CHAPTER › 06

Molecular Basis of Inheritance

NEET KEY NOTES

- **Mendel** suggested that there are some factors or genes which help to maintain the phenotypes and genotypes of organisms for generation after generation.
- It was later established that DNA (Deoxyribonucleic Acid) is the genetic material in majority of organisms, while RNA acts as the genetic material in some viruses, but has additional roles as well. RNA functions as adapter, structural and in some cases as catalytic molecule.

DNA (Deoxyribonucleic Acid)

- It is a long polymer of deoxyribonucleotides. The length of DNA is usually defined as number of nucleotides (or a pair of nucleotide referred to as base pairs) present in it.
- For example, a bacteriophage known as $\phi \times 174$ has 5386 nucleotides, bacteriophage lambda has 48502 bp, *Escherichia coli* has 4.6×20^6 bp and haploid content of human DNA is 3.3×10^9 bp.

Discoveries Related to Structure of DNA

- **Friedrich Miescher** in 1869, first identified DNA as an acidic substance present in the nucleus and named it as 'nuclein'.
- **James Watson** and **Francis Crick**, proposed a very simple **double helix model** for the structure of DNA in 1953 based on X-ray diffraction data.
- **Erwin Chargaff** proposed that for a double-stranded DNA, the ratio between adenine and thymine and guanine and cytosine are constant and equals one.

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

Structure of a Polynucleotide Chain

A nucleotide is composed of a nitrogenous base, pentose sugar and a phosphate group.

1. **A nitrogenous base** It is the nitrogen containing organic molecule having similar physical properties of a base.
   - There are two types of nitrogenous bases
     - **Purines** Adenine and Guanine.
     - **Pyrimidines** Cytosine, Uracil and Thymine.
   - Thymine is present in DNA, while uracil is present in RNA in place of thymine (5-methyl uracil, another name for thymine).
2. **A pentose sugar** Two types of sugars are present
   - **Ribose** (in case of RNA)
   - **Deoxyribose** (in case of DNA)
3. **A phosphate group** It is in the form of H_3PO_4.
   - **Nucleoside and nucleotide** A nucleoside is formed when a nitrogenous base is linked to a pentose sugar through N-glycosidic linkage.
   - **Nucleotides** are the phosphoric esters of nucleosides.
     - Nucleotides are joined by 3′–5′ phosphodiester bonds to form a dinucleotide.
     - Alternate deoxyribose and phosphate residues joins to form the polynucleotide chain.

Double Helix Structure of DNA

- DNA is made up of two polynucleotide chains, where the backbone is constituted by sugar, phosphate and the bases project inside.
- The two chains have anti-parallel polarity, i.e. 5′→ 3′ for one, 3′→ 5′ for another.

- The bases in two strands are paired through hydrogen bond (H—bonds) forming base pairs (bp). Adenine forms two hydrogen bonds with thymine and *vice-versa*. Guanine bonds with cytosine by three H—bonds and *vice-versa*. Thus, a purine always comes opposite to a pyrimidine forming a uniform distance between the two strands.
- The two chains are coiled in a right-handed fashion. The pitch of the helix is 3.4 nm and there are roughly 10 bp in each turn. Due to this, the distance between a base pair in a helix is about 0.34 nm.
- The plane of one base pair stacks over the other in double helix. This confers stability to the helical structure in addition to H—bonds.

Central Dogma

- In 1957, **Francis Crick** proposed the central dogma in molecular biology. According to this, the genetic information flows from DNA → RNA → Protein.

Central dogma

- The flow of information can be in reverse direction also, i.e. from RNA to DNA in some viruses, such as TMV.

Packaging of DNA Helix

- In **prokaryotes**, such as *E. coli*, the DNA is not scattered throughout the cell even though they do not have a defined nucleus. DNA (being negatively charged) is held with some proteins (that are positively charged) in a region termed as nucleoid. The DNA in nucleoid is organised in large loops held by proteins.
- In **eukaryotic cells**, there is a set of positively charged proteins called **histones**. Histones are rich in basic amino acid residuces lysine and arginine. These are organised to form a unit of eight molecules called **histone octamer**.
- The negatively charged DNA is wrapped around the positively charged histone octamer to form a structure called **nucleosome**. A typical nucleosome contains 200 bp of DNA helix.
- Nucleosome constitutes the repeating unit of a structure in the nucleus called **chromatin**, thread-like stained (coloured) bodies seen in nucleus.
- The 'beads-on-string' structure of nucleosome in chromatin are packaged to form chromatin fibres which further coil and condense at metaphase stage of cell division to form the **chromosomes**. The packaging of chromatin at higher level requires additional set of proteins that collectively are referred to as **Non-Histone Chromosomal** (NHC) **proteins**.
- Some regions of chromatin which are loosely packed (stain light) are called **euchromatin** (active chromatin). In some regions, chromatin is densely packed (stain dark), it is called **heterochromatin** (inactive chromatin).

The Search for Genetic Material

The experiments given below established that DNA is the genetic material in majority of organisms.

Transforming Principle

- **Frederick Griffith** (1928) carried out a series of experiments with *Streptococcus pneumoniae* (bacterium causing pneumonia).
- He used two strains of this bacterium, i.e. one forming smooth colonies with capsule (S-type) and the other forming rough colonies without capsule (R-type) and gave the following observations

S-strain $\xrightarrow{\text{Injection}}$ Mice ⟶ Mice died

R-strain $\xrightarrow{\text{Injection}}$ Mice ⟶ Mice lived

S-strain $\xrightarrow{\text{Injection}}$ Mice ⟶ Mice live
(Heat-killed)

S-strain $\xrightarrow{\text{Injection}}$ Mice ⟶ Mice die
(Heat-killed)
+
R-strain (Live)

- He concluded that the R-strain bacteria had somehow been transformed by the heat-killed S-strain bacteria, which must be due to the transfer of the genetic material (transforming principle).

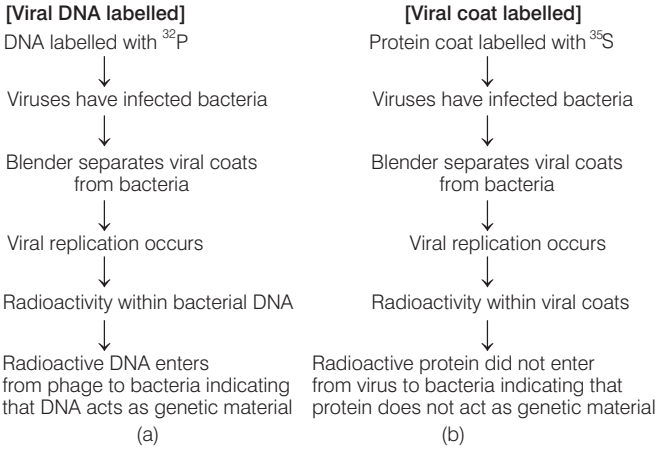
Biochemical Characterisation of Transforming Principle

- **Oswald Avery**, **Colin MacLeod** and **Maclyn McCarty** (1933-44) worked to determine the biochemical nature of 'transforming principle' in Griffith's experiment in an *in vitro* system.
- From the heat-killed S-cells, they purified biochemicals (proteins, DNA, RNA, etc.) to observe, which biochemical could transform live R-cells into S-cells.
- They discovered that DNA alone from heat-killed S-type bacteria caused the transformation of non-virulent R-type bacteria into virulent S-type bacteria.
- Protein-digesting enzymes (proteases) and RNA digesting enzymes (RNases) did not cause this transformation. This proved that the 'transforming substance' was neither protein nor RNA.
- DNA-digesting enzyme (DNase) caused inhibition of transformation, which suggested that DNA caused the transformation. Thus, it was concluded that DNA is the hereditary material.

The Genetic Material is DNA

- **Alfred Hershey** and **Martha Chase** gave another definitive evidence for DNA as genetic material in 1952.
- In their work, they described that the phage DNA enters the host cell and works as a genetic material.

- Outline of their experiment is given below



The Hershey and Chase experiment

Properties of Genetic Material (DNA *v/s* RNA)

- **Genetic material** is the substance which controls the inheritance of traits from one generation to next.
- Following are the criteria that a molecule must fulfil to act as a genetic material
  - It should be able to replicate itself.
  - It should be stable both chemically and structurally.
  - It should provide the scope for slow changes (mutation), which are required for evolution.
  - It should be able to express itself in the form of 'Mendelian characters'.

Differences between DNA and RNA

DNA	RNA
It is double-stranded with exception of some viruses.	It is generally single-stranded.
It is the genetic material in all living organisms.	It is the genetic material in some viruses only.
The sugar is deoxyribose.	The sugar is ribose.
Nitrogenous bases present are adenine, guanine, thymine and cytosine.	Nitrogenous bases present are adenine, guanine, cytosine and uracil.
It is chemically less reactive and structurally more stable.	It is chemically more reactive and structurally less stable.
It usually occurs inside the nucleus and in some cell organelles.	Small amount of RNA occurs inside the nucleus. Most of it is found in the cytoplasm.

RNA World

- **Ribonucleic Acid (**RNA) is said to be the first genetic material.
- It is evident through various scientific researches that essential life processes such as metabolism, translation and splicing, etc., evolved around, RNA. RNA used to act as genetic material as well as a catalyst. But RNA being a catalyst was reactive and hence unstable.
- Therefore, DNA has evolved from RNA with chemical modifications which make it more stable.
- There are following three types of RNA, i.e. **messenger RNA** (*m*RNA), which provides the template for transcription, **transfer RNA** (*t*RNA) which brings amino acids and reads the genetic code and **ribosomal RNA** (*r*RNA), which plays structural and catalytic role during translation.

DNA Replication

- Scheme for replication of DNA termed as **semiconservative DNA replication** was proposed by **Watson** and **Crick** (1953). According to this, the two strands would separate and act as a template for the synthesis of new complementary strands. Thus, each DNA molecule formed would have one parental and one newly synthesised strand.

The Experimental Proof

Matthew Meselson and **Franklin Stahl** (in 1958) conducted the following experiment with *Escherichia coli* to prove that DNA replicates semiconservatively.

- They grew many generations of *E. coli* in a medium that contained $^{15}NH_4Cl$ (^{15}N is the heavy isotope of nitrogen) as the only source of nitrogen.
- They observed that ^{15}N was incorporated into the newly synthesised strand of DNA. This heavy DNA could be distinguished from the normal DNA by centrifugation in a cesium chloride (CsCl) density gradient.
- DNA from such bacterium had an intermediate density (hybrid), one generation after the transfer from ^{15}N to ^{14}N. After another generation, it was composed of equal amount of hybrid DNA and light DNA.
- Similar experiments on '*Vicia faba*' (faba beans) were conducted by **Taylor** and colleagues in 1958, involving the use of radioactive thymidine. The results were that the DNA in chromosomes also replicate semiconservatively.

The Machinery and the Enzymes

The process of replication requires a set of catalysts (enzymes) which are given below

- **DNA-dependent DNA polymerase** It is the main enzyme which uses a DNA template to catalyse the polymerisation of deoxynucleotides.
  These enzymes are highly efficient and also help in removing mismatched nucleotides by a mechanism called **proof reading**.
- **Helicase** This enzyme unwinds the DNA strand, i.e. separates the two strands from one point, for the formation of a **replication fork**.

- **Topoisomerase** The unwinding of DNA creates a tension in the DNA strands, which gets released by the enzyme topoisomerase.
- **DNA ligase** It facilitates the joining of DNA strands together by catalysing the formation of phosphodiester bond. It also repairs single strand breaks in duplex DNA.

Process of DNA Replication

- Replication is an energy expensive process, **deoxyribonucleoside Triphosphates** (*d*NTPs) serve the dual purpose of acting as a substrate and providing energy (from two terminal phosphates).
- In a long DNA molecule, replication takes place within a small opening of the DNA helix, known as **replication fork**.
- DNA-dependent DNA polymerases catalyse polymerisation only in one direction, i.e. 5′→3′.
- Due to this, on one strand called the **leading strand** with polarity 3′→5′, replication is **continuous**. While on the other strand called the **lagging strand** with polarity 5′ → 3′ replication is **discontinuous**, i.e. in small fragments called **Okazaki fragments**. The fragments synthesised are joined by DNA ligase.
- Replication begins at a definite region in a *E. coli*, DNA molecule known as **origin of replication** *(ori)*, which has recognition site for DNA polymerase and also provides site for attachment of **RNA primer**.

Transcription

It is the process of copying genetic information from one strand of the DNA into RNA. This process is governed by the principle of complementarity, except adenosine now forms base pair with uracil instead of thymine.

Transcription Unit

- A transcription unit of DNA is defined primarily by three regions in the DNA
  - A promoter
  - The structural gene
  - A terminator
- The enzyme **DNA-dependent RNA polymerase** catalyses the polymerisation in only one direction (i.e. 5′→ 3′ direction).
- The strand with 3′ → 5′ polarity is known as the **template strand**. The strand with 5′ → 3′ polarity and same sequence as RNA (except thymine at the place of uracil) displaced during transcription, is known as **coding strand**.
- A **promoter** is a DNA sequence that provides binding site for RNA polymerase. It is located at 5′ end (upstream) of the structural gene and its presence defines the template and coding strands.
- The **structural gene** in a transcription unit is flanked by the promoter and terminator.
- A **terminator** is located towards the 3′ end (downstream) of the coding strand. It usually defines the end of transcription.

Transcription Unit and The Gene

- **Gene** is the functional unit of inheritance. The DNA sequence coding for *t*RNA or *r*RNA molecule also defines a gene.
- **Cistron** is the segment of DNA which codes for a polypeptide.
- In a transcription unit, the structural gene could be
  - **Monocistronic** (mostly in eukaryotes).
  - **Polycistronic** (mostly in bacteria or prokaryotes).
- The monocistronic structural genes in eukaryotes have interrupted coding sequences. They are of two types
  - **Exons** are the coding sequences or expressed sequences that appear in mature or processed RNA.
  - **Introns** are the intervening sequences which do not appear in mature or processed RNA. These only interrupt exons. The **split gene**, i.e. gene with both exons and introns is a characteristic of eukaryotic DNA.
- The **promoter** and **regulatory sequences** of a structural gene also affect the inheritance of a character. Hence, the regulatory sequences are sometimes loosely defined as **regulatory genes**.

Transcription in Prokaryotes

- **DNA-dependent RNA polymerase** is the single enzyme that catalyses transcription of all types of bacterial RNA, and takes place in the following three steps
  - **Initiation** RNA polymerase binds to promoter and initiates transcription by associating transiently with **initiation factor (σ).**
  - **Elongation** Chain elongation proceeds in the 5′→ 3′ direction and the **transcription bubble** travels with RNA polymerase. The RNA polymerase after initiation of transcription loses the σ factor, but continues the polymerisation of ribonucleotides to form RNA.
  - **Termination** When RNA polymerase reaches the terminator region of DNA, which is GC rich and has a hairpin-like structure, the nascent RNA separates and the RNA polymerase falls off resulting in termination of transcription.

Transcription in Eukaryotes

The process of transcription in eukaryotes is similar to that in prokaryotes. Structural genes are monocistronic in eukaryotes. Two additional complexities are present in eukaryotes as given below

- The first complexity is that there are atleast three RNA polymerases in nucleus in addition to RNA polymerase found in organelles and these are
  - **RNA polymerase-I** transcribes ***r*RNAs** (28S, 18S, 5.8S).

- **RNA polymerase-II** transcribes precursor of *m*RNA, which is called **heterogeneous nuclear RNA** (*hn*RNA).
- **RNA polymerase-III** transcribes *t*RNA, **5*sr*RNA** (small ribosomal RNA) and ***sn*RNAs** (small nuclear RNAs).

- The second complexity is that the primary transcript contains both exons and introns. Thus, the process of **splicing** is performed to remove the **introns** and join the **exons** in a proper order to allow translation.
- The RNA formed is called *hn*RNA, which undergoes additional processing as follows
  - **Capping** In capping, methyl guanosine triphosphate, an unusual nucleotide is added to the 5′ end of *hn*RNA.
  - **Tailing** In tailing, adenylate residues are added at 3′ end in a template independent manner.
- The fully processed *hn*RNA, now called ***m*RNA**, gets transported out of the nucleus for translation.

Genetic Code

- It is the relationship between the sequence of nucleotides on *m*RNA and the sequence of amino acids in the polypeptide.
- Important features of genetic code include
  - The codon is triplet. 61 codons code for all amino acids and 3 codons do not code for any amino acids, hence, they function as stop codons.
  - Some amino acids are coded by more than one codon hence, the code is **degenerate**.
  - Genetic code is unambiguous and specific, i.e. one codon codes for only one amino acid and is read in a contiguous fashion without any punctuation marks.
  - The genetic code is nearly **universal**, i.e. one codon codes for the same amino acid in all organisms.
  - AUG codon has dual function, i.e. it codes for the amino acid methionine (*met*) and also acts as an **initiation codon**.
  - Three codons function as **stop codon** or **non-sense codons**, which are **UAA** (ochre), **UGA** (amber), **UAG** (opal).

Mutations and Genetic Code

The sudden inheritable change in the genetic material is defined as **mutation**. These include

- **Point mutation** is mutation in a single base pair, which is replaced by another base pair, e.g. in **sickle-cell anaemia**, a point mutation in β-globin chain results in the change of amino acid residue glutamate to valine.
- **Frameshift mutation** is a change in the reading frame because of insertion or deletion of base pairs.

*t*RNA : The Adapter Molecule

- The presence of an adapter molecule, which could read the code and would bind to specific amino acids during translation was proposed by **Francis Crick** in 1961.
- *t*RNA was known before genetic code and was called *s*RNA (soluble RNA), but later its role as an adapter molecule was reported.
- The *t*RNA has a secondary structure like **clover leaf**. But its three dimensional structure depicts it as an inverted **L-shaped molecule.** *t*RNA has five arms or loops, as follows
  - **Anticodon loop** has bases complementary to the code. *t*RNAs are specific for specific amino acid.
  - **Amino acid acceptor end** where amino acids bind.
  - **T-loop** helps in binding to ribosome.
  - **D-loop** helps in binding aminoacyl synthetase.
  - **Variable loop** is variable in both nucleotide composition and in length.

