Molecular Basis of Inheritance

CHAPTER 6

EXAM DRILL

ANSWERS

1. **(b) :** RNA splicing represents a post-transcriptional mechanism to generate multiple functional RNAs or proteins from a single transcript. It is a process that removes the intervening, non-coding sequences of genes (introns) from pre-*m*RNA and joins the protein-coding sequences (exons) together in order to enable translation of *m*RNA into a protein.

2. **(a) :** Sense strand or coding strand has 5′ → 3′ polarity. A pyrimidine is a six-membered single ring.
In prokaryotes, a cistron has a continuous coding sequence from beginning to end whereas in eukaryotes, a cistron contains non-coding regions also.

OR

(d) : The chemical structure of RNA is very similar to that of DNA : each nucleotide consists of a nitrogenous base, a sugar and a phosphate group. There are two differences that distinguish DNA from RNA : (a) RNA contains the sugar ribose, while DNA contains the slightly different sugar deoxyribose and (b) RNA has the nucleobase uracil while DNA contains thymine.

3. **(d) :** The bond found between the pentose sugar and the nitrogen base is glycosidic bond. The bond found between the nitrogen bases is hydrogen bond and the bond found between the sugar moiety and the phosphate molecule is phosphodiester bond.

4. **(c) :** When the DNA is stained and observed under the light microscope, it exhibits two regions, on the ground of concentration or intensity of staining. The dark stained areas are said as heterochromatin and light stained areas are said as euchromatin. Euchromatin is loosely packed and heterochromatin is densely packed.

5. **(a) :** Transcription is catalysed by the enzyme DNA dependent RNA polymerase. The DNA have two strands with opposite polarity but only one strand works as template. Similar to DNA polymerase, DNA-dependent RNA polymerase also catalyse the polymerisation in 5′ → 3′ only, therefore, the strand with 3′ → 5′ polarity acts as a template and is referred to as template strand for *m*RNA synthesis.

6. **(d) :** RNA is less stable than DNA so RNA may get destroyed by heat.

7. Capping and tailing of hnRNA occur respectively at 5′ end and 3′ end.

8. DNA Polymerase II is responsible for primer extension, editing and proofreading.

9. Length of DNA segment is usually calculated by finding the number of base pairs and multiplying it by the distance between adjoining base pairs.

10. In prokaryotes and eukaryotes, the termination of translation occurs when a nonsense codon (UAA, UAG, or UGA) is encountered for which there is no complementary *t*RNA. On aligning with the A site, these nonsense codons are recognised by release factors in prokaryotes and eukaryotes that result in the P-site amino acid detaching from its *t*RNA, releasing the newly made polypeptide.

11. **(a) :** When bacteria *Streptococcus pneumoniae* are grown on a culture plate, some produce smooth shiny colonies (S) while others produce rough colonies (R). This is because the S strain bacteria have a mucous (polysaccharide) coat, while R strain does not. Mice infected with the S strain (virulent) die from pneumonia infection but mice infected with the R strain do not develop pneumonia. In Griffith's experiment, some 'transforming principle', transferred from the heat-killed S strain, had enabled the R strain to synthesise a smooth polysaccharide coat and become virulent which must be due to the transfer of the genetic material. This is known as transformation.

12. **(a)**

13. **(c) :** Replication in eukaryotes occurs in the nucleus during S phase of cell cycle.

14. **(b)**

15. **(i) (b) :** In the presence of an inducer, such as lactose or allolactose, the repressor is inactivated by interaction with the inducer. This allows RNA polymerase access to the promoter and transcription proceeds.
(ii) (b) : *E.coli* will use all the glucose in the media to derive energy. Only when they sense a low glucose level they search alternative energy source like lactose, fructose or galactose.
(iii) (a) : z gene codes for the enzyme β-galactosidase which is responsible for the hydrolysis of lactose into its monomeric units, galactose and glucose. So, *E. coli* cells with a mutated

gene and having only lactose as a source of energy could not grow.

(iv) (d) : In *lac* operon, activator is positive regulator and acts as a glucose sensor while, repressor is a negative regulator and acts as a lactose sensor.

(v) (c) : If there is a mutation in the operator gene, the repressor cannot bind to it. Thus, the operon will express constitutively.

