nucleotide. DNA polymorphisms are the different DNA sequences among individuals, groups, or populations. Polymorphism at the DNA level includes a wide range of variations from single base pair change, many base pairs, and repeated sequences. DNA polymorphisms are endless, and more discoveries continue at a rapid rate. These are called as polymorphic DNA.

155 DNA strands on a gel stained with ethidium bromide when viewed under UV radiation, appear as [NEET 2021]

- (a) yellow bands
- (b) bright orange bands
- (c) dark red bands
- (d) bright blue bands

Ans. (b)

To make the DNA visible in the gel, ethidium bromide is added to the gel solution and the buffer. This positively charged polycyclic aromatic compound

binds to DNA by inserting itself between the basepairs (intercalation). The DNA fragments when exposed to ultraviolet light appear as orange colour bands, due to the large increase in fluorescence of the ethidium bromide upon binding to the DNA.

156 Which is the basis of genetic mapping of human genome as well as DNA fingerprinting? [NEET (Oct.) 2020]

- (a) Polymorphism in DNA sequence
- (b) Single nucleotide polymorphism
- (c) Polymorphism in *hnRNA* sequence
- (d) Polymorphism in RNA sequence

Ans. (a)

Polymorphism in DNA sequence is the basis of genetic mapping of human genome as well as DNA fingerprinting. Polymorphism simply means variation at genetic level which arises due to mutations.

157 Which of the following is not required for any of the techniques of DNA fingerprinting available at present? [NEET 2016, Phase I]

- (a) Zinc finger analysis
- (b) Restriction enzymes
- (c) DNA-DNA hybridisation
- (d) Polymerase chain reaction

Ans. (a)

A zinc finger is a small protein structural motif that is characterised by the coordination of one or more Zn ions in order to stabilise the folds.

158 Satellite DNA is important because it [CBSE AIPMT 2015]

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

Ans. (b)

Satellite DNA forms the minor peak after centrifugation of DNA. These are repetitive DNA sequences that do not code for any protein. They show high degree of polymorphism and heritable from parents to children, thus form the basis of DNA fingerprinting.

159 DNA fingerprinting refers to [CBSE AIPMT 2004]

- (a) molecular analysis or profiles of DNA samples
- (b) analysis of DNA samples using imprinting device
- (c) techniques used for molecular analysis of different specimens of DNA
- (d) techniques used for identification of finger-prints of individuals

Ans. (a)

DNA fingerprinting refers to molecular analysis of DNA samples. Alec Jeffreys [1985, 86] discovered this technique for the first time.

160 Nucleus of a donor embryonal cell/somatic cell is transferred to an enucleated egg cell. Then after the formation of organism, what shall be true? [CBSE AIPMT 2002]

- (a) Organism will have extra-nuclear genes of the donor cell
- (b) Organism will have extra-nuclear genes of recipient cell
- (c) Organism will have extra-nuclear genes of both donor and recipient cell
- (d) Organism will have nuclear genes of recipient cell

Ans. (b)

The organism will have extranuclear genes of recipient cell. Since, the recipient cell has already been enucleated (its nucleus is removed), the organism developing from it would have the nuclear genes of donor cell.

161 The basis for DNA fingerprinting is [CBSE AIPMT 1996]

- (a) occurrence of Restriction Fragment Length Polymorphism (RFLP)
- (b) phenotypic differences between individuals
- (c) availability of cloned DNA
- (d) knowledge of human karyotype

Ans. (a)

The basis of DNA fingerprinting is the occurrence of restriction fragment length polymorphism which are distributed throughout human genome. DNA fingerprinting was developed by a British geneticist Prof. Alec Jeffreys in 1984.

The chromosomes of every human cell contain short, highly repeated 15 nucleotide segments called 'mini-satellites' or variable number tandem repeats scattered through their DNA.