Translation

The process by which the triplet base sequence (codon) on *m*RNA guides the linking of a specific sequence of amino acids to form a polypeptide on ribosomes is known as **translation**.

Translation Machinery

Translation requires a machinery which consists of ribosome, *m*RNA, *t*RNAs, aminoacyl *t*RNA synthetase (enzyme that helps in combining amino acid to particular *t*RNA) and amino acids.

- **Initiator *t*RNA** It is a specific *t*RNA for the process of initiation and there are no *t*RNAs for stop codons.
- **Ribosome** It is responsible for protein synthesis. Ribosome exists as two subunits in its inactive stage
  - **Small subunit** When the small subunit encounters an *m*RNA, translation of *m*RNA to protein begins.
  - **Large subunit** It consists of two sites, where amino acids can bind to and be close to each other for the formation of a **peptide bond**. Ribosome also acts as a catalyst (23S *r*RNA in bacteria is the enzyme, **ribozyme**) for peptide bond formation.
- **Translational unit** It is the sequence of RNA flanked by the start codon (AUG) and the stop codon in *m*RNA. It codes for the polypeptide to be produced.
- **Untranslated Regions** (UTRs) These are some additional sequences in an *m*RNA which are not translated. These are present at both the ends, i.e. at 5′ end (before start codon) and at 3′ end (after stop codon). These improve the efficiency of translation process.

Stages of Protein Synthesis

Synthesis of proteins takes place in three stages which are as follows

1. **Initiation** In prokaryotes, initiation requires ribosome (large and small subunits), *m*RNA, initiation *t*RNA and three Initiation Factors (IFs). For initiation to take place, the ribosome first binds to *m*RNA at the start codon (AUG) that is recognised only by the initiator *t*RNA.

- **Activation of amino acid** The formation of peptide bond requires energy and in first phase, the amino acids are activated in the presence of ATP and linked to their cognate *t*RNA by a process known as **charging of *t*RNA** or **aminoacylation of *t*RNA**. In the presence of ATP and Mg^{2+}, amino acids become activated by binding with **aminoacyl *t*RNA synthetase** enzyme.
- The amino acids – AMP– enzyme complex is called an **activated amino acid**.

2. **Elongation of polypeptide chain** In this step, another charged aminoacyl *t*RNA complex binds to the A-site of the ribosome.
   - A peptide bond forms between carboxyl group (—COOH) of amino acid at P-site and amino group ($—NH_3$) of amino acid at A-site in a reaction catalysed by the enzyme **peptidyl transferase**.
   - During this stage, ribosome moves from one codon to another codon along the *m*RNA in the 5′ ⟶ 3′ direction. Amino acids are then added one-by-one in the sequence of codons and translated into a polypeptide sequences, dictated by DNA and represented by *m*RNA.
3. **Termination of polypeptide** When the A-site of ribosome reaches a termination codon, then no *t*RNA binds to the A-site of ribosome. At the end, a release factor binds to the stop codon and which terminates translation and releases the complete polypeptide from the ribosome.

Regulation of Gene Expression

- **Gene expression** results in the formation of a polypeptide. **Gene regulation** is the mechanism of switching 'off ' and switching 'on' of the genes depending upon the requirement of the cells and the stage of development. The regulation of gene expression may occur at various levels.
- **In eukaryotes**, it takes place at the following levels
  - **Transcriptional level** A primary transcript is formed.
  - **Processing level** Regulation of splicing.
  - **Transport of *m*RNA** From nucleus to the cytoplasm.
  - **Translational level**
- **In prokaryotes**, control of the transcriptional rate of initiation is the predominant site for control of gene expression. In a transcription unit, the activity of RNA polymerase at a given promoter is in turn regulated by the interaction with accessory proteins, which affect its ability to recognise start sites.
- The accessibility of promoter regions of prokaryotic DNA in many cases is regulated by the interaction of **operators**.
- The operator region is adjacent to the promoter elements in most operons and in most cases operator bind a repressor protein. Each operon has its specific operator and specific repressor, e.g. *lac* operator is present only in the *lac* operon and it interacts with *lac* repressor only.

Lac Operon

- **Francois Jacob** and **Jacque Monod** in 1961 were the first to propose the concept of a transcriptionally regulated system, where a polycistronic structural gene is regulated by a common promoter and regulatory genes.
- Such an arrangement is referred as an **operon**, e.g. *lac* (lactose) operon, *trp* (tryptophan) operon, *ara* (arabinose) operon, *his* (histidine) operon and *val* (valine) operon, etc.
- Let us take the example of *lac* operon. Its structure consists of various genes as follows
- One regulatory gene (the *i* gene), which codes for the repressor of the *lac* operon. The term *i* refers to the word inhibitor.
- Three structural genes are
  - ***z* gene** codes for β-galactosidase (β-gal), that helps in the hydrolysis of disaccharide into its monomeric units, i.e. lactose into galactose and glucose.
  - ***y* gene** codes for permease, that increases the permeability of the cell to β-galactosides.
  - ***a* gene** codes for a transacetylase.
- An inducer, i.e. lactose here which is the substrate for the enzyme β-galactosidase.
- If lactose is provided as the carbon source in the growth medium then in the absence of the preferred carbon source such as glucose, the lactose is transported into the cells by the action of enzyme permease. The lactose then induces the operon.
- The *i* gene synthesises the repressor of the operon. Repressor binds to the operator region of the operon, preventing RNA polymerase from transcribing the operon. However, when inducer such as lactose or allolactose is present, it binds with the repressor and inactivates it. Now, that the repressor is inactivated, RNA polymerase is allowed access to the promoter and transcription proceeds.
- Regulation of *lac* operon by repressor is referred to as **negative regulation**. *Lac* operon can work under the control of **positive regulation** also**.**

Human Genome Project (HGP)

- In 1990, a mega project was started to determine the nucleotide sequence of the entire human nuclear genome. It was called as Human Genome Project (HGP).
- In addition, HGP was also entrusted to elucidate the genomes of several other model organisms, e.g. *E. coli, Saccharomyces cerevisiae* (yeast), roundworm and mouse. It was closely associated with the rapid development of a new area in biology called **bioinformatics**.

Goals of HGP

Important goals of HGP were

- To identify all the approximately 20,000-25,000 genes in human DNA.
- To determine the sequences of the 3 billion chemical base pairs that constitute human DNA.
- To store this information in databases in digital format.
- To improve the tools required for data analysis.
- To transfer the related technologies to other sectors (like industries).
- To address the Ethical, Legal and Social Issues (ELSI) that could arise from the project.

Methodologies of HGP

Two major approaches involved were as follows

- **Expressed Sequence Tags** (ESTs) This method was focused on identifying all the genes that are expressed as RNA.
- **Sequence annotation** This method involved sequencing the whole set of genome (that contained all coding and non-coding sequence) and then assigning functions to the different regions in the sequence.

Sequencing of Genome

- For the process of sequencing, the entire DNA from a cell is isolated and broken into relatively smaller fragment.
- DNA fragments are cloned in a suitable host, (such as bacteria and yeast) using specialised vectors such as **BAC** (Bacterial Artificial Chromosome) and **YAC** (Yeast Artificial Chromosome).
- Fragments of DNA are then sequenced by automated DNA sequencers, which work on the principle of a method developed by Frederick Sanger.
- These sequences were arranged accordingly on the basis of overlapping regions of DNA fragments and were then aligned using special computer programmes.
- At last, the genetic and physical maps of the genome were constructed by collecting information about certain repetitive DNA sequences and DNA polymorphism.

Salient Features/Observations of Human Genome

- There are 3164.7 million nucleotide bases in the human genome.
- In an average gene, there are 3000 bases. The largest known human gene is **Dystrophin** (2.4 million bases).
- Total number of genes in human genome are estimated at 30,000. Almost, all (99.9%) of the nucleotide bases are exactly same in every human individual.
- For over 50% of the discovered genes, the functions are unknown.
- Less than 2% of the genome codes for proteins.
- Repeated sequences are stretches of DNA sequences, which are repeated many times (some times 100-1000 times). These have no direct coding functions, but help in understanding chromosome structure, dynamics and evolution.
- **Chromosome-1** has the maximum number of genes (2968) and **Chromosome-Y** has the least number of genes (231).
- There are about 1.4 million locations in human genome, where single-base DNA differences occur (SNPs– Single Nucleotide Polymorphisms). This information is helpful in finding chromosomal locations for disease-associated sequences and tracing human history.

Applications and Future Challenges

- Its knowledge is helpful in research involving biological systems including human biology.
- All the genes in a genome, e.g. all the transcripts in a particular tissue/organ/tumour, can be studied.

DNA Fingerprinting

- It also called **DNA typing** or **DNA profiling** and is a technique of determining nucleotide sequences of certain areas of DNA which are unique to each individual.
- It uses satellite DNA as probe showing high degree of polymorphism and called it **Variable Number of Tandem Repeats** (VNTRs). It was discovered by Alec Jeffreys in 1985.
- The technique has the following steps
  - **DNA isolation** DNA is extracted from the cells in a high speed centrifuge.
  - **Amplification** Many copies of the extracted DNA can be made by the use of Polymerase Chain Reaction (PCR).
  - **Digestion** of DNA by restriction endonucleases.
  - **Separation** of DNA fragments by electrophoresis.
  - **Blotting-transfer** of the separated DNA fragments to synthetic membranes like nylon or nitrocellulose (Southern blotting).
  - **Hybridisation** with the help of a radiolabelled VNTR probe. These proteins target a specific nucleotide sequence that is complementary to them.
  - **Autoradiography** Detection of hybridised DNA fragments by autoradiography.

Applications of DNA Fingerprinting

- It helps to settle paternity or maternity disputes.
- It is used to identify perpetrators of sexual assault cases.
- It is used identify racial groups.

Mastering NCERT

MULTIPLE CHOICE QUESTIONS

TOPIC 1 ~ *The DNA*

1 DNA is a
(a) long polymer of deoxyribonucleotides
(b) short polymer of deoxyribonucleotides
(c) monomer polymer of deoxyribonucleotides
(d) long polymer of ribonucleotides

2 The length of DNA usually depends on
(a) position of nucleotides
(b) number of nucleotides
(c) Both (a) and (b)
(d) None of the above

3 Find the incorrect match.
(a) A bacteriophage ($\phi \times 174$) –5386 nucleotides
(b) Bacteriophage lamda – 48502 base pairs
(c) *E. coli* – 4.6×10^6 bp
(d) Haploid content of human DNA – 3.3×10^6 bp

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

5 Nitrogenous bases are linked to sugar by
(a) hydrogen bond (b) phosphodiester bond
(c) N-glycosidic bond (d) O-glycosidic bond

6 Nucleoside is formed when the nitrogenous bases are linked to
(a) sugar (b) phosphate
(c) proteins (d) fats

7 What is the difference between adenosine and deoxyadenosine?
(a) Only sugar (b) Only purine
(c) Only phosphate (d) All of these

8 When a phosphate group is linked to ...*A*... group of nucleoside through ...*B*... bond, a corresponding ...*C*... is formed.
Choose the correct option for *A*, *B* and *C*.
(a) A–5′ OH, B–phosphodiester bond, C–nucleotide
(b) A–3′ OH, B–phosphodiester bond, C–nucleotide
(c) A–2′ OH, B–phosphodiester bond, C–nucleotide
(d) A–5′ OH, B–phosphodiester bond, C–nucleoside

9 Choose the correct option.
(a) Pyrimidines include adenine and guanine
(b) Pyrimidines include cytosine, uracil and thymine
(c) Purines include adenine and thymine
(d) Purines include guanine and cytosine

10 Which of the following are all nucleotides?
(a) Adenosine, cytidilic acid, cytosine ***AIIMS 2019***
(b) Adenylic acid, cytidilic acid, guanylic acid
(c) Cytidine, adenine, adenylic acid
(d) Uracil, thymidine, thymidylic acid

11 A polymer or a polynucleotide chain has at one end a free .....*A*..... at 5′ end of sugar, similarly at the other end of the polymer the sugar has a free .....*B*..... of 3′ group.
(a) A – Phosphate moiety, B – OH
(b) A – OH, B – Phosphate moiety
(c) A – COOH, B – Phosphate moiety
(d) A – Phosphate moiety, B–COOH

12 Backbone of DNA is formed by
(a) sugar
(b) phosphates
(c) Both (a) and (b)
(d) nitrogenous bases (purine and pyrimidine)

13 Thymine is also called
(a) 2 methyl uracil (b) 3 methyl uracil
(c) 4 methyl uracil (d) 5 methyl uracil

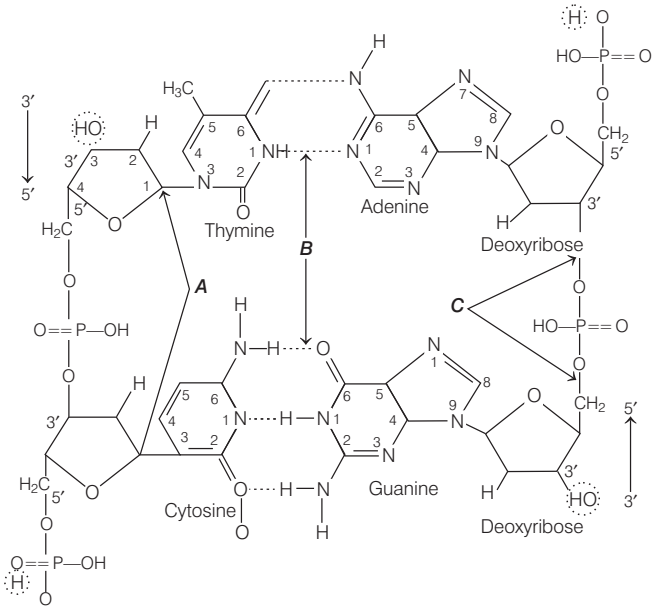
14 Choose the incorrect option.
(a) Friedrich Miescher in 1869 identified DNA as an acidic substance and named it nuclein
(b) Erwin Chargaff said, the ratio between A and T and G and C of *ds*DNA are constant and equals one
(c) The two strands of *ds*DNA are complementary to each other
(d) None of the above

15 X-ray data diffraction of DNA was produced by
(a) Watson and Crick (b) Wilkins and Franklin
(c) Bateson and Punnett (d) Both (a) and (b)

16 In DNA 20% bases are adenine. What percentage of bases are pyrimidines? ***JIPMER 2019***
(a) 30% (b) 60% (c) 50% (d) 20%

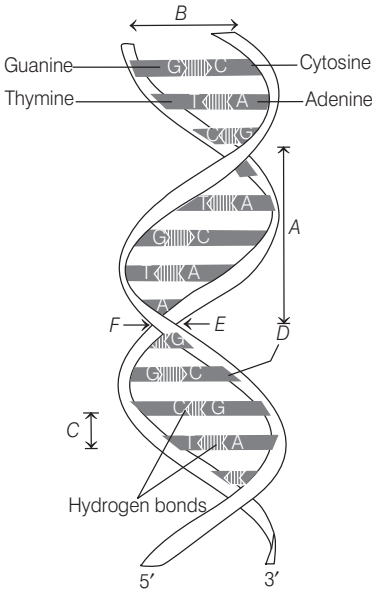
17 In sea urchin DNA, which is double-stranded 17% of the bases were shown to be cytosine. The percentages of the other three bases expected to be present in this DNA are ***CBSE-AIPMT 2015***
(a) G/34%, A/24.5%, T/24.5%
(b) G/17%, A/16.5%, T/32.5%
(c) G/17%, A/33%, T/33%
(d) G/8.5%, A/50%, T/24.5%

18 In the given diagram of chemical structure of DNA, identify the type of bonding shown by *A, B* and *C*.



(a) A–N-glycosidic bonding, B–Phosphodiester bonding, C–Hydrogen bonding
(b) A–N-glycosidic bonding, B–Phosphodiester bonding, C–Covalent bonding
(c) A–N-glycosidic bonding, B–Phosphodiester bonding, C–Coordinate bonding
(d) A–N-glycosidic bonding, B–Hydrogen bonding, C–Phosphodiester bonding

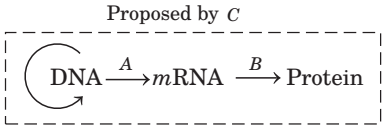
19 Given the diagram showing Watson and Crick model of DNA structure. Identify the parameters of *A, B* and *C*.



(a) A–0.34 Å, B–20 Å, C–3.4 Å, D–Phosphate backbone, E–Major groove, F–Minor groove
(b) A–3.4 Å, B–20 Å, C–34 Å, D–Sugar backbone, E–Major groove, F–Minor groove
(c) A–34 Å, B–20 Å, C–3.4 Å, D–Sugar phosphate backbone, E–Major groove, F–Minor groove
(d) A–34 Å, B–20 Å, C–0.34 Å, D–Major groove, E–Minor groove, F–Sugar phosphate bone

20 Which of the following is not the correct salient feature of double-helix structure of DNA?
(a) Two polynucleotide chains have backbone of sugar and phosphate and bases project inside
(b) Two chains have antiparallel polarity, i.e. one is $5' \rightarrow 3'$ and other is $3' \rightarrow 5'$
(c) Adenine forms three hydrogen bonds with thymine and guanine forms two hydrogen bonds with cytosine
(d) The plane of one base pair stacks over the other in double helix in addition to H-bond to confer extra statbility to helical structure

21 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

22 In some viruses, the flow of information is in reverse direction, i.e. from RNA to DNA. Can you suggest a simple name to the process?
(a) Transcription (b) Transception
(c) Reverse transcription (d) Translation

23 The length of DNA in a human cell is about
(a) 2.3 m (b) 2.4 m (c) 2.2 m (d) 2.0 m

24 Find out the number of base pairs in *E. coli* DNA if its DNA is 1.36 mm long.
(a) 4×10^6 bp (b) 3×10^6 bp
(c) 2×10^6 bp (d) 7×10^6 bp

25 In prokaryotes (such as *E. coli*) ...*A*... nucleus is not present, the DNA is not scattered throughout the cell. DNA is ...*B*... charged and holded by the ...*C*... charged proteins. This structure in prokaryotes is called ...*D*... .