16. (i) (b) : The central dogma of molecular biology explains the flow of genetic information from DNA to RNA to make functional product, a protein.

DNA $\rightarrow$ RNA $\rightarrow$ Protein

(ii) (a) : Reverse transcriptase also called RNA directed DNA polymerase, is an enzyme encoded from the genetic material of retroviruses that catalyses the transcription of retrovirus RNA into DNA. This catalysed transcription is the reverse process of normal cellular transcription of DNA into RNA.

(iii) (c)

(iv) (a)

(v) (b) : A type of virus that has RNA instead of DNA as its genetic material uses enzyme called reverse transcriptase to become part of host cell's DNA. The virus that causes AIDS, the human immunodeficiency virus (HIV) is a type of retrovirus.

17. Tetracycline, neomycin, erythromycin and rifampicin are inhibitors of protein synthesis. Their modes of action are as follows :

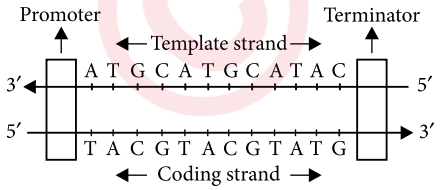
(i) Tetracycline inhibits binding of aminoacyl-*t*RNA to ribosome.

(ii) Neomycin inhibits the interaction of *t*RNA with *m*RNA.

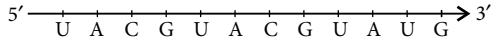
(iii) Erythromycin inhibits the translocation of *m*RNA along ribosome.

(iv) Rifampicin inhibits RNA synthesis by inhibiting RNA polymerase.

18. (a)



(b)



19. (a) *i* = Regulator gene

p = Promoter gene

(b) 'Inducer' for the given operon is 'lactose'. Its role is to bind with repressor, change the latter into non-DNA binding state so as to free the operator gene and switch on the *lac* operon.

OR

From the given example it is inferred that genetic code is degenerate, universal and unambiguous.

Unambiguous codon : Codons that specify only one amino acid and not any other. *E.g.*, AUG codes for methionine.

Non overlapping code : Successive triplets are read in order. Each nucleotide is part of only one triplet codon.

Universal codon : A codon that is applicable universally *i.e.*, specifies the same amino acid from a virus to a tree or human being.

20. The DNA molecule is taken and digested into fragments with the help of restriction endonuclease. These fragments are separated through electrophoresis and transferred on nylon membrane. Further these fragments are hybridised with VNTR probes and analysed through autoradiography.

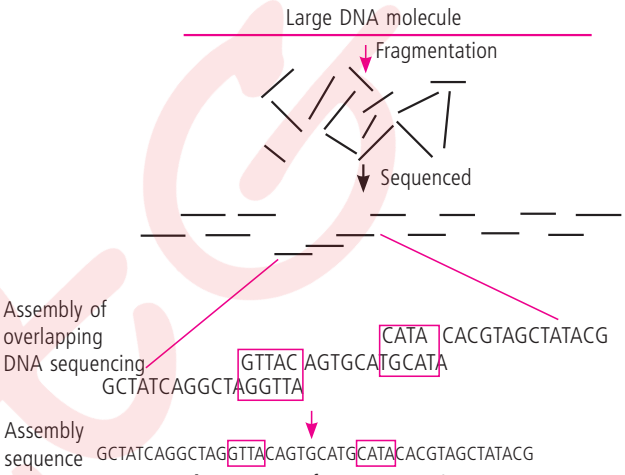


Fig.: Process of DNA sequencing

21. (i) DNA is double-stranded, but only one strand serves as a template for transcription at any given time and is called template strand. The non template strand is referred to as the coding strand because its sequence will be the same as that of the new RNA molecule. It seems reasonable that only one strand of DNA is transcribed, because transcription of RNA from both strands would produce two complementary RNA strands from the same stretch of DNA, and these strands presumably would produce two different kinds of protein (with different amino acid sequences).

(ii) Polycistronic *m*RNA is a RNA that encodes several proteins and is characteristic of many bacterial and chloroplast *m*RNAs. Monocistronic *m*RNA is a RNA that encodes only one protein and all eukaryotic *m*RNAs are monocistronic.