Choose the correct option for *A*, *B*, *C* and *D*.
(a) A–undefined, B–negatively, C–positively, D–nucleoid
(b) A–undefined, B–negatively, C–positively, D–nucleus
(c) A–defined, B–negatively, C–positively, D–nucleoid
(d) A–defined, B–positively, C–negatively, D–nucleoid

26 Positively charged basic proteins that are found in eukaryotes are called
(a) histones (b) protamine
(c) arginine (d) lysine

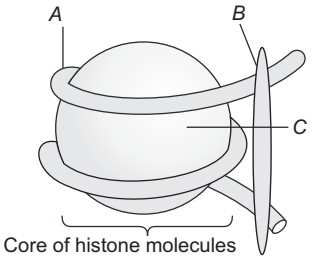
27 Choose the incorrect pair.
(a) Basic amino residues in histones — Lysine and arginine
(b) Unit of 8 molecules in histones — Histone octamer
(c) Negative charged DNA wrapped around positive charged DNA — Nucleosome
(d) Thread-like, colourless unit of structure — Chromatin in nucleus

28 Linker-DNA is attached to ***JIPMER 2018***
(a) H1 (b) H2A (c) H2B (d) H3

29 The packaging of chromatin at higher level requires an additional set of proteins that are collectively referred to as
(a) histone proteins (b) non-histone proteins
(c) basic proteins (d) acidic packaging proteins

30 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

31 In the given diagram, identify *A, B* and *C*.



(a) A–DNA, B–H1 histone, C–Histone octamer
(b) A–RNA, B–H1 histone, C–Histone octamer
(c) A–DNA, B–H1 histone, C–Histone tetramer
(d) A–RNA, B–H1 histone, C–Histone tetramer

32 Lightly stained part of chromatin which remains loosely packed and is transcriptionally active named as
(a) euchromatin
(b) heterochromatin
(c) chromatosome
(d) chromonemata

33 Part of chromatin which is densely packed, stain darkly and is transcriptionally inactive is called
(a) euchromatin (b) chromatosome
(c) heterochromatin (d) chromosome

TOPIC 2 ~ *The Search for Genetic Material and RNA World*

34 Experimental organism of Frederick Griffith was
(a) Variola virus (b) Tuberculosis bacteria
(c) Actinomycetes (d) *Streptococcus pneumoniae*

35 What was unique in Griffith's experiments?
(a) DNA was found to be the genetic material
(b) RNA was found to be the genetic material
(c) Something from dead organisms could change the living cells
(d) Viruses can live in bacteria

36 In Griffith experiment, what would be the effect of following conditions on mice?

Form of *Pneumococcus* Injected	Effect on Mice
I. Live R-strain	*A*
II. Live S-strain	*B*
III. Heat-killed S-strain	*C*
IV. Heat-killed S-strain + live R-strain	*D*

Choose the correct option for effect on mice.
(a) A–Survived, B–Died, C–Died, D–Survived
(b) A–Survived, B–Died, C–Survived, D–Died
(c) A–Died, B–Survived, C–Survived, D–Died
(d) A–Died, B–Survived, C–Died, D–Died

37 Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? ***NEET (Odisha) 2019, 17***
(a) Beadle and Tatum (b) Meselson and Stahl
(c) Hershey and Chase (d) Jacob and Monod

38 Isotopes used by Hershey and Chase were
(a) ^{32}P and ^{35}S (b) ^{35}P and ^{32}S
(c) ^{34}P and ^{31}S (d) ^{30}P and ^{32}S

39 Bacteriophage nucleic acids were labelled as (in Hershey and Chase experiment)
(a) ^{32}P labelled phosphate (b) ^{3}H labelled H_2O
(c) ^{35}S labelled sulphate (d) ^{14}C labelled CO_2

40 Bacteriophage protein coat was labelled by growing *E. coli* on
(a) radioactive sulphur-35
(b) radioactive sulphur-32
(c) radioactive sulphur-30
(d) radioactive phosphorus-32

41 Hershey and Chase concluded that viral infecting agent in their experiment was
(a) Protein (b) DNA
(c) RNA (d) Both (b) and (c)

42 Hershey and Chase used ^{35}S and ^{32}P to prove that DNA is the genetic material. Their experiments proved that DNA is genetic material because
(a) progeny viruses retained ^{32}P but not ^{35}S
(b) retention of ^{32}P in progeny viruses indicated that DNA was passed on
(c) loss of ^{35}S in progeny viruses indicated that proteins were not passed on
(d) All of the above

43 RNA is the genetic material in
(a) All bacteria
(b) Tobacco Mosaic Viruses (TMV)
(c) QB bacteriophage
(d) Both (b) and (c)

44 A molecule that can act as a genetic material must fulfill the traits given below, except ***NEET 2016***
(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

45 Which group present in RNA nucleotide is very reactive and makes RNA liable and easily degradable than DNA?
(a) 3–OH′ group at every nucleotide
(b) 2–OH′ group on ribose sugar
(c) 3–OH′ group on ribose sugar
(d) 4–OH′ group on ribose sugar

46 Stability of DNA is due to
(a) deoxyribose sugar
(b) presence of thymine in place of uracil
(c) Both (a) and (b)
(d) None of the above

47 Viruses having RNA genome and having shorter lifespan, mutate and evolve faster because
(a) RNA is unstable and mutates at faster rate
(b) RNA is stable and mutates at faster rate
(c) RNA is stable and mutates at slower rate
(d) RNA is unstable and mutates at slower rate

48 DNA is dependent on ...*A*... for synthesis of proteins. DNA and RNA both can function as genetic material. But ...*B*... being more stable, preferred for the storage of genetic information. For the transmission of genetic information, ...*C*... is better. Choose the correct option for *A*, *B* and *C*.
(a) A–DNA, B–RNA, C–RNA
(b) A–RNA, B–DNA, C–RNA
(c) A–RNA, B–RNA, C–DNA
(d) A–DNA, B–RNA, C–DNA

49 The first genetic material was
(a) RNA
(b) DNA
(c) Both (a) and (b)
(d) None of the above

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

51 Which one of the following option is correct?
(a) DNA has evolved from RNA with chemical modifications
(b) DNA being complementary double-stranded resists changes by a process of repair
(c) RNA being a catalyst is reactive and unstable
(d) All of the above

TOPIC 3 ~ *Replicaton*

52 DNA replication is semiconservative. It was shown first in
(a) fungi (b) *E. coli* (c) *Vicia faba* (d) algae

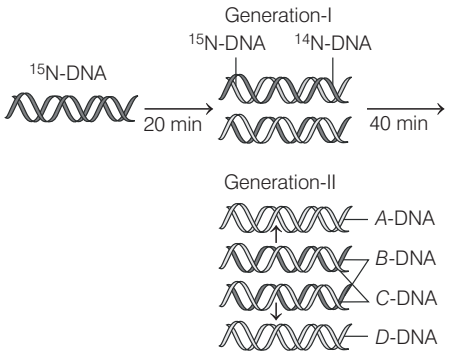
53 Who experimentally proved the semiconservative mode of DNA replication?
(a) Mathew Meselson
(b) Franklin Stahl
(c) Both (a) and (b)
(d) Watson and Crick

54 Name the heavy isotope used by Meselson and Stahl for proving the semiconservative mode of DNA.
(a) $^{15}NH_4Cl$ (b) $^{14}NH_3Cl_2$
(c) $^{13}NH_2Cl_3$ (d) All of these

55 Heavy DNA can be differentiated from normal DNA by which centrifugation technique?
(a) AgCl density gradient (b) $CaSO_4$ density gradient
(c) CsCl density gradient (d) KCl density gradient

56 In Meselson and Stahl's experiment (1958), DNA extracted from the culture one generation after the transfer from ^{15}N to ^{14}N medium had a hybrid (or intermediate) density. Why?
(a) Because the generation time of *E. coli* (culture) was about 20 minutes
(b) Because it would take 20 minutes for RNA replication
(c) Because it would take 20 minutes for replication of DNA to RNA (transcription)
(d) Because it would take 20 minutes for translation RNA to protein

57 Given diagram depicts the experiment of Meselson and Stahl. Identify the type of isotopic DNA formed after 40 minutes (*A, B, C* and *D*).



(a) A–^{14}N-DNA, B–^{15}N-DNA, C–^{14}N-DNA, D–^{15}N-DNA
(b) A–^{14}N-DNA, B–^{15}N-DNA, C–^{14}N-DNA, D–^{14}N-DNA
(c) A–^{14}N-DNA, B–^{14}N-DNA, C–^{15}N-DNA, D–^{15}N-DNA
(d) A–^{14}N-DNA, B–^{15}N-DNA, C–^{15}N-DNA, D–^{15}N-DNA

58 Similar experiments like Meselson and Stahl was performed by Taylor in 1958. The experimental organism of Taylor was
(a) *Vicia faba* (b) Fungi
(c) *E. coli* (d) Protista

59 Radioisotope used by Taylor in his experiment was
(a) iron (b) titanium
(c) thymidine (d) copper

60 DNA polymerase is
(a) DNA dependent
(b) DNA independent
(c) RNA dependent
(d) RNA independent

61 DNA polymerisation rate of DNA polymerase is
(a) 1000 bp/s (b) 2000 bp/s
(c) 3000 bp/s (d) 5000 bp/s

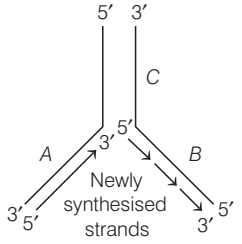
62 For long DNA molecules, the two strands of DNA cannot be separated in its entire length due to the requirement of
(a) enzymes
(b) high energy
(c) RNA
(d) phosphate and nucleotide

63 Replication occurs within the small opening of DNA helix referred to as
(a) replication fork (b) duplication fork
(c) DNA fork (d) RNA fork

64 DNA-dependent DNA polymerases catalyses polymerisation in which direction?
(a) $3' \rightarrow 5'$ (b) $5' \rightarrow 2'$
(c) $5' \rightarrow 3'$ (d) $2' \rightarrow 5'$

65 On which strand of DNA, replication is continuous?
(a) $5' \rightarrow 3'$ polarity strand
(b) $3' \rightarrow 5'$ polarity strand
(c) $3' \rightarrow 2'$ polarity strand
(d) $3' \rightarrow 4'$ polarity strand

66 Identify *A, B* and *C* strands.



(a) A–Continuous strand, B–Discontinuous strand, C–Template strand
(b) A–Leading strand, B–Lagging strand, C–Parental strand
(c) A– 5′–3′ strand, B– 3′–5′ strand, C–Parental strand
(d) All of the above

67 During DNA replication, supercoiling is relaxed by ***JIPMER 2019***
(a) primase (b) polymerase
(c) DNA topoisomerase (d) SSBPs

68 During DNA replication, okazaki fragments are used to elongate ***NEET 2017***
(a) The leading strand towards replication fork
(b) The lagging strand towards replication fork
(c) The leading strand away from replication fork
(d) The lagging strand away from the replication fork

69 Deoxyribonucleoside triphosphate serve dual purposes. The purposes are
(a) act as substrate and decrease reaction rate
(b) provide energy for polymerisation and act as substrate
(c) decrease reaction rate and provide energy for polymerisation
(d) Synthesise RNA primer and decrease reaction rate

TOPIC 4~ *Transcription*

70 Which one of the following is wrongly matched? ***CBSE-AIPMT 2014***

(a) Transcription – Writing information from DNA to *t*RNA
(b) Translation–Using information in *m*RNA to make proteins
(c) Repressor protein – Binds to operator to stop enzyme synthesis
(d) Operon – Structural genes, operator and promoter

71 Why both the strands of DNA are not copied during transcription?

(a) Because RNA molecule with different sequences will be formed
(b) Because RNA molecule with same sequences will be formed
(c) Because RNA molecule with identical sequences will be formed
(d) Because DNA molecule with different sequences will be formed

72 If both the strands copied during transcription, then what will happen?

(a) The segment of DNA would be coding for two different proteins
(b) Two RNA will be produced simultaneously complementary to each other
(c) There will be formation of double helical RNA
(d) All of the above

73 What will happen if the double-stranded RNA is produced during transcription?

(a) This would prevent RNA from being translated into protein
(b) This would not prevent RNA from being translated into protein
(c) There will be the continuous synthesis of RNA
(d) Double-stranded RNA will have lower stability. It will be degraded very fastly

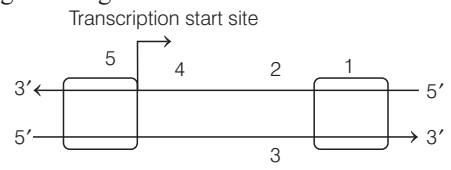
74 Which strand of DNA works as template strand?

(a) 5′ – 3′ polarity strand (b) 3′ – 5′ polarity strand
(c) Both (a) and (b) (d) None of these

75 The strand which do not code for anything is called

(a) coding strand (b) non-coding strand
(c) template strand (d) antisense strand

76 In given diagram find out



A. Promoter site B. Structural gene
C. Terminator site D. Template strand
E. Coding strand

Codes

	A	B	C	D	E
(a)	5	1	4	2	3
(b)	5	1	4	3	2
(c)	5	4	1	2	3
(d)	5	4	1	3	2

77 If the coding strand has the sequence 5′–ATCGATCG–3′ then find out the sequence of non-coding strand.

(a) 3′ – TAGCTAGC – 5′
(b) 5′– TACGTACG – 3′
(c) 5′– UAGGUACG – 3′
(d) 5′– UACFUACG – 3′

78 AGGTATCGCAT is a sequence from the coding strand of a gene. What will be the corresponding sequence of the transcribed *m*RNA? ***NEET 2018***

(a) ACCUAUGCGAU (b) UGGTUTCGCAT
(c) AGGUAUCGCAU (d) UCCAUAGCGUA

79 Which of the following *m*RNA can be transcripted? ***JIPMER 2018***

(a) AUG.UGA.UUU (b) UAA.UAV.UGG
(c) UAG.UGA.UUV (d) UGA.UUV.UGG

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

3'–ATGCATGCATGCATG–5' Template strand

5'–TACGTACGTACGTAC–3' Coding strand

(a) 3'–AUGCAUGCAUGCAUG–5' ***NEET (Odisha) 2019***
(b) 5'–UACGUACGUACGUAC–3'
(c) 3'–UACGUACGUACGUAC–5'
(d) 5'–AUGCAUGCAUGCAUG–3'

81 Promoter and terminator flanks the

(a) house-keeping gene (b) structural gene
(c) recon (d) transcription unit

82 Choose the incorrect pair.

(a)	Promoter	—	Binding site for RNA polymerase
(b)	Terminator	—	Define the end of transcription process
(c)	Cistron	—	Segment of RNA coding for a polypeptide
(d)	Regulatory genes	—	Do not code for any RNA or protein

83 Identify the correct pair of *m*RNA type and its function.

(a) Messenger RNA — Provides the template
(b) Transfer RNA — Brings amino acids and reads genetic code
(c) Ribosomal RNA — Plays catalytic role during translation
(d) All of the above

84 Which of the following RNAs should be most abundant in animals cell? ***NEET 2017***

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

85 DNA-dependent RNA polymerase catalyses transcription on one strand of the DNA which is called the ***NEET 2016***

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

86 In bacteria, which enzyme catalyses the transcription of all types of RNA (*m*RNA, *t*RNA and *r*RNA)?

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

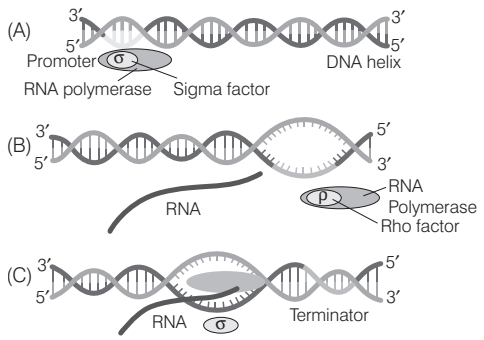
87 In prokaryotes, which process of transcription is catalysed by RNA polymerase only?

(a) Initiation (b) Elongation
(c) Termination (d) Aminoacylation

88 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

89



Identify *A, B* and *C*. ***AIIMS 2019***

(a) A–Elongation, B–Termination, C–Initiation
(b) A–Initiation, B–Termination, C–Elongation
(c) A–Initiation, B–Elongation, C–Termination
(d) A–Termination, B–Elongation, C–Initiation

90 In bacteria, transcription and translation takes place in the same compartment. Why?

(a) No separation of cytosol and nucleus
(b) *m*RNA does not require any processing to become active
(c) Both (a) and (b)
(d) Due to the presence of nucleus

91 In the process of transcription in eukaryotes, the RNA polymerase-I transcribes ***NEET (Odisha) 2019***

(a) *m*RNA with additional processing, capping and tailing
(b) *t*RNA, 5 *sr*RNA and *sn*RNAs
(c) *r*RNAs-28 S, 18 S and 5.8 S
(d) precursor of *m*RNA, *hn*RNA

92 In splicing, the sequences which are kept and those which are removed, respectively, are

(a) exons and introns (b) introns and exons
(c) exons and cistrons (d) introns and cistrons

93 Spliceosomes are not found in cells of ***NEET 2017***

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

94 Name the nucleotide added to 5′ end of *hn*RNA in capping.

(a) Ethyl cytosine triphosphate
(b) Ethyl guanosine triphosphate
(c) Methyl guanosine triphosphate
(d) Methyl cytosine triphosphate

95 Which is present at 5′ end of eukaryotic *m*RNA? ***JIPMER 2018***

(a) Poly-A tail (b) Modified C at 5′
(c) 7 mG (d) Poly-C

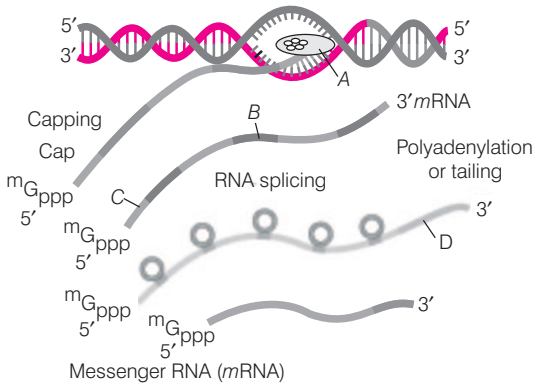
96 What happens in the tailing process of transcription?

(a) Adenylate residues added at 5′ end of RNA
(b) Adenylate residues added at 3′ end of RNA
(c) Guanylate residues added at 5′ end of RNA
(d) Guanylate residues added at 3′ end of RNA

97 Fully processed *hn*RNA to undergo translation is called

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

98 The following diagram refers to the process of transcription in eukaryotes. Identify *A*, *B*, *C* and *D*.



(a) A–RNA polymerase-II, B–Exon, C– Intron, D–Poly-A tail
(b) A–RNA polymerase-III, B–Intron, C– Exon, D–Poly-A tail
(c) A–RNA polymerase-II, B–Intron, C– Exon, D–Poly-A tail
(d) A–RNA polymerase-III, B–Intron, C– Exon, D–Poly-G tail

99 Choose the correct option.

(a) Splicing represent the dominance of RNA world
(b) The presence of introns is reminiscent of antiquity
(c) Split gene arrangements represent an ancient feature of the genome
(d) All of the above

TOPIC 5 ~ *Genetic Code*

100 Genetic code
(a) is a relationship between sequence of DNA or *m*RNA to polypeptide
(b) triplet base on *m*RNA
(c) determines the sequence of amino acid in polypeptide
(d) All of the above

101 In order to code for all the 20 amino acids, the code should be made up of three nucleotides.
This statement was suggested by
(a) Har Gobind Khorana (b) George Gamow
(c) Marshall Nirenberg (d) Servo Ochoa

102 Who developed the technique of synthesising RNA molecules with well-defined combination of bases (homopolymers and copolymers) to develop genetic code?
(a) Crick *et. al* (b) Har Gobind Khorana
(c) Matthaei (d) Nirenberg

103 Who used cell free system for protein synthesis?
(a) Marshall Nirenberg (b) Ochoa
(c) Khorana (d) Gamow

104 Polynucleotide phosphorylase enzymes are also called
(a) Crick *et. al* enzymes (b) Servo Ochoa enzymes
(c) James Watson enzymes (d) Mendel enzymes

105 How many codons codes for amino acids?
(a) 25 (b) 50 (c) 61 (d) 60

106 The genetic codes of arginine are ***AIIMS 2019***
(a) CGU, CGC, CGA (b) CAU, CAC, CAA
(c) AGU, AGC, AAC (d) GAU, GAC, GAA

107 Codons of glycine are ***AIIMS 2018***
(a) CCU, CCC, CCA, CCG
(b) CGU, CGC, CGA, CGG
(c) GGU, GGC, GGA, GGG
(d) ACU, ACC, ACA, ACG

108 The codon AUG codes for (in eukaryotes)
(a) methionine (b) histidine
(c) tryptophan (d) alanine

109 Which of the following is not a stop condon? ***JIPMER 2019***
(a) UAA (b) UAC (c) UAG (d) UGA

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

111 Codons are non-ambiguous, which means that one codon codes for
(a) more than one amino acid
(b) two amino acids
(c) Only one amino acid
(d) non-sense amino acid

112 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

113 Degeneracy refers to
(a) one amino acid has more than one code triplet
(b) one amino acid has only one code triplet
(c) codons which specify the same amino acids differ only in the third base of the triplet
(d) Both (a) and (c)

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

115 The relationship between genes and DNA are best understood by
(a) mutation
(b) recombination
(c) enzymatic synthesis of amino acid
(d) enzymatic synthesis of codons

116 Sickle-cell anaemia is a classical example of point mutation in which valine amino acid comes in place of
(a) glutamate (b) tryptophane (c) alanine (d) guanine

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

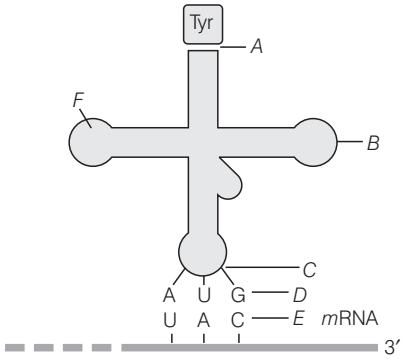
118 If there are 999 bases in an RNA that codes for a protein with 333 amino acids and the base at position 901 is deleted such that the length of the RNA becomes 998 bases, how many codons will be altered? ***NEET 2017***
(a) 1 (b) 11
(c) 33 (d) 333

119 Which mutation of the genetic bases gives the proof that codon is triplet and reads in a contagious manner?
(a) Frameshift mutation (b) Point mutation
(c) Both (a) and (b) (d) Inversion mutation

120 The presence of an adapter molecule that would on one hand read the code and on other hand would bind to specific amino acids was postulated by
(a) Francis Crick (b) James Watson
(c) Rosalind Franklin (d) Griffith

121 Before the genetic code was postulated, the *t*RNA was called
(a) *r*RNA (ribosomal RNA)
(b) *m*RNA (messenger RNA)
(c) *s*RNA (soluble RNA)
(d) *s*RNA (sedimentary RNA)

122 Study the given figure and identify *A* to *F*.



(a) A–Variable arm, B–D-loop, C–T-loop, D–Anticodon arm, E–Codon, F–Variable arm
(b) A–Amino acid arm, B–T-loop, C–Variable arm, D–Anticodon arm, E–Codon, F–D- loop
(c) A–Amino acid arm, B–T-loop, C–Anticodon loop, D–Anticodon, E–Codon, F–D-loop
(d) A–Amino acid arm, B–T-loop, C–Anticodon loop, D–Anticodon, E–Codon, F–Variable arm

123 Choose the incorrect option for *t*RNA molecule.
(a) It has an anticodon loop that has bases complementary to the code
(b) It has an amino acid acceptor end to which it binds to amino acids
(c) *t*RNA are not specific for each amino acid
(d) *t*RNA looks like a clover leaf

124 *t*RNA is a compact molecule which looks like
(a) M-shaped (b) P-shaped (c) L-shaped (d) K-shaped

125 RNA binds to *m*RNA through ***JIPMER 2019***
(a) anticodon loop
(b) T ψ C loop
(c) amino acid binding loop
(d) D-loop

126 Removal of RNA polymerase-III from nucleoplasm will affect the synthesis of ***CBSE-AIPMT 2012***
(a) *t*RNA (b) *hn*RNA (c) *m*RNA (d) *r*RNA

TOPIC 6 ~ *Translation*

127 The process of polymerisation of amino acids to form a polypeptide is
(a) transcription (b) replication
(c) translation (d) polymerisation

128 Many ribosomes may associate with a single *m*RNA to form multiple copies of a polypeptide simultaneously. Such strings of ribosomes are termed as ***NEET 2018, 16***
(a) plastidome (b) polyhedral bodies
(c) polysome (d) nucleosome

129 In the protein synthesis, *t*RNA carrying the amino acid enters from which site of the ribosome?
(a) A-site (b) P-site
(c) Anticodon site (d) R-site

130 The order and sequences of amino acids are defined by the sequences of the bases in
(a) *r*RNA (b) *m*RNA (c) *t*RNA (d) All of these

131 Which of the following enzymes are required in protein synthesis?
I. Ligase II. Permease
III. Endonuclease IV. Ribozyme
V. RNA polymerase VI. Peptidyl transferase
VII. Amino acid activating enzyme
Choose the correct option.
(a) IV, VI and VII (b) I, II and III
(c) II, III, IV and V (d) All of these

132 Which among the following process occur(s) during charging or aminoacylation of *t*RNA?
(a) Activation of amino acids in the presence of ATP
(b) Linking of amino acids to their cognate *t*RNA
(c) Both (a) and (b)
(d) None of the above

133 The cellular factory responsible for the synthesis of proteins is
(a) mitochondria
(b) endoplasmic reticulum
(c) Golgi body
(d) ribosome

134 Which of the following *r*RNAs act as structural RNA as well as ribozyme in bacteria? ***NEET 2016***
(a) 5 *sr*RNA (b) 18 *sr*RNA
(c) 23 *sr*RNA (d) 5.8 *sr*RNA

135 UTRs present on *m*RNA refer to
(a) Untranscribed regions at both 5′ end and 3′ end
(b) Untranslated regions at 5′ end
(c) Untranslated regions at both 5′ end and 3′ end
(d) Untranslated regions at 3′ end

136 For initiation, the ribosomes binds to the ...*A*... at the start codon and ...*B*... is recognised by the ...*C*... . Choose the correct option for *A*, *B* and *C*.

(a) A–*m*RNA, B–AUG, C–initiator *t*RNA
(b) A–*m*RNA, B–AUG, C–*t*RNA
(c) A–*r*RNA, B–AUG, C–*t*RNA
(d) A–*r*RNA B–AUG, C–initiator *m*RNA

137 Choose the incorrect pair.

(a)	Untranslated regions	—	Required for efficient translation process
(b)	Release factor	—	Kind to stop codon for terminating translation
(c)	Translational unit	—	Sequence of RNA with start codon only
(d)	Elongation phase	—	Ribosome moves from codons to codons along *m*RNA

138 For the given DNA sequence

3′–TACATGGGTCCG–5′.

Choose the correct sequential code of *t*RNA anticodon.

I. UAC II. AUG
III. GGC IV. CCA

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

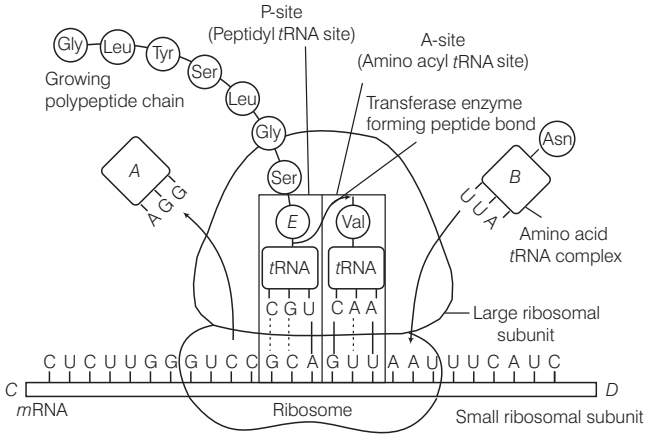
139

RNA molecule	Anti-codon pairing
I	UCA
II	AUG
III	AUU
IV	AUC

Which of the following *t*RNA molecules does not exist?

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

140 Study the diagram given below of translation and choose the correct option for labels *A, B, C, D* and *E*.



	A	B	C	D	E
(a)	Charged/ Aminoacylated *t*RNA	Uncharged *t*RNA	5′ end	3′ end	Glycine
(b)	Uncharged *t*RNA	Charged/Aminoacy-lated *t*RNA	5′ end	3′ end	Alanine
(c)	Uncharged *t*RNA	Charged/Aminoacy-lated *t*RNA	3′ end	5′ end	Glycine
(d)	Uncharged *t*RNA	Charged/Aminoacy-lated *t*RNA	5′ end	3′ end	Lysine

141 Termination of protein synthesis or translation requires

(a) Both stop signal and starting codon
(b) Both starting codon and release factor
(c) Both release factor and stop codon
(d) GUG and AUG codon

TOPIC 7 ~ *Regulation of Gene Expression*

142 The regulation of gene expression in eukaryotes can be exerted at

I. transcriptional level.
II. processing level.
III. transport of *m*RNA (from nucleus to cytoplasm).
IV. translational level.

Choose the correct combination to complete the statement.

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

143 In prokaryotes, control of the rate of ...*A*... is the pre-dominant site for the control of gene expression. In a transcription unit, the activity of ...*B*... at a given promoter is in turn regulated by interaction with ...*C*... proteins, which affects its ability to recognise the start sites.

Complete the statement filling the correct options in given blanks.

(a) A–RNA replication, B–DNA polymerase, C–accessory
(b) A–transcriptional initiation, B–RNA polymerase, C–accessory
(c) A–translational initiation, B–RNA polymerase, C–accessory
(d) A–DNA replication, B–RNA polymerase, C–accessory

144 Positively regulatory proteins are called

(a) activator
(b) repressors
(c) necessary proteins
(d) accessory proteins

145 The accessibility of the promoter regions of prokaryotic DNA is (in many cases) regulated by the interaction of proteins with the sequences termed as

(a) regulator (b) promoter
(c) operator (d) structural genes

146 An operon is considered to regulate a

(a) translational unit (b) genetic unit
(c) protein unit (d) enzymatic unit

147 1st operon model was

(a) *trp* operon (b) *lac* operon
(c) *his* operon (d) *val* operon

148 Select the correct match. ***NEET 2018***

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

149 Number of regulatory and structural genes present in *lac* operon are

(a) one and two (b) one and three
(c) one and one (d) three and one

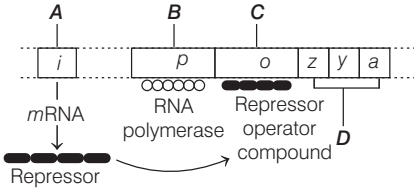
150 Gene regulation governing lactose operon of *E. coli* that involves the *lac i* gene products is ***CBSE-AIPMT 2015***

(a) positive and inducible because it can be induced by lactose
(b) negative and inducible because its repressor protein prevents transcription
(c) negative and repressible because its repressor protein prevents transcription
(d) feedback inhibition because excess of β-galactosidase can switch off transcription

151 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

152 Identify *A, B, C* and *D* in the given diagram of a *lac* operon.



(a) A–Regulatory gene, B–Promoter, C–Operator, D–Structural gene
(b) A–Regulatory gene, B–Promoter, C–Structural gene, D–Operator
(c) A–Regulatory gene, B–Structural gene, C–Pormoter, D–Operator
(d) A–Regulatory gene, B–Structural gene, C–Operator gene, D–Promoter gene

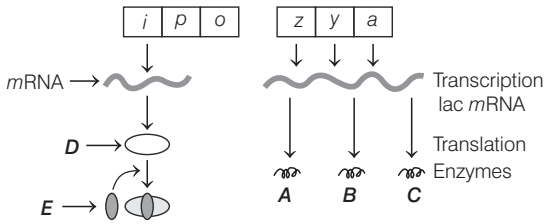
153 Lactose is a substrate for

(a) galactosidase
(b) α-galactosidase
(c) β-galactosidase
(d) γ-galactosidase

154 Lactose is transported into cells through

(a) β-galactosidase
(b) permease
(c) transacetylase
(d) transferase

155 The given diagram of the *lac* operon showing an operon of inducible enzymes. Identify components and enzymes (*A, B, C, D* and *E*).



(a) A–Galactosidase, B–Permease, C–Transacetylase, D–Repressor protein, E–Inducer (lactose)
(b) A–Galactosidase, B–Permease, C–Transacetylase, D–Inducer (lactose), E–Repressor protein
(c) A–Galactosidase, B–Transacetylase, C–Permease, D–Repressor protein, E–Inducer (lactose)
(d) A–Permease, B–Transacetylase, C–-Galactosidase, D–Repressor protein, E–Inducer (lactose)

156 To, which of the following, repressor protein is attached? ***JIPMER 2018***

(a) Operator (b) Inducer
(c) Promoter (d) Structural gene

157 Why glucose and galactose cannot act as an inducer for *lac* operon?

(a) Because they cannot bind with the repressor
(b) Because they can bind with the repressor
(c) Because they can bind with the operator
(d) Because they can bind with the regulator

TOPIC 8 ~ *Human Genome Project*

158 Which of the following option is true for Human Genome Project (HGP)?
(a) It was launched in the year 1990 and was called mega project
(b) Total estimated cost of the project would be 9 billion US dollars
(c) It aims to identify all 20000-25000 genes in human DNA
(d) All of the above

159 Human genome project was co-ordinated by
(a) Europian Department of Energy
(b) US Department of Energy
(c) National Institute of Health
(d) Both (b) and (c)

160 Identify the incorrect option regarding human genome project.
(a) It was completed in 2003
(b) It aims to determine the sequence of 3 billion chemical base pairs and store it in data bases
(c) It associated ethical legal and social issues arising from the project
(d) It is not associated with non-human organisms DNA sequences

161 Gene library or DNA library has the collection of
(a) DNA and RNA ***AIIMS 2019***
(b) Any one type of gene of organism
(c) *c*DNA
(d) All possible genes are organisms

162 Which among the following are non-human model whose genome are sequenced?
(a) *Caenorhabditis elegans* (b) *Drosophila*
(c) Plants (rice and *Arabidopsis*) (d) All of these

163 Identify the incorrect pair.
(a) Expressed sequence tags — Genes that are express as RNA
(b) Sequence annotation — Sequencing genome with coding sequences
(c) Automated DNA sequences — Work on the principle developed by Frederick Sanger
(d) None of the above

164 How genetic and physical maps were generated in HGP?
(a) By using DNase
(b) By using RNase
(c) By using restriction endonuclease
(d) By using automated DNA sequences

165 To make chromosomal studies easier, chromosomes are classified into certain groups. So, the chromosome number 21, 22 and Y are listed in ***JIPMER 2019***
(a) A (b) D (c) E (d) G

166 Exact number of nucleotides contained in human genome, revealed by human genome project are
(a) 3164.7 million bp (b) 3163.7 million bp
(c) 3162.7 million bp (d) 3160.7 million bp