22. Genetic code refers to the relationship between the sequence of nitrogenous bases in *m*RNA and the sequence of amino acids in a polypeptide chain.

The important properties of genetic code are as follows :

(i) Code is a triplet.

(ii) The code is degenerate.

(iii) The code is non-overlapping.

(iv) The code is commaless.

(v) The code is unambiguous.

(vi) The code is universal.

(vii) Genetic code has polarity.

23. *Lac* operon is composed of an operator site, regulatory gene and structural genes. Operator site is a DNA sequence that regulates transcription of the structural genes. The regulatory gene encodes for the repressor protein and regulates the transcription of structural genes. There are three structural genes (z, y, and a) in *lac* operon. All the three gene products in *lac* operon are required for metabolism of lactose. The z gene codes for beta-galactosidase (β-gal), primarily responsible for the transformation of lactose into allolactose and hydrolysis of lactose into galactose and glucose. The y gene codes for permease, which increases permeability of the cell to β-galactosides. The a gene encodes transacetylase.

24. Differences between prokaryotic and eukaryotic transcription are as follows:

	Prokaryotic transcription	**Eukaryotic transcription**
(i)	Transcription and translation are continuous process and occur simultaneously in the cytoplasm.	They are two separate processes, transcription occurs in the nucleus whereas translation occurs in the cytoplasm.
(ii)	Transcription initiation machinery is simple since DNA is not associated with any histone proteins.	Transcription initiation machinery is very complex since the genetic material is associated with proteins.
(iii)	σ factor present, which is essential for transcription initiation.	σ factor absent and it is not required for transcription initiation.
(iv)	RNA polymerase can recognise and bind to the promoter region with the help of σ factor.	RNA polymerase cannot recognise the promoter region directly unless the promoter is pre occupied by transcription initiation factors.
(v)	Promoter region contain pribnow box at -10 positions. TATA box and CAT box are absent in the promoter region of prokaryotes.	Promoter region contains; TATA box located 35 to 25 upstream; CAT box located ~70 nucleotide upstream; GC box located ~110 nucleotide upstream. Pribnow box absent in eukaryotes.

25. Like B-DNA, A-DNA is a right-handed double helix. A-DNA was discovered by Rosalind Franklin. Dehydrated DNA takes an A form that protects the DNA during extreme condition such as desiccation. Protein binding also removes the solvent from DNA and the DNA takes an A form. The helix diameter of A-DNA is 26 Å and the helix pitch (height of a turn) of A-DNA is 28.6 Å. A DNA is 20 to 25% shorter than B-DNA due to the smaller rise per turn. A-DNA contains 11.6 base pairs per turn. The distance between the adjacent base pairs is 2.9 Å. The helical twist per base pair in A-DNA is 31°.

26. (a) The given figure represents the band pattern based on DNA fingerprinting technique. DNA fingerprinting is a technique that simultaneously detects lots of minisatellites in the genome to produce a pattern unique to an individual.
(b) Paternity, can be legally established in several ways. Usually blood-group studies, which commonly employ the ABO system, cannot establish paternity but can conclusively exclude an alleged father from being a candidate. A typical population frequency for conventional blood typing might be one in 200, for DNA one in 5,000,000. This means that only one in 5,000,000 people would have the same DNA profile. Adequate samples for DNA typing can be collected from blood, blood stain and oral swab easily. DNA typing compares strands of genetic material between the child and alleged father comparing strands from various locations of the genetic material allows accuracy ratings of 99.9%. DNA typing allows an alleged father to be excluded with 100% certainty.
(c) According to the given figure, Dad 2 would be the actual father of the baby as it shows maximum similarity with baby in DNA bands.

27. (a) The given figure represents two molecules A-Guanine, B-Thymine. Guanine is a kind of purine (a two ringed, heterocyclic nitrogenous compound) and thymine is a kind of pyrimidine (single ringed nitrogenous compound).
(b) Purines (adenine and guanine) and pyrimidine (thymine, cytosine and uracil) are involved in making nucleic acids-DNA and RNA. Purines and pyrimidines are an important ingredient of the DNA along with the phosphate and the pentose sugar. They form the backbone of nucleic acid as nucleotides. Thymine is found in DNA only.
(c) In DNA, guanine pairs with cytosine with three hydrogen bonds and thymine pairs with adenine with two hydrogen bonds.