167 Average gene consists of ...*A*... bases, but their size vary greatly, with the largest known human gene being ...*B*... with ...*C*... bases.
Complete the statement filling the correct option in the given blanks.
(a) A–3000 bases, B–dystrophin, C–2.4 million
(b) A–2000 bases, B–dystrophin, C–2.4 million
(c) A–1000 bases, B–dystrophin, C–2.0 million
(d) A–3000 bases, B–dystrophin, C–2.0 million

168 Percentage of similarity between the nucleotides of two individuals is
(a) 98% (b) 99% (c) 99.9% (d) 99.8%

169 Total percentage of genes, which codes for proteins is
(a) 2% (b) 3% (c) 4% (d) 5%

170 Repetitive DNA make up very large portion of human genome and are important for studying
(a) chromosome structure (b) chromosome dynamics
(c) evolution (d) All of these

171 Choose the incorrect option.
(a) HGP is closely associated with bioinformatics
(b) HGP will help in developing new ways to diagnose, treat and some day prevent disorders affecting humans
(c) Fragment sequenced during HGP are done by method developed by Frederick Sanger
(d) Repetitive DNA sequences are stretches of DNA repeated 2-3 times in a DNA sequence

172 SNP–Single Nucleotide Polymorphisms is
(a) location on RNA where the single base differs
(b) location on proteins where the single base differs
(c) location on genome where the single base of DNA differs
(d) location on genome where many bases of DNA differs

173 SNPs can be used for
(a) finding chromosome locations for disease associated sequences
(b) tracing human history
(c) evolution
(d) All of the above

TOPIC 9 ~ *DNA Fingerprinting*

174 DNA fingerprinting involves identifying the differences in some specific regions in DNA sequence called
(a) non-repetitive DNA
(b) coding DNA
(c) non-coding DNA
(d) repetitive DNA

175 The bulk of DNA (other than repetitive) forms the major peaks during density gradient centrifugation. The other small peaks are referred to as
(a) satellite DNA (b) non-satellite DNA
(c) exonic DNA (d) intronic DNA

176 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

177 Basis of DNA fingerprinting
(a) high degree of polymorphism in sequences
(b) low degree of polymorphism in sequences
(c) intermediate degree of polymorphism in sequences
(d) sequences show no polymorphism

178 The technique of DNA fingerprinting was initially developed by
(a) Lalji Singh (b) Alec Jeffreys
(c) Frederick Sanger (d) Jacob and Monod

179 Alec Jeffreys used a satellite DNA as probe that shows very high degree of polymorphism. It was called as
(a) Short Number of Tandem Repeats (SNTRs)
(b) Large Number of Tandem Repeats (LNTRs)
(c) Variable Number of Tandem Repeats (VNTRs)
(d) All of the above

180 VNTR belongs to the class of satellite DNA referred to as
(a) microsatellite DNA
(b) minisatellite DNA
(c) megasatellite DNA
(d) repetitive DNA

181 VNTR varies in size from
(a) 0.1-20 kb (b) 0.2-10 kb
(c) 0.3-30 kb (d) 0.4-15 kb

182 The sensitivity of DNA fingerprinting can be increased by
(a) using intron sequences
(b) using exon sequences
(c) using polymerase chain reactions
(d) All of the above

183 Southern blotting technique involves the transfer of DNA from
(a) gel to membrane
(b) membrane to gel
(c) solution to gel
(d) gel to solution

184 Steps in DNA fingerprinting are

Isolation of DNA
↓
Digestion of DNA by (*A*)
↓
Separation of DNA by (*B*)
↓
Transfering of DNA to (*C*)
↓
DNA hybridisation using (*D*)
↓
Detecting of hybridised DNA by (*E*)

Complete the accompanying *A*, *B*, *C*, *D* and *E* in the flowchart are
(a) A–Restriction endonuclease, B–Electrophoresis, C–Nitrocellulose or nylon, D–Labelled VNTR probe, E–Autoradiography
(b) A–Electrophoresis, B–Restriction endonuclease, C–Nitrocellulose or nylon, D–Labelled VNTR probe, E–Autoradiography
(c) A–Restriction endonuclease, B–Electrophoresis, C–Labelled VNTR probe, D–Nitrocellulose or nylon, E–Autoradiography
(d) A–Restriction endonuclease, B–Electrophoresis, C–Nitrocellulose or nylon, D–Autoradiography, E–Labelled VNTR probe

NEET

SPECIAL TYPES QUESTIONS

I. Assertion and Reason

■ **Directions** (Q. No. 185-199) *In each of the following questions, a statement of Assertion (A) is given by corresponding statement of Reason (R). Of the statements, mark the correct answer as*

(a) If both A and R are true and R is the correct explanation of A
(b) If both A and R are true, but R is not the correct explanation of A
(c) If A is true, but R is false
(d) If A is false, but R is true

185 **Assertion** (A) DNA acts as a genetic material in all organisms.
Reason (R) It is a double-stranded biomolecule in most organisms.

186 **Assertion** (A) DNA has two chains having antiparallel polarity.
Reason (R) In one chain of DNA at one end has a free phosphate moiety 5′ end of ribose sugar and at other end the ribose has a free 3′ OH group.

187 **Assertion** (A) Adenine cannot pair with cytosine.
Reason (R) Adenine and cytosine do not have complementarity between their respective hydrogen donor and hydrogen acceptor sites.

188 **Assertion** (A) Histones are basic in nature.
Reason (R) These are rich in the amino acids lysine and arginine.

189 **Assertion** (A) Heterochromatin is transcriptionally inactive.
Reason (R) It is densely packed.

190 **Assertion** (A) Viruses having RNA genome and shorter lifespan, mutate and evolve faster.
Reason (R) RNA is unstable and thus mutates faster.

191 **Assertion** (A) Replication on one strand of DNA is continuous and on another it is discontinuous.
Reason (R) The DNA polymerase works in 3′ → 5′ direction.

192 **Assertion** (A) Replication and transcription occur in the nucleus, but translation takes place in the cytoplasm.
Reason (R) *m*RNA is transferred from the nucleus into cytoplasm where ribosomes and amino acids are available for protein synthesis.

193 **Assertion** (A) *hn*RNA is larger than *m*RNA.
Reason (R) *hn*RNA has non-coding introns which are not required for translation.

194 **Assertion** (A) Polycistronic *m*RNA is capable of forming a number of different polypeptide chains.
Reason (R) Polycistronic *m*RNA has terminator codons.

195 **Assertion** (A) In transcription, the strand with 3′ → 5′ polarity acts as the template strand.
Reason (R) The enzyme RNA polymerase catalyses the polymerisation in only one direction, i.e. 5′ → 3′.

196 **Assertion** (A) In eukaryotes, transcription occurs in nucleus. ***AIIMS 2019***
Reason (R) In bacteria, transcription and translation occur in cytoplasm.

197 **Assertion** (A) The genetic code is degenerate.
Reason (R) Most amino acids are coded by more than one codon.

198 **Assertion** (A) *m*RNA has some untranslated regions that are not translated.
Reason (R) UTRs are required for efficient translation.

199 **Assertion** (A) DNA fingerprinting is very well-known for its application in paternity testing in case of disputes.
Reason (R) It employs the principle of DNA polymorphism.

II. Statement Based Questions

200 Read the following statements.

I. A purine is heterocyclic, 9-membered double ring structure with nitrogen at 1st, 3rd, 7th and 9th positions.
II. A pyrimidine is heterocyclic, 6-membered single ring structure with nitrogen at 1st and 3rd positions.
III. Purine nucleosides have 1′-9 glycosidic linkage whereas pyrimidine nucleosides have 1′-1-glycosidic linkage.
IV. Two nucleosides are linked by 3′-5′ phosphodiester linkage to form a dinucleotide.
V. Ribose sugar can be represented as $C_5H_{10}O_4$ whereas deoxyribose sugar can be represented as $C_5H_{10}O_5$.

Which of the above statement(s) is/are correct?

(a) Only I (b) I, II, III and IV
(c) III, IV and V (d) IV and V

201 Choose the incorrect statement.

(a) A nucleotide contains ribose sugar or deoxyribose sugar
(b) A nucleotide contains pyrimidine bases and purine bases
(c) A nucleotide contains protein, carbohydrates and fats
(d) A phosphate group is present in a nucleotide

202 Which of the following statements about Griffith's experiment are correct?

I. S-strain have mucus (polysaccharide) coat.
II. S-strain are virulent is cause pneumonia infection, while R-strain do not.
III. Transforming principle is associated with genetic material of R-strain.
IV. Transformation of R-strain into S-strain can take place in a test tube.

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

203 Choose the correct statements about biochemical characterisation of transforming principle in Griffith's experiment.

I. It was done by Oswald Avery, Colin MacLeod and Maclyn McCarty.
II. Scientists purified biochemicals (proteins, DNA, RNA, etc.) from heat killed S-cell.
III. It was seen that DNA alone from S-bacteria caused R-bacteria to become transformed .
IV. Proteases and RNases did not affect transformation.

(a) I and II
(b) III and IV
(c) I and III
(d) All statements are correct

204 Which of the following statements about Hershey and Chase experiment are correct?

I. Sulphur is present in proteins, but not in DNA.
II. Phosphorus is present in DNA, but not in proteins.
III. ^{32}P will end up in the supernatant after centrifugation.
IV. Progeny generation of T_2-bacteriophage contains ^{32}P.

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

205 Choose the incorrect statement(s) about the experiment conduted by Meselson and Stahl's that

(a) equal amount of light DNA and hybrid DNA was observed in *E. coli* culture after two generations
(b) the generation time of *E. coli* culture was 40 minutes
(c) the equal amount of light DNA and hybrid DNA was observed in *E. coli* culture after three generations
(d) Both (a) and (b)

206 J Watson and F Crick proposed the double helix model of DNA. Choose the correct statements with respect to their model of DNA.

I. Based on X-ray diffraction of DNA produced by M Wilkins and R Franklin.
II. One of the hall marks of their proposition was base pairing between the two strands of polynucleotide chains.
III. The two polynucleotide chains are antiparallel to each other .
IV. Based on Chargaff's rule $(A+G/T+C=1)$

Choose the correct option.

(a) I, II and III
(b) II, III and IV
(c) I, II, III and IV
(d) All of the above

207 Choose the incorrect statement about the semiconservative scheme of DNA replication.

(a) Watson and Crick proposed the scheme for replication of DNA in 1953
(b) The scheme suggested that the two strands would separate and act as a template for the synthesis of new complementary strands
(c) Griffith proposed the scheme of semiconservative DNA replication
(d) After the completion of replication, each DNA molecule would have one parental and one newly synthesised strand

208 Arrange the following events of replication of DNA.

I. Bonds between complementary bases breaks.
II. Bonds between complementary bases forms.
III. DNA molecules uncoils.
IV. Opposite strands separates.
V. Sugar phosphate bonds forms.
VI. Free nucleotides align with the complementary nucleotides on each strand.

Choose the correct option.

(a) VI → I → III → IV → V → II
(b) III → VI → I → IV → V → II
(c) I → III → VI → IV → II → V
(d) III → I → IV → VI → II → V

209 Choose the correct statements about DNA replication.

I. Discontinuously synthesised fragments are later joined by the enzyme DNA ligase.
II. There is a definite region in *E. coli* DNA where the replication originates, known as origin of replication.
III. In eukaryotes, the replication of DNA takes place at S-phase of the cell cycle.
IV. Failure of cell division after DNA replication results in polyploidy.
V. *E. coli* having 4.6×10^6 bp completes DNA replication within 38 minutes.

(a) I and II (b) III and IV
(c) I and V (d) All of these

210 Choose the correct statement.

(a) The regions of transcriptional units are promoter, structural gene and terminator

(b) The region of transcriptional units are exon, intron and cistron

(c) The region of DNA where transcription stops is present on promoter

(d) The terminator codes for enzyme or protein

211 Consider the following statements.

I. The presence of a promoter in a transcription unit defines the template and coding strands.

II. DNA-dependent RNA polymerase catalyse the polymerisation in only one direction that is 5′→3′.

III. The DNA sequence coding for *t*RNA or *r*RNA molecules also define a gene.

IV. Regulatory sequences are loosely defined as regulatory genes and these sequences do not code for any RNA or protein.

Choose the correct statements.

(a) I and IV (b) I, II and III

(c) II and IV (d) I, II, III and IV

212 Which one of the following statement is incorrect?

(a) Structural gene in transcription unit is monocistronic in eukaryotes and polycistronic in bacteria

(b) Monocistronic genes in eukaryotes are split

(c) Exons are non-coding and introns are coding sequences of gene

(d) Intervening sequences do not appear in mature or processed RNA

213 Choose the correct statement(s).

(a) The factors required for the synthesis of protein are initiation code and ribosomes

(b) The factors required for the synthesis of protein are GTP, ATP and amino acid pool

(c) The factors required for the synthesis of protein are *t*RNA and *m*RNA

(d) All of the above

214 Consider the following statements.

I. *r*RNA provides the template for synthesis of proteins.

II. *t*RNA brings amino acids and reads the genetic code.

III. RNA polymerase binds to promoter and initiates transcription.

IV. A segment of DNA coding for polypeptide is called intron.

Which of the statements given above are correct?

(a) I and III (b) I and II (c) I, II and III (d) II and III

215 Following are the stages in the cellular synthesis of a protein.

I. Movement of *m*RNA from the nucleus to cytoplasm.

II. Linking of adjacent amino acid molecules.

III. Transcription of *m*RNA from a DNA template.

IV. Formation of the polypeptide chain.

V. Attachment of the *m*RNA strand to a ribosome.

In which order do these stages take place?

(a) III I V II IV

(b) I III II V IV

(c) I V III IV II

(d) III IV I II V

216 The difference(s) between *m*RNA and *t*RNA is/are that

I. *m*RNA has more elaborated 3-dimensional structure due to extensive base pairing.

II. *t*RNA has more elaborated 3-dimensional structure due to extensive pairing.

III. *t*RNA is usually smaller than *m*RNA.

IV. *m*RNA contains anticodons, but *t*RNA contains codons.

Choose the correct statements.

(a) I, II, III and IV (b) II and III

(c) I and III (d) I, II and III

217 Few steps involved in polypeptide synthesis are given below. In which of the following steps does *t*RNA participates?

I. Activation of amino acids by binding with aminoacyl *t*RNA synthetase enzyme.

II. Elongation of polypeptide chain.

III. Translation of *m*RNA to form a polypeptide.

IV. Transcription of DNA into RNA.

(a) I, III and IV (b) II, III and IV

(c) I, II and IV (d) I, II and III

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

I. Glucose or galactose may bind with the repressor and inactivate it.

II. In the absence of lactose, the repressor binds with the operator region.

III. Tryptophan acts as an inducer for the gene expression.

IV. Regulatory gene is the one that produces the repressor molecule.

Choose the correct option.

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

219 Which of the following statements concerning the regulatory genes (R), associated with the *lac* operon are incorrect?

I. *m*RNA is transcribed from the R gene whether lactose is present or not.

II. *m*RNA is transcribed from the R gene only when the lactose is present.

III. *m*RNA is transcribed from the R gene only when the lactose is not present.

IV. Lactose inhibits the translation of R gene *m*RNA.

(a) I and II (b) II and III

(c) III and IV (d) II, III and IV

220 Identify the incorrect statement for *lac* operon model.

(a) Lactose acts as inducer which inactivates repressor
(b) RNA polymerase stay away from promoter in the presence of repressor
(c) Regulation of *lac* operon by repressor is referred to as negative regulation
(d) The repressor of the operon is synthesised during specific periods from *r*-gene

221 Select the incorrect statement from the following.

AIIMS 2019

(a) The human genome contains 3164.7 million nucleotide bases
(b) Less than 10% of the genome codes for proteins
(c) Repeated sequences make up very large portion of the human genome
(d) Chromosome 1 has most genes (2968) and Y has the fewest (231)

222 Consider the following statements.

I. Major countries who contributed or participated in human genome project were Japan, France, Germany and China.
II. Human genome project was a mega project of 13 years.

Choose the correct option.

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

223 Choose the incorrect statement about Human Genome Project (HGP).

(a) Commonly used host for cloning in HGP were PAC (Plasmic Artificial Chromosome) and GMO (Genetically Modified Organisms)
(b) The alignment of sequences obtained was done by computer based programs
(c) The developed sequences were annotated and were assigned to each chromosome
(d) The human genome has 22 autosomes, X and Y

224 Steps in sequencing Human Genome Project (HGP) are

I. isolation of total DNA.
II. cloning in suitable vectors.
III. sequence arrangment by computer.
IV. formation of physical and genetic maps.
V. converting the fragments.
VI. using automated sequencer.
VII. using restriction endonuclease recognition sites.
VIII. completition of human genome sequencing.

Choose the correct option in which the above given steps are arranged properly.

(a) I, II, III, IV, V, VI, VII, VIII
(b) I, V, II, VI, III, VII, IV, VIII
(c) I, II, V, VI, III, IV, VIII, VII
(d) I, II, V, VI, III, VII, VIII, IV

225 Tandem Repeat DNA

I. is classified as microsatellites and minisatellites.
II. normally does not code for any protein.
III. shows polymorphism.
IV. is used in fingerprinting.

Choose the correct option to complete the statement.

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

III. Matching Type Questions

226 Match the following columns.

	Column I (Scientists)		**Column II** (Discoveries)
A.	F Miescher	1.	DNA double helix
B.	Griffith	2.	Nuclein
C.	Hershey and Chase	3.	*Streptococcus pneumoniae*
D.	Watson and Crick	4.	Bacteriophage
E.	Wilkins and Franklin	5.	X-ray diffraction studies

Codes

	A	B	C	D	E
(a)	5	4	3	1	2
(b)	1	4	3	2	5
(c)	2	3	4	1	5
(d)	1	3	4	2	5

227 Match the following columns.

	Column I (Features)		**Column II** (Associated enzymes)
A.	RNA digesting enzymes	1.	Lipase
B.	Protein digesting enzymes	2.	DNase
C.	DNA digesting enzymes	3.	Protease
D.	Fat digesting enzymes	4.	RNase

Codes

	A	B	C	D		A	B	C	D
(a)	3	4	2	1	(b)	1	2	4	3
(c)	4	3	2	1	(d)	1	2	3	4

228 Match the following columns.

	Column I (Enzymes)		**Column II** (Functions)
A.	Topoisomerase	1.	Relaxes the DNA from its super-coiled nature.
B.	DNA gyrase	2.	Relieves strain of unwinding by DNA helicase; this is a specific type of topoisomerase.
C.	DNA ligase	3.	Re-anneals the semiconservative strands and joins okazaki fragments of the lagging strand.
D.	Telomerase	4.	Provides a starting point of RNA (or DNA) for DNA polymerase to begin synthesis of the new DNA strand.

Codes

	A	B	C	D		A	B	C	D
(a)	1	2	4	3	(b)	1	2	3	4
(c)	2	4	3	1	(d)	1	3	2	4

229 Match the following columns.

	Column I		Column II
A.	Splicing	1.	*Lac* operon
B.	Okazaki fragment	2.	Lagging strand
C.	Jacob and Monod	3.	Lactose
D.	Inducer	4.	Removal of introns

Codes

	A	B	C	D		A	B	C	D
(a)	1	2	3	4	(b)	4	2	1	3
(c)	4	2	3	1	(d)	2	4	3	1

230 Match the given enzymes with their respective function in DNA replication.

	Column I		Column II
A.	DNA helicase	1.	A protein which prevents DNA polymerase-III form dissociating from the DNA parent strand.
B.	DNA polymerase	2.	Bind to *ss*DNA and prevent the DNA double helix from re-annealing after DNA helicase unwinds it thus maintaining the strand separation.
C.	DNA clamp	3.	Also known as helix destabilising enzyme and unwinds the DNA double helix at the replication fork.
D.	Single-Strand Binding (SSB) Proteins	4.	Build a new duplex DNA strand by adding nucleotides in the 5′ to 3′ direction. Also performs proofreading and error correction.

Codes

	A	B	C	D		A	B	C	D
(a)	1	2	4	3	(b)	3	4	1	2
(c)	4	3	2	1	(d)	1	2	3	4

231 Match the following columns.

	Column I		Column II
A.	Sigma factor	1.	5′–3′
B.	Capping	2.	Initiation
C.	Tailing	3.	5′ end
D.	Coding strand	4.	3′ end

Codes

	A	B	C	D		A	B	C	D
(a)	4	1	2	3	(b)	2	4	3	1
(c)	1	3	4	2	(d)	3	2	1	4

232 Match the following columns.

	Column I		Column II
A.	*t*RNA	1.	Linking of amino acids
B.	*m*RNA	2.	Transfer of genetic information
C.	*r*RNA	3.	Nucleolar organising region
D.	Peptidyl transferase	4.	Transfer of amino acid from cytoplasm to ribosome

Codes

	A	B	C	D
(a)	4	2	3	1
(b)	1	4	3	2
(c)	1	2	3	4
(d)	1	3	2	4

233 Match the following columns.

	Column I		Column II
A.	Exon	1.	Coding sequence
B.	Intron	2.	Non-coding sequence
C.	Genetic code	3.	Triplet bases on *m*RNA
D.	DNA packaging	4.	Nucleosome

Codes

	A	B	C	D		A	B	C	D
(a)	1	3	2	4	(b)	1	4	2	3
(c)	1	2	3	4	(d)	4	1	2	3

234 Match the following columns.

	Column I		Column II
A.	5′–AUG–3′	1.	Segment of DNA
B.	RNA with introns and exon	2.	Chromatin
C.	Gene	3.	*hn*RNA
D.	Nucleosomes	4.	Initiation codon

Codes

	A	B	C	D		A	B	C	D
(a)	4	3	1	2	(b)	4	2	1	3
(c)	2	1	4	3	(d)	2	3	1	4

235 Match the following columns.

	Column I (Functions)		Column II (Segments of DNA)
A.	Segment of DNA coding for polypeptide	1.	Recon
B.	Segment of DNA goes for recombination	2.	Muton
C.	Segment of DNA goes for mutation	3.	Cistron

Codes

	A	B	C		A	B	C
(a)	1	2	3	(b)	3	2	1
(c)	3	1	2	(d)	1	3	2

236 Match the following RNA polymerases with their transcribed products. ***NEET (Odisha) 2019***

	Column I		Column II
A.	RNA polymerase-I	1.	*t*RNA
B.	RNA polymerase-II	2.	*r*RNA
C.	RNA polymerase-III	3.	*hn*RNA

Codes

	A	B	C		A	B	C
(a)	1	3	2	(b)	1	2	3
(c)	2	3	1	(d)	3	2	1

237 Match the following genes of the *lac* operon with their respective products. ***NEET 2019***

	Column I		Column II
A.	*i* gene	1.	β-galactosidase
B.	*z* gene	2.	Permease
C.	*a* gene	3.	Repressor
D.	*y* gene	4.	Transacetylase

Codes

	A	B	C	D		A	B	C	D
(a)	1	2	3	4	(b)	3	1	4	2
(c)	3	4	1	2	(d)	1	3	2	4

238 Match the following columns.

	Column I (Enzymes)		Column II (Functions)
A.	β-galactosidase	1.	Joining of DNA fragments
B.	Permease	2.	Peptide bond formation
C.	Ligase	3.	Hydrolysis of lactose
D.	Ribozyme	4.	Increase permeability to β-lactose

Codes

	A	B	C	D
(a)	1	2	3	4
(b)	3	4	1	2
(c)	3	2	1	4
(d)	4	1	2	1

239 Match the following columns.

	Column I		Column II
A.	Termination (Translation)	1.	Aminoacyl *t*RNA synthatase
B.	Translation	2.	Okazaki fragments
C.	Transcription	3.	GTP dependent release factor
D.	DNA replication	4.	RNA polymerase

Codes

	A	B	C	D
(a)	3	1	4	2
(b)	2	3	1	4
(c)	4	3	1	2
(d)	2	1	3	4

240 Identify the correct match between the codons and coding functions.

	Column I		Column II
A.	AUG	1.	Phenylalanine
B.	UAA	2.	Methionine
C.	UUU	3.	Tryptophan
D.	UGG	4.	Termination

Codes

	A	B	C	D
(a)	1	4	2	3
(b)	2	4	1	3
(c)	4	3	2	1
(d)	4	1	3	2

NCERT Exemplar

MULTIPLE CHOICE QUESTIONS

241 In a DNA strand the nucleotides are linked together by
(a) glycosidic bonds (b) phosphodiester bonds
(c) peptide bonds (d) hydrogen bonds

242 A nucleoside differs from a nucleotide. It lacks the
(a) base (b) sugar
(c) phosphate group (d) hydroxyl group

243 Both deoxyribose and ribose belong to a class of sugars called
(a) trioses (b) hexoses
(c) pentoses (d) polysaccharides

244 The fact that a purine always paired base through hydrogen bonds with a pyrimidine base leads to, in the DNA double helix
(a) the antiparallel nature
(b) the semiconservative nature
(c) uniform width throughout DNA
(d) uniform length in all DNA

245 Which of the following are the functions of RNA?
(a) It is carrier of genetic information from DNA to ribosomes synthesising polypeptides
(b) It carries amino acids to ribosomes
(c) It is a constituent component of ribosomes
(d) All of the above

246 Who amongst the following scientists had no contribution in the development of the double helix model for the structure of DNA?
(a) Rosalind Franklin (b) Maurice Wilkins
(c) Erwin Chargaff (d) Meselson and Stahl

247 While analysing the DNA of an organism a total number of 5386 nucleotides were found out of which the proportion of different bases were Adenine = 29%, Guanine = 17%, Cytosine = 32%, Thymine = 17%. Considering the Chargaff's rule it can be concluded that
(a) it is a double-stranded circular DNA
(b) it is single-stranded DNA
(c) it is a double-stranded linear DNA
(d) No conclusion can be drawn

248 In some viruses, DNA is synthesised by using RNA as template. Such a DNA is called
(a) A-DNA (b) B-DNA (c) *c*DNA (d) *r*DNA

249 The net electric charge on DNA and histones is
(a) positive
(b) negative
(c) negative and positive, respectively
(d) zero

250 The first genetic material could be
(a) protein (b) carbohydrates
(c) DNA (d) RNA

251 If Meselson and Stahl's experiment is continued for four generations in bacteria, the ratio of $^{15}N/^{15}N : ^{15}N/^{14}N : ^{14}N/^{14}N$ containing DNA in the fourth generation would be
(a) 1:1:0 (b) 1:4:0 (c) 0:1:3 (d) 0:1:7

252 DNA is a polymer of nucleotides which are linked to each other by 3′–5′ phosphodiester bond. To prevent polymerisation of nucleotides, which of the following modifications would you choose?
(a) Replace purine with pyrimidines
(b) Remove/Replace 3′ OH group in deoxyribose
(c) Remove/Replace 2′ OH group with some other group in deoxyribose
(d) Both (b) and (c)

253 Discontinuous synthesis of DNA occurs in one strand, because
(a) DNA molecule being synthesised is very long
(b) DNA-dependent DNA polymerase catalyses polymerisation only in one direction (5′ → 3′)
(c) it is a more efficient process
(d) DNA ligase has to have a role

254 If the sequence of nitrogen bases of the coding strand of DNA in a transcription unit is
5' – A T G A A T G – 3',
the sequence of bases in its RNA transcript would be
(a) 5′ – A U G A A U G – 3′ (b) 5′ – U A C U U A C – 3′
(c) 5′ – C A U U C A U – 3′ (d) 5′ – G U A A G U A – 3′

255 The promoter site and the terminator site for transcription are located at
(a) 3′ (downstream) end and 5′ (upstream) end, respectively of the transcription unit
(b) 5′ (upstream) end and 3′ (downstream) end, respectively of the transcription unit
(c) the 5′ (upstream) end
(d) the 3′ (downstream) end

256 The RNA polymerase holoenzyme transcribes
(a) the promoter, structural gene and the terminator region
(b) the promoter and the terminator region
(c) the structural gene and the terminator regions
(d) the structural gene only

257 Which one of the following steps in transcription is catalysed by RNA polymerase?
(a) Initiation (b) Elongation
(c) Termination (d) All of these

258 Which one of the following is true with respect to AUG?
(a) It codes for methionine only
(b) It is also an initiation codon
(c) It codes for methionine in both prokaryotes and eukaryotes
(d) All of the above

259 With regard to mature *m*RNA in eukaryotes
(a) exons and introns do not appear in the mature RNA
(b) exons appear, but introns do not appear in the mature RNA
(c) introns appear, but exons do not appear in the mature RNA
(d) Both exons and introns appear in the mature RNA

260 To initiate translation, the *m*RNA first binds to
(a) the smaller ribosomal subunit
(b) the larger ribosomal subunit
(c) the whole ribosome
(d) No such specificity exists

261 If the base sequence of a codon in *m*RNA is 5'–AUG–3', the sequence of *t*RNA pairing with it must be
(a) 5′ – UAC – 3′ (b) 5′ – CAU – 3′
(c) 5′ – AUG – 3′ (d) 5′ – GUA – 3′

262 The amino acid attaches to the *t*RNA at its
(a) 5′-end (b) 3′-end
(c) Anticodon site (d) DHU loop

263 Control of gene expression takes place at the level of
(a) DNA-replication (b) transcription
(c) translation (d) None of these

264 In *E. coli*, the *lac* operon gets switched on when
(a) lactose is present and it binds to the repressor
(b) repressor binds to operator
(c) RNA polymerase binds to the operator
(d) lactose is present and it binds to RNA polymerase

265 Regulatory proteins are the accessory proteins that interact with RNA polymerase and affect its role in transcription. Which of the following statements is correct about regulatory protein?
(a) They only increase expression
(b) They only decrease expression
(c) They interact with RNA polymerase, but do not affect the expression
(d) They can act both as activators and as repressors

266 Which was the last human chromosome to be completely sequenced?
(a) Chromosome 1 (b) Chromosome 11
(c) Chromosome 21 (d) Chromosome-X

267 The human chromosome with the highest and least number of genes in them are respectively
(a) chromosome 21 and Y (b) chromosome 1 and X
(c) chromosome 1 and Y (d) chromosome X and Y

Answers

› Mastering NCERT with MCQs

1 (a)	**2** (b)	**3** (d)	**4** (a)	**5** (c)	**6** (a)	**7** (a)	**8** (a)	**9** (b)	**10** (b)	**11** (a)	**12** (c)	**13** (d)	**14** (d)	**15** (b)
16 (c)	**17** (c)	**18** (d)	**19** (c)	**20** (c)	**21** (c)	**22** (c)	**23** (c)	**24** (a)	**25** (c)	**26** (a)	**27** (d)	**28** (a)	**29** (b)	**30** (c)
31 (a)	**32** (a)	**33** (c)	**34** (d)	**35** (c)	**36** (b)	**37** (c)	**38** (a)	**39** (a)	**40** (a)	**41** (b)	**42** (d)	**43** (d)	**44** (c)	**45** (b)
46 (b)	**47** (a)	**48** (b)	**49** (a)	**50** (d)	**51** (d)	**52** (b)	**53** (c)	**54** (a)	**55** (c)	**56** (a)	**57** (b)	**58** (a)	**59** (c)	**60** (a)
61 (b)	**62** (b)	**63** (a)	**64** (c)	**65** (b)	**66** (a)	**67** (c)	**68** (d)	**69** (b)	**70** (a)	**71** (a)	**72** (d)	**73** (a)	**74** (b)	**75** (a)
76 (c)	**77** (a)	**78** (c)	**79** (a)	**80** (b)	**81** (b)	**82** (c)	**83** (d)	**84** (a)	**85** (a)	**86** (a)	**87** (b)	**88** (*)	**89** (c)	**90** (c)
91 (c)	**92** (a)	**93** (d)	**94** (c)	**95** (c)	**96** (b)	**97** (a)	**98** (c)	**99** (d)	**100** (d)	**101** (b)	**102** (b)	**103** (a)	**104** (b)	**105** (c)
106 (a)	**107** (c)	**108** (a)	**109** (b)	**110** (b)	**111** (c)	**112** (d)	**113** (d)	**114** (b)	**115** (a)	**116** (a)	**117** (c)	**118** (c)	**119** (a)	**120** (a)
121 (c)	**122** (c)	**123** (c)	**124** (c)	**125** (a)	**126** (a)	**127** (c)	**128** (c)	**129** (a)	**130** (b)	**131** (a)	**132** (c)	**133** (d)	**134** (c)	**135** (c)
136 (a)	**137** (c)	**138** (d)	**139** (c)	**140** (b)	**141** (c)	**142** (d)	**143** (b)	**144** (a)	**145** (c)	**146** (b)	**147** (b)	**148** (d)	**149** (b)	**150** (b)
151 (a)	**152** (a)	**153** (c)	**154** (b)	**155** (a)	**156** (a)	**157** (a)	**158** (d)	**159** (d)	**160** (d)	**161** (c)	**162** (d)	**163** (b)	**164** (c)	**165** (d)
166 (a)	**167** (a)	**168** (c)	**169** (a)	**170** (d)	**171** (d)	**172** (c)	**173** (d)	**174** (d)	**175** (a)	**176** (b)	**177** (a)	**178** (b)	**179** (c)	**180** (b)
181 (a)	**182** (c)	**183** (a)	**184** (a)											

› NEET Special Types Questions

185 (d)	**186** (a)	**187** (a)	**188** (a)	**189** (a)	**190** (a)	**191** (a)	**192** (a)	**193** (a)	**194** (b)	**195** (a)	**196** (b)	**197** (a)	**198** (b)	**199** (a)
200 (b)	**201** (c)	**202** (c)	**203** (d)	**204** (d)	**205** (c)	**206** (d)	**207** (c)	**208** (d)	**209** (d)	**210** (a)	**211** (d)	**212** (c)	**213** (d)	**214** (d)
215 (a)	**216** (b)	**217** (d)	**218** (c)	**219** (d)	**220** (d)	**221** (b)	**222** (c)	**223** (a)	**224** (b)	**225** (d)	**226** (c)	**227** (c)	**228** (b)	**229** (b)
230 (b)	**231** (b)	**232** (a)	**233** (c)	**234** (a)	**235** (c)	**236** (c)	**237** (b)	**238** (b)	**239** (a)	**240** (b)				

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241 (b)	**242** (c)	**243** (c)	**244** (c)	**245** (d)	**246** (d)	**247** (b)	**248** (c)	**249** (c)	**250** (d)	**251** (d)	**252** (b)	**253** (b)	**254** (a)	**255** (b)
256 (c)	**257** (b)	**258** (d)	**259** (b)	**260** (a)	**261** (b)	**262** (b)	**263** (b,c)	**264** (a)	**265** (d)	**266** (a)	**267** (c)			

Answers & Explanations

1 (*a*) DNA is a long chain of polymer of deoxyribonucleotide in which a phosphate group is attached to 5′−OH of nucleoside through phosphodiester linkage.

2 (*b*) Length of DNA is directly proportional to the number of nucleotides. As the number of nucleotides increases, the length of DNA also increases.

3 (*d*) Option (d) is the incorrect match and can be corrected as

Haploid content of human DNA is 3.3×10^9 bp.

Rest of the matches are correct.

4 (*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.

7 (*a*) Adenosine and deoxyadenosine differ in only sugar. Nitrogenous bases are attached to the pentose sugar by N-glycoside bond.

If ribose sugar is present then it is called nucleoside and when deoxyribose sugar is present then it is called deoxynucleoside, i.e. adenoside (sugar is ribose), deoxyadenoside (sugar is deoxyribose), cytidine, deoxycytidine, uridine or deoxythymine.

10 (*b*) Adenylic acid, cytidilic acid and guanylic acid are nucleotides. A nucleotide is composed of three components – nitrogen base (adenosine, cytosine, guanine), ribose sugar and a phosphate group. These are monomer unit of nucleic acid, i.e. RNA and DNA.

Adenine, cytidine, thymidine are nucleosides.

Uracil, cytosine and adenosine are nitrogenous bases.

13 (*d*) Thymine and uracil, both have similar structures and are pyrimidine. Thymine ring has one additional methyl group at 5′ position in its pyrimidine ring. Therefore it is also called 5 methyl uracil.

16 (*c*) The percentage of bases which are pyrimidines is 50%. According to Chargaff's rule

$$\underset{\text{(Purines)}}{A + G} = \underset{\text{(Pyramidines)}}{C + T} = 50\%$$

$\therefore$ If A = 20%, then T = 20%

$$C + T = 50\%$$

$$C = 50\% - 20\% = 30\%$$

Total percentage of pyrimidine bases (T + C) are 20 + 30 = 50%

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

i.e. (A + T) = (G + C)

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

If cytosine = 17%, then G = 17%

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

then $A + 17 + 17 + T = 100$

$$A + T + 34 = 100$$

$$A + T = 100 - 34$$

$$A + T = 66$$

$$A = T = 66/2 = 33\%$$

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

20 (*c*) Option (c) is incorrect and can be corrected as

Adenine forms two hydrogen bonds with thymine of the opposite strand and *vice-versa*. On the other hand, guanine is bounded with cytosine with three H-bonds.

Rest of the options are correct.

23 (*c*) The length of DNA in a human cell is about 2.2 m. It can be calculated as

The distance between two consecutive base pairs = 0.34 nm or 0.34×10^{-9} m

If the length of DNA double helix in a typical mammalian cell

= The total number of bp × Distance between two consecutive bp

$= 6.6 \times 10^9$ bp $\times 0.34 \times 10^{-9}$ m/bp = 2.2 m

24 (*a*) In the given case, the number of base pairs for *E. coli* would be 4×10^6 bp. It can be calculated as

Average distance between two base pairs of DNA is 3.4 Å. Length of *E. coli* DNA is $= 1.36 \times 10^7$ Å

So, number of nucleotides $= \frac{1.36 \times 10^7 \text{ Å}}{3.4 \text{Å}} = 0.39 \times 10^7$

$$= 3.9 \times 10^6 \cong 4 \times 10^6 \text{ bp}$$

26 (*a*) In a eukaryotic cell, the DNA packaging has positively charged basic proteins called as histones. A protein acquires charge depending upon the abundance of amino acids residues with charged side chains. Histones are rich in basic amino acid residues lysine and arginine and hence are positively charged.

27 (*d*) Option (d) is the incorrect match and can be corrected as

Chromatin are thread-like stained (coloured) bodies seen in nucleus. The nucleosomes in chromatin are seen as 'beads on string' when viewed under electron microscope.

Rest of the matches are correct.

28 (*a*) Linker-DNA is attached to H_1 histone protein.

Linker DNA connects two adjacent nucleosomes. Its length is varied (about 145 Å with 70 bp). Nucleosome and linker DNA together constitute chromatosome. Chromatosome contains a histone octamer and DNA.

29 (*b*) The packaging of chromatin at higher level requires an additional set of proteins that are collectively called non-histone proteins (i.e. H2A and H2B).

30 (*c*) The association of H1 histone with nucleosome indicates that DNA is condensed into chromatin fibre. 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 (H2A, H2B, H3 and H4). The linker DNA, consisting of H1 histone connects two adjacent nucleosomes.

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

34 (*d*) Frederick Griffith (1920) conducted a series of experiments on the bacterium *Streptococcus pneumoniae*. Through his experiment he found out that the heat-killed S-strain bacteria had changed the R-strain to virulent form. He called this the transforming principle.

35 (*c*) In Griffith's experiment, he found out that something from dead organism could change the living cells. From his experiment he showed that dead S-bacteria (virulent) are changing (transforming) the R-bacteria (non-virulant) into S-type, i.e. the virulent strain.

37 (*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.

38 (*a*) Hershey and Chase grew cultures of *Escherichia coli*. One culture was supplied with radioactive sulpur (^{35}S) and the another with radioactive phosphorus (^{32}P).

44 (*c*) Option (c) is the incorrect trait and can be corrected as

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

Rest of the options are correct.

47 (*a*) Both DNA and RNA are able to mutate. Infact RNA being unstable, mutates at a faster rate. Consequently, viruses having RNA genome and shorter lifespan, mutate and evolve faster.

49 (*a*) RNA was the first genetic material. There is now enough evidence to suggest that the essential life processes has evolved around RNA.

50 (*d*) Chargaff's rule is not applicable to RNA. It is the generalised formula about DNA structure. The rule states that DNA from any cell of an organism 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.

55 (*c*) Heavy DNA molecule could be distinguished from the normal DNA by centrifugation in a cesium chloride (CsCl) density gradient.

56 (*a*) In Meselson and Stahl's experiment, the generation time (replication time) of *E. coli* culture is about 20 minutes. Therefore, the DNA extracted after the interval of 20 minutes in the experiment had heavy ^{15}N incorporated in its genetic material and had a hybrid density.

58 (*a*) An experiment similar to Meselson and Stahl experiment was performed on *Vicia faba* (faba beans) by Taylor and colleagues in 1958. The experiments proved that the DNA in chromosomes also replicate semiconservatively.

60 (*a*) DNA polymerase is DNA dependent because it uses DNA template to catalyse the polymerisation of deoxynucleotides.

62 (*b*) Separation of the entire length of DNA helix needs a large amount of energy. Hence, only up to certain extent separation of DNA helix can take place.

63 (*a*) Replication fork is a Y-shaped structure formed due to small opening of DNA helix for replication to take place. This is formed because long DNA molecules cannot be separated along the entire length (due to very high energy requirement).

65 (*b*) The replication is continuous on $3' \rightarrow 5'$ polarity strand because DNA polymerase can catalyse polymerisation in $5' \rightarrow 3'$ direction only and we know that DNA strands are complementary to each other. Thus, continuous synthesis occurs in $3' \rightarrow 5'$ direction.

67 (*c*) During DNA replication, super coiling is relaxed by DNA topoisomerase. These enzymes participate in underwinding of DNA.

Other options functions as,

- SSBPs are single strand binding proteins which stabilises the unwound parental DNA.
- Primase is the enzyme which synthesise RNA primer on DNA template to initiate DNA synthesis.
- RNA polymerase enzyme helps in synthesis of new DNA strand during replication.

68 (*d*) Okazaki fragments are short segments of replicating DNA. These have 1000-2000 bp in prokaryotes and 100-200 bp in eukaryotes. These fragments are formed discontinuously and are used to elongate the lagging strand away from the replication fork.

69 (*b*) Option (b) is correct. The phosphorylated nucleotides are *de*ATP (deoxy Adenosine Triphosphate), *de*CTP (deoxy Cytidine Triphosphate), *de*TTP (deoxy Thymidine Triphosphate). These triphosphates serve dual purpose. These act as substrate as well as provide energy for polymerisation of nucleotides by releasing energy after dissociating the phosphate group.

70 (*a*) Option (a) contains the wrongly matched pair and can be corrected as

Transcription is a process of RNA synthesis from a DNA template.

Rest of the options contain correct pairs.

71 (*a*) The strands in the DNA are complementary to each other, not identical. If the two RNAs are formed from both strands then RNAs with different sequences would be formed.

72 (*d*) Option (d) is correct.

If both strands are copied during transcription, then two complementary RNA strands will be produced simultaneously. These would have the tendency to form double-stranded RNA and if these two RNA strands do not form double helix these would code for two different types of proteins. Then, the whole exercise of transcription would be futile.

73 (*a*) If double-stranded RNA is produced during transcription this would prevent RNA from being translated into proteins. Double-stranded RNA have more stability than single-stranded RNA. If double-stranded RNA is formed from transcription, then it is difficult to separate the strands of RNA due to which translation would be halted.

75 (*a*) The strand, which does not code for anything is referred to as coding strand. All the reference point, while defining a trancription unit is made with the coding strand.

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

79 (*a*) Among the given options, only the *m*RNA given in option (a) can be transcripted because it possesses an initiation codon-AUG which codes for methionine. Rest of the *m*RNA sequences start with termination codons, i.e. UAA (Ochre), UAG (Amber) and UGA (Opal). Therefore, these cannot be transcripted.

80 (*b*) Option (b) gives the sequence of *m*RNA produced by the given stretch of DNA. The *m*RNA 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 *m*RNA for the given DNA strand will be 5′–UACGUACGUACGUAC–3'.

81 (*b*) Promoter is present at the 5′-site of structural gene and terminator is present at the 3′-site of structural genes. Thus, we can say that promoter and terminator flanks the structural genes.

82 (*c*) Option (c) is incorrect and can be corrected as Cistron is a segment of DNA coding for a polypeptide.

Rest of the options are correct.

84 (*a*) *r*RNA is the most abundant form of RNA; because it is responsible for coding and protein synthesis in the cell and is also associated with ribosomes.

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

87 (*b*) RNA polymerase only catalyses the elongation process of transcription. The initiation of transcription is done by sigma (σ) unit. The termination of the transcription is acheived by rho (ρ) factor. These two structures are not a part of RNA polymerase. Thus, RNA polymerase can perfom the function of elongation only.

88 (*) This question is incorrect because out of the given initiation and termination factors, none is involved in transcription in eukaryotes.

However, option (a) contains 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 II H) and Transcription Termination Factor-1 (TTF-1), respectively.

90 (*c*) Option (c) is correct.

In prokaryotes, *m*RNA does not require any processing to become active and there is no clear demarcation between the nucleus and cytoplasm. Genetic material is dispersed through out the cytoplasm. Thus, transcription and translation takes place in the same compartment in prokaryotes.

91 (*c*) In the process of transcription (i.e. copying of genetic information from one strand of the DNA into RNA) in eukaryotes, the enzyme RNA polymerase-I transcribes *r*RNA - 28S, 18S and 5.8S.

On the other hand, *t*RNA, 5*s*rRNA and *sn*RNAs are transcribed by RNA polymerase III. RNA polymerase-II transcribes precursor of *m*RNA, i.e. *hn*RNA.

92 (*a*) RNA undergoes a process where the introns (non-coding parts) are removed and exons (coding sequence) are joined to form *m*RNA. This process is called splicing.

93 (*d*) Spliceosome is absent in cells of bacteria. It is a large molecular complex found in nucleus of eukaryotic cells of plants, animals and fungi. It is assembled from *sn*RNAs and protein complexes which play an important role in splicing of introns.

95 (*c*) At the 5′ end of eukaryotic *m*RNA, 7 mG (7-methyl guanosine) is present. In eukaryotes, primary transcript is often larger than the functional RNAs. Therefore, post-transcription processing is required to convert primary transcript of all types of RNAs into functional RNAs. It is of four types; cleavage, splicing, terminal addition and nucleotide modification.

The terminal additions include capping and tailing. In capping, 7 mG is added to 5′ end of *m*RNA.

97 (*a*) Fully processed *hn*RNA to undergo translation is called *m*RNA. *hn* (heterogenous nuclear) RNA is the raw form of *m*RNA containing both introns and exons. After splicing and post-transcriptional modification of *hn*RNA, *m*RNA is formed.

104 (*b*) Polynucleotide phosphorylase enzyme is used in polymerising RNA with defined sequences in a template independent manner (enzymatic synthesis of RNA). It is also called Servo Ochoa enzyme.

105 (*c*) 61 codons code for amino acids out of the total 64 codons. The rest three are non-sense codons which are used for stopping translation. These are also called stop codons.

109 (*b*) UAC is not a stop codon. It codes for tyrosine amino acid.

The last codon of a functional gene which helps in termination of the polypeptide chain, is termed as stop or termination codon. These are UAA, UAG and UGA. These codons do not have *t*RNA to be translated.

113 (*d*) Degeneracy refers to the fact that one amino acid has more than one code triplet and the codons which specify the same amino acids differ only in the third base of the triplet, e.g. both CAC and CAU code for the amino acid histidine.

114 (*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, e.g. in mitochondria, the stop codon UGA for humans specifies amino acid tryptophan.

115 (*a*) Mutation gives rise to alterations in the phenotype. This is the reason as to why mutation is best for studying the relationship between genes and DNA for their expression.

117 (*c*) The reading frame of given *m*RNA will not change even after the deletion of GGU from 7th, 8th and 9th positions. However, only the amino acid glycine will not be formed at third position in this case which is being coded by GGU.

In rest of the cases, insertion or deletion of one or two nucleotide bases would result in the complete alteration in the reading frame of *m*RNA.

118 (*c*) 33 codons will be altered if the base at position 901 is deleted from an *m*RNA having 999 bases. This can be calculated as

Total number of bases in the given *m*RNA = 999

Number of codons for this *m*RNA $= \frac{999}{3} = 333$

If one base is deleted at position 901 then the number bases unchanged are 900 which codes for $\frac{900}{3}$

$= 300$ amino acids

Thus, number of altered codons will be

$$333 - 300 = 33$$

119 (*a*) Frameshift mutation of the genetic bases (deletion or addition) gives the proof that codon is triplet and reads in contagious manner. Deletion or addition of a base pair disturb the reading frame of DNA or *m*RNA.

121 (*c*) *t*RNA was known as *s*RNA (soluble RNA) before the genetic code was postulated. Its role as an adaptor molecule was reported later.

123 (*c*) Option (c) is incorrect and can be corrected as

*t*RNA are specific for each amino acid, e.g. for initiation there is a specific initiator *t*RNA.

Rest of the options are correct for *t*RNA.

124 (*c*) Three dimensional structure or compact form of *t*RNA was given by Klug in 1974. It looks like the letter 'L' of English alphabet. Hence, it is called as the L-form model of *t*RNA.

125 (*a*) *t*RNA binds to *m*RNA through anticodon loop, as it bears bases complementary to those on *m*RNA being translated.

The amino acid loop of *t*RNA is involved in binding the respective amino acid. The T ψ C loop helps in binding the amino acid, while the D-loop of *t*RNA is the binding site for aminoacyl synthetase.

126 (*a*) RNA polymerase-III transcribes the synthesis of *t*RNA, therefore *t*RNA synthesis will be affected if it is removed from nucleoplasm. RNA polymerase-II synthesises *m*RNA while, RNA polymerase-I synthesis *r*RNA in eukaryotes.

128 (*c*) Polysome is a string of ribosomes associated with a single *m*RNA. Polysome helps to produce a number of copies of the same polypeptide.

129 (*a*) In the process of protein synthesis, *t*RNA carrying the amino acids enters the A-site of the ribosome. Peptide bonds that are formed between the amino acids are present on P and A-site.

130 (*b*) According to the sequences present on the *m*RNA, amino acids are produced. Thus, the order and the sequence of the amino acids are defined by *m*RNA.

135 (*c*) UTRs present on *m*RNA refer to Untranslated Regions present at both 5′–end (before start codon) and 3′–end (after stop codon). These are the additional sequences that are not translated. These are required for efficient translation process.

137 (*c*) Option (c) contains the incorrect match and can be corrected as

A translational unit in *m*RNA is the sequence of RNA that is flanked by the start codon (AUG) and ends at the stop codon and codes for a polypeptide.

Rest of the matches are correct.

138 (*d*) Option (d) represents the correct sequential code of *t*RNA. DNA and *m*RNA have complementary base pairs.

If the DNA is 3′–TAC ATG GGT CCG–5′

than *m*RNA will have

II I IV III

5′–AUG UAC CCA GGC–3′

*t*RNA and *m*RNA have complementary base pairs.

139 (*c*) Option (c) is correct as UAA, UAG and UGA are stop codons on *m*RNA for which no *t*RNA molecules are present. *t*RNA molecules have anticodon, therefore anticodons for the mentioned stop codons will AUU, AUC and ACU which does not exist.

144 (*a*) Positively regulatory proteins are called activators. These activator proteins bind to regulatory sites on DNA near to the promoter regions which act as on / off switches. This binding facilitates RNA polymerase activity and transcription of nearby genes.

145 (*c*) In the operon system, the promoter is generally situated beside the operator genes. In the prokaryotes, the working of promoter region (binding of RNA polymerase) is coordinated by the operator genes, e.g. if operator genes are occupied by the repressor proteins then RNA polymerase does not bind to the promoter gene and there is no transcription.

146 (*b*) An operon is considered to regulate genetic unit or DNA. It act as a single regulatory unit having one or more structural genes, an operator gene, regulator genes, a repressor and an inducer.

148 (*d*) Option (d) is the correct match.

Jacob and **Monod** (1916) discovered the ***lac* operon**.

Rest of the matches are incorrect and can be corrected as

- **Matthew Meselson** and **F Stahl** discovered the semiconservative 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.

149 (*b*) A *lac* operon has one regulatory gene (i.e. *i*-gene) and three structural genes (i.e. *z*, *y* and *a* genes).

150 (*b*) Gene regulation governing lactose operon of *E. coli* that involves the *Lac i* gene products is negative and inducible because its repressor protein prevents transcription.

Lac i gene produces an inhibitor or repressor that induces negative regulation of *lac* operon.

The repressor binds to the operator gene and stops its working. Repressor is meant to block the operator gene, so that structural genes are unable to form *m*RNA, thus stopping the transcription of genes.

On the other hand, lactose operon is inducible operon system. It is a regulated unit of genetic material which is switched on in response to the presence of a chemical.

151 (*a*) β-galactosidase enzyme will be produced in a cell in which non-sense mutation takes place in the *lac y* gene. Non-sense mutation stops polypeptide synthesis due to the formation of non-sense codon. In *lac* operon, sequence of structural genes is *z* (codes for β-galactosidase), *y* (permease) and *a* gene (transacetylase). Due to non-sense mutation at *y*-gene, permease synthesis will be stopped resulting in non-expression of both *y* and successive gene *a* also. Thus, only β-galactosidase enzyme will be produced.

153 (*c*) Lactose is the substrate for the enzyme beta (β) galactosidase and it regulates the switching on and off of the *lac* operon. Hence, it is termed as inducer.

156 (*a*) Repressor protein attaches to the operator gene. It is a regulatory protein synthesised by regulator gene. Repressor is meant for blocking the operator gene, so that the structural genes are unable to form *m*RNA.

157 (*a*) An inducer binds with the repressor protein and prevents the repressor protein from binding to the operator.

Glucose and galactose cannot act as an inducer because these do not have the binding sites for attaching the repressor protein.

160 (*d*) Option (d) is incorrect and can be corrected as During human genome project many non-human organisms such as bacteria, yeast, *C. elegans*, *Drosophila*, plants, etc. DNA were also sequenced.

Rest of the options are correct.

161 (*c*) Gene or DNA library is a collection cloned or copied DNA (*c*DNA) of cells or tissues, organs of an organism in a preserved form for future use.

163 (*b*) Option (b) is the incorrect match and can be corrected as

Sequence annotation is simply sequencing the whole set of genome that contained all the coding and non-coding sequence and later assigning different regions in the sequence with functions.

Rest of the matches are correct.

164 (*c*) For generating genetic and physical maps, restriction endonuclease was used. For sequencing the human DNA, the entire DNA from a cell is isolated and converted into random fragments of relatively smaller size by using restriction endonuclease enzyme and cloned in suitable host using specialised vectors.

165 (*d*) Chromosome number 21, 22 and Y are listed in G group. To make chromosomal studies easier, chromosomes are classified into Groups A to G as given below.

Group A contains 1-3 chromosomes

B contains 4-5 chromosomes

C contains 6-12 chromosomes and X-chromosome

D contains 13-15 chromosomes

E contains 16-18 chromosomes

F contains 19-20 chromosomes

G contains 21-22 chromosomes and Y- chromosome

166 (*a*) Human genome is said to have approximately 3×10^9 bp, but the exact number is 3164.7 million bp.

170 (*d*) Option (d) is correct as reptitive sequences are stretches of DNA sequences that are repeated many times, (sometimes hundred to thousand times). These are thought to have no direct coding functions, but these shed light on chromosome structure, dynamics and evolution.

171 (*d*) Option (d) is incorrect and can be corrected as

Repetitive DNA sequences are stretches of DNA sequences that are repeated many times, sometimes hundred to thousand times.

Rest of the options are correct.

172 (*c*) There are about 1.4 million locations where single base DNA differences occurs. These locations are called SNPs (snips) or Single Nucleotide Polymorphism in humans.

176 (*b*) Sattelite DNA is important because it shows high degree of polymorphism (variation at genetic level) in population and also the same degree of polymorphism in an individual, which is heritable from parents to children. Also satellite DNA does not code for proteins or enzymes but are different in all the members of a population.

182 (*c*) PCR (Polymerase Chain Reaction) is the technique in which many copies of DNA can be produced in a short period of time. It can increase the sensitivity of DNA fingerprinting.

183 (*a*) In Southern blotting DNA is transferred from electrophoresis gel plate to the nitrocellulose or nylon membrane sheet.

185 (*d*) Assertion is false, but Reason is true. Assertion can be corrected as

DNA serves as the genetic material in most organisms, but in some viruses like TMV, RNA acts as the genetic material. DNA is a double-stranded biomolecule, but can also exist as a single-stranded biomolecule.

186 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

The two chains of DNA have antiparallel polarity. This is because one chain has a free phosphate moiety at the 5′ end of the ribose sugar and another chain has a free phosphate moiety at the 3′ end.

187 (*a*) Both Assertion and Reason are correct and Reason is the correct explanation of Assertion.

Adenine cannot pair with cytosine. Adenine pairs with thymine and cytosine pairs with guanine. This occurs because adenine pairs with thymine with two hydrogen bonds, i.e. have only two hydrogen donor / hydrogen acceptor sites whereas cytosine has three hydrogen donor / hydrogen acceptor sites. Thus, due to lack of complementarity between the hydrogen donor and hydrogen acceptor sites between adenine and cytosine, these cannot pair.

188 (*a*) Both Assertion and Reason are correct and Reason is the correct explanation of Assertion.

Histones are basic in nature because these are rich in amino acids lysine and arginine which are basic in nature.

189 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

Heterochromatin is densely packed and inaccessible to transcription factors. Hence, it is rendered transcriptionally silent or inactive.

190 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

RNA is an unstable catalytic molecule. It mutates at a faster rate than DNA. Thus, viruses having RNA genome and shorter lifespan, mutate and evolve faster due to this unstability.

191 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

The DNA-dependent DNA polymerase works in the 5′ → 3′ direction requiring a free 3′–OH of a pre-existing polynucleotide for initiating DNA replication. Thus, it continuously synthesises the strand having polarity 3′ → 5′.

Replication of the lagging strand (5′→ 3′) generates small polynucleotide fragments, okazaki fragments. The replication of this strand is discontinuous.

192 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

In eukaryotes, replication and transcription take place in the nucleus.

The fully processed *hn*RNA now called *m*RNA, is transferred from the nucleus into the cytoplasm, where translation occurs.

This is because all the amino acids, *t*RNA and ribosomes required for translation are present in the cytoplasm.

193 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

The primary transcript in eukaryotes, i.e. the *hn*RNA is much larger as it contains both introns and exons. It is the precussor of *m*RNA. During post-transcriptional modification. Introns (the intervening sequences), which do not code for proteins are removed and all exons are joined to form fully prossessed *m*RNA.

194 (*b*) Both Assertion and Reason are true, but Reason is not the correct explanation of Assertion.

Polycistronic *m*RNA, commonly found in prokaryotes, two or more coding regions are present and can specify a number of polypeptide chains or proteins. It further contains multiple (open) reading frames to enable the formation of two or more proteins.

Both polycistronic and monocistronic *m*RNAs have a 5′ leader sequence, the coding region (containing initiation codon and termination codon) and a non-translated 3′ trailer sequence.

195 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

In transcription, the strand with 3′ → 5′ polarity acts as the template from which *m*RNA is transcribed as is called the template strand.

This is because the enzyme DNA-dependent RNA polymerase catalyses polymerisation in only 5′ → 3′ direction.

196 (*b*) Both the Assertion and Reason are true, but Reason is not the correct explanation of Assertion.

In eukaryotes, transcription, i.e. synthesis of RNA from DNA, occurs inside nucleus, because the genetic material DNA is enclosed within the nucleus in eukaryotes.

In prokaryotes like bacteria, the genetic material, DNA remains suspended within the cytoplasm. Thus, in prokaryotes the processes of transcription and translation occur in cytoplasm.

197 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

The genetic code is degenerate. It means that a given amino acid can be coded by more than one codon. For example, serine is an amino acid coded by UCU, UCC, UCA, UCG, AGU and AGC.

198 (*b*) Both Assertion and Reason are true, but Reason is not the correct explanation of Assertion.

*m*RNA has some additional sequences that are not translated known as Untranslated Regions (UTR). The UTRs are present at both 5′ end (before start codon) and at 3′ end (after stop codon). These are required for efficient translation process.

199 (*a*) Both Assertion and Reason are true and Reason is the correct explanation of Assertion.

DNA fignerprinting is very well-known for its application in paternity testing as it employs the principle of DNA polymorphism. DNA fingerprinting involves the use of satellite DNA. These sequences do not code for any proteins, but show high degree of polymorphism.

These serve as the basis of DNA fingerprinting. These polymorphisms are inheritable from parents to children and thus DNA fingerprinting is the basis of paternity testing.

200 (*b*) Statements I, II, III and IV are correct.

Statement V is incorrect and can be corrected as

Ribose sugar can be represented as $C_5H_{10}O_5$ whereas deoxyribose sugar (has deficit of one oxygen atom) can be represented as $C_5H_{10}O_4$.

201 (*c*) The statement in option (c) is incorrect and can be corrected as

Nucleotides do not have proteins, carbohydrates and fats. Nucleotides contain a sugar, a phosphate group and a nitrogenous base.

Rest of the statements are correct.

202 (*c*) Statements I, II and IV are correct. Statement III is incorrect and can be corrected as

Transforming principle is associated with genetic material of S-strain.

204 (*d*) Statements I, II and IV are correct.

Statement III is incorrect and can be corrected as

^{35}S will end up in the supernatant after centrifugation as sulphur is present in proteins.

205 (*c*) The statement in option (c) is incorrect and can be corrected as

Equal amount of heavy DNA and light DNA was observed in *E. coli* culture after the two generations.

Rest of the statements are correct.

207 (*c*) The statement in option (c) is incorrect and can be corrected as

Meselson and Stahl proposed the semiconservative DNA replication scheme.

Rest of the statements are correct.

210 (*a*) The statement in option (a) is correct.

Rest of the statements are incorrect and can be corrected as

- Exon is the coding or expressed sequence, intron is the non-coding sequence and cistron is the segment of DNA which codes for a polypeptide.
- The region of DNA where transcription starts is promoter.
- The terminator codes for the end of transcription.

212 (*c*) The statement in option (c) is incorrect and can be corrected as

The coding sequences or expressed sequences are called exons. Intervening sequences or non-coding sequences in an unprocessed RNA are called introns.

Rest of the statements are correct.

214 (*d*) Statements II and III are correct. Statements I and IV are incorrect and can be corrected as

- *r*RNA provides the site for protein synthesis.
- A segment of DNA coding for polypeptide is called cistron.

216 (*b*) Statements II and III are correct.

Statements I and IV are incorrect and can be corrected as

- *m*RNA does not have an elaborated 3 D structure, it is a linear chain.
- *m*RNA contains codons and *t*RNA contains anticodons.

217 (*d*) Steps in statements I, II and III are related with *t*RNA as these are steps of polypeptide synthesis, i.e. translation. Steps in statement IV is not related with *t*RNA.

This is because transcription involves copying of genetic information from the template DNA strand to RNA. *t*RNA does not participates inthis process.

218 (*c*) Statements II and IV are correct. Statements I and III are incorrect and can be corrected as

- Glucose and galactose are formed from allolactose by β-galactosidase. These bind with the lactose repressor and activate it is enable the transcription process.
- Tryptophan acts as repressor to stop gene expression.

219 (*d*) Statement II, III and IV are incorrect and only statement I is correct.

This can be explained as in *lac* operon model, regulatory gene is continuously working, whether lactose (inducer) is present or not. It transcribes *m*RNA which codes for repressor.

When this repressor binds with lactose (inducers) it inhibits translation of operator gene (not R gene). Thus, lactose presence affects operator gene not R gene.

220 (*d*) The statement in option (d) is incorrect and can be corrected as

The repressor of the operon is synthesised (all-the-time-constitutively) from the *i* gene. The repressor protein binds to the operator region of the operon and prevents RNA polymerase from transcribing the operon.

Rest of the statements are correct.

221 (*b*) The statement in option (b) is incorrect and can be corrected as

Less than 2% of the genome codes for proteins.

In most of organisms more than 98% of human genome is composed of non-coding DNA (or Junk DNA).

Rest of the statements are correct.

223 (*a*) The statement in option (a) is incorrect and can be corrected as

BAC or Bacterial Artificial Chromosome and YAC or Yeast Artificial Chromosome are the two vectors generally used in human genome project for cloning the large fragments of human DNA.

Rest of the statements are correct.

242 (*c*) A nitrogenous base is attached to the pentose sugar by an N-glycosidic linkage to form a nucleoside, i.e. Nucleoside=Nitrogen base + Pentose sugar.

When a phosphate group is attached to the 5′-OH of a nucleoside through phosphodiester linkage, a nucleotide is formed, i.e. Nucleotide = Nitrogen base + Pentose sugar + Phosphate (PO_4).

So, a nucleoside differs from a nucleotide as it lacks phosphate group.

243 (*c*) Both deoxyribose and ribose belong to the class of sugar called pentoses as these sugars contain five carbon atoms.

244 (*c*) The diameter of the strand is always constant due to the pairing of a purine (adenine and guanine) with a pyrimidine (cytosine and thymine). This specific bonding gives uniform width throughout the DNA.

245 (*d*) Option (d) is correct. *r*RNA, *m*RNA and *t*RNA are the major classes of RNAs that are involved in gene expression. Their functions include

*r*RNA binds protein molecules and forms a ribosome.

*m*RNA carries coded information for translation and polypeptide formation.

*t*RNA is called soluble or adaptor RNA which carries amino acids to ribosomes during protein synthesis.

246 (*d*) Meselson and Stahl had no contribution in the development of double helix model. In 1958, Meselson and Stahl performed experiments on *E. coli* to prove that DNA replication is semiconservative.

247 (*b*) According to Chargaff's rule of base pairing

i.e. $$\frac{A}{T}=\frac{G}{C}=1$$

For the given organism, the DNA does not follow Chargaff's rule as $\frac{A}{T}=\frac{27}{17}\neq\frac{32}{17}=\frac{G}{C}\neq 1$

Hence, it can be concluded that it is a single-stranded DNA, not double-stranded.

248 (*c*) In some viruses, like retroviruses (e.g. HIV), complementary DNA (*c*DNA) is synthesised by using an RNA template. This process is termed reverse transcription and an enzyme called reverse transcriptase is used.

249 (*c*) The net electric charge on DNA and histones is negative and positive, respectively.

DNA consists of a nitrogenous base, pentose sugar and a phosphate group. DNA has negative charge due to the presence of phosphate group (PO_4^{3-}). Histones are rich in basic amino acid residues lysine and arginine, which carry positive charge in their side chains. Therefore, histones are positively charged.

250 (*d*) The first genetic material could be RNA. We know that RNA is present as a genetic material in some viruses, and it also works as a catalyst (there are some important biochemical reactions in living systems that are catalysed by RNA catalysts and not by protein enzymes). But, RNA being a catalyst is reactive and hence unstable.

Therefore, it is considered that DNA has evolved from RNA thereby making RNA the first genetic material.

251 (*d*) Option (d) is correct.

Meselson and Stahl found that DNA of the first generation was hybrid or intermediate (^{15}N and ^{14}N).

It settled in caesium chloride at a level higher than the fully labelled DNA of parent bacteria (^{15}N ^{15}N).

The second generation of bacteria after 40 minutes, contained two types of DNA, 50% light (N^{14} N^{14}) and 50% intermediate (N^{15} N^{14}).

The third generation of bacteria after 60 minutes contained two types of DNA, 25% intermediate (N^{15} N^{14}) and 75% light (N^{14} N^{14}) in 1 : 3 ratio.

It can be assumed that the fourth generation after 80 minutes would contain 12.5% N^{15} N^{14} and 87.5% N^{14} N^{14} DNA in 1:7 ratio.

Thus, if Meselson and Stahl's experiment is continued for four generations in bacteria, the ratio of $^{15}N/\ ^{15}N$: $^{15}N/\ ^{14}N$: $^{14}N/\ ^{14}N$ containing DNA in the fourth generation would be 0 : 1 : 7.

252 (*b*) To prevent polymerisation of nucleotides, 3′ OH group in deoxyribose should be replaced/removed. This is because DNA polymerase enzyme requires a free 3′–OH end of pre-existing polynucleotide to enable polymerisation, leading to the formation of a continuous strand in the 5′→ 3′ direction.

254 (*a*) Option (a) gives the correct sequence of bases in the RNA transcript for the given DNA coding strand.

5′ - A T G A A T G - 3′ (coding strand)

↓

3′- T A C T T A C - 5′ (template strand)

↓

5′ -A U G A A U G - 3′ (RNA)

255 (*b*) The promoter is located towards 5′ end (upstream) of the structural gene of coding strand and provides the binding site for RNA polymerase to initiate transcription. The terminator region is where the transcription stops and it is present at the 3′ end (downstream).

257 (*b*) RNA polymerase catalyses elongation during transcription. During elongation RNA polymerase 'walks' along one strand of DNA known as the template strand in the 3' → 5' direction. For each nucleotide in the template RNA polymerase adds a matching (complementary) RNA nucleotide to the 3' end of the RNA strand. It associates transiently with initiation factor (σ) and termination factor (ρ) to initiate and terminate the transcription, respectively.

259 (*b*) In *m*RNA of eukaryotes exons appear, but introns do not. This is because introns are intervening or non-coding sequences and exons are coding or expressed sequences. Through splicing introns are removed and exons are joined to form *m*RNA.

260 (*a*) To initiate translation, the *m*RNA first binds to the smaller ribosomal subunit.

Ribosome consists of structural RNAs and about 80 different proteins. In its inactive state, it exist as two subunits, a large subunit and a small subunit. When the smaller subunit encounters the *m*RNA, the process of translation of the *m*RNA to protein begins with the binding of the *m*RNA to the smaller ribosome unit.

261 (*b*) The first base of anticodon in 5′ → 3′ direction binds with the third base in codon (reading in 5′ → 3′ direction). Thus, if the base sequence in codon of *m*RNA is 5′ – AUG – 3′ the complementary anticodon will be 3′ – UAC – 5′ or 5′ – CAU – 3′.

262 (*b*) AA-binding site (amino acid binding site) lies at the 3′ end opposite the anticodon and has CCA-OH group. Thus, the site where amino acid attaches to the *t*RNA is the 3′ end of the *t*RNA molecule.

263 (*b, c*) Both options (b) and (c) are correct.

In eukaryotes, the regulation of gene expression is exerted at transcriptional level (formation of primary transcript), processing level (regulation of splicing), transport of mRNA from nucleus to the cytoplasm and translational level.

While, in prokaryotes, control of the rate of transcriptional initiation is the predominant site for control of gene expression.

264 (*a*) When lactose is present, it act as an inducer and binds to the repressor and inactivates it. This repressor fails to bind to operator. Therefore, the RNA polymerase binds to the promoter and transcript *lac m*RNA thus switching on the *lac* operon and allowing transcription to proceed.

265 (*d*) Option (d) is correct.

In a transcription unit, the activity of RNA polymerase at a given promoter is regulated by interaction with accessory proteins, which affects its ability to recognise start sites. These regulatory proteins can act both positively (activators) and negatively (repressors).

266 (*a*) Chromosome 1 was the last completed chromosome, sequenced two decades after the beginning of the human Genome Project (hGP). It is designated as the largest human chromosome.

267 (*c*) The human chromosomes having the highest and least number of genes, respectively are chromosome 1 with 2968 genes and chromosome-Y with 231 genes.