28. Differences between deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) are as follows :

	DNA	**RNA**
(i)	DNA is universal genetic material with some exceptions. It is a blueprint for all genetic information contained within an organism.	RNA is genetic material in some organisms such as viruses.
(ii)	DNA consists of two strands, arranged in a double helix.	RNA has single strand.

(iii)	The sugar in DNA is deoxyribose, which contains one hydroxyl group less than ribose.	RNA contains ribose sugar molecules.
(iv)	The bases in DNA are Adenine ('A'), Thymine ('T'), Guanine ('G') and Cytosine ('C').	RNA shares Adenine ('A'), Guanine ('G') and Cytosine ('C') with DNA, but contains Uracil ('U') rather than Thymine ('T').
(v)	DNA is found in the nucleus, with a small amount of DNA also being present in mitochondria.	RNA forms in the nucleolus, and then moves to specialised regions of the cytoplasm depending on the type of RNA formed.
(vi)	Due to its deoxyribose sugar, DNA is a more stable molecule than RNA, and is useful as a molecule which has the task of keeping genetic information safe.	RNA containing a ribose sugar is more reactive than DNA and is not stable in alkaline conditions. RNA's larger helical grooves mean it is more easily subject to attack by enzymes.

29. All organisms contain the genes which determine their phenotypic as well as genotypic characters. The DNA in the genes contains instructions for all the proteins that are made in an organism. Proteins, in turn, determine the structure and function of all cells. Protein's structure is determined with the sequence of amino acids that make up the protein. The instructions for making proteins with the correct sequence of amino acids are encoded in DNA. In eukaryotic cells, DNA is found in chromosomes which always remain in the nucleus, but proteins are made at ribosomes in the cytoplasm. Therefore, the instructions in DNA reach to the site of protein synthesis outside the nucleus in the form of RNA (ribonucleic acid). RNA is a small molecule that can squeeze through pores in the nuclear membrane. It carries the information from DNA in the nucleus to a ribosome in the cytoplasm and then helps assemble the protein.

In short : DNA $\rightarrow$ RNA $\rightarrow$ Protein

The central dogma of molecular biology describes the two-step process, transcription and translation, by which the information in genes flows into proteins. Discovering this sequence of events was a major milestone in molecular biology.

30. The most challenging task during the human genome project was to assign the genetic and physical maps on the genome, which was generated by using information on polymorphism of restriction endonuclease recognition sites, and some repetitive DNA sequences known as microsatellites. Collectively, the sequence-tagged sites, DNA fingerprint, and Fluorescence *in situ* hybridization (FISH) data allowed the researchers to generate contigs, which consisted of multiple overlapping bacterial artificial chromosome (BAC) library clones spanning each of the 24 different human chromosomes (*i.e.*, 22 autosomes and the X and Y chromosomes).

OR

(a) Paternity disputes can be resolved with the help of DNA fingerprinting, in which differences in repetitive DNA sequence of bases in the DNA strands of chromosomes are used to compare one biological sample with another to investigate genetic relationship. These sequences show high degree of polymorphism which arises due to genetic mutation and forms the basis of DNA fingerprinting. Using these sequences of base pairs, every person could be identified solely by the sequence of their base pairs. The composition of DNA molecule does not vary from cell to cell thus; DNA in blood is identical to that in other biological material such as hair, semen, skin, and bone marrow.

(b) The technique used in paternity identification, *i.e.*, DNA fingerprinting also has applications in paleontology, archaeology, various fields of biology, and medical diagnostics. In the medical field, researchers have made possible the mapping quantitative trait loci involved in biological pathways of diseases such as diabetes mellitus, cancers, obesity, osteoporosis and coronary heart disease.

31. Watson and Crick Model of DNA structure was proposed by James D. Watson and Francis H. C. Crick in 1953. The major features of Watson and Crick model are as follows:

- DNA is made up of two polynucleotide chains containing sugar phosphate backbone and nitrogenous bases inside.
- DNA is a double-stranded helix, with the two strands connected by hydrogen bonds. Adenine are always paired with thymine, and cytosine are always paired with guanine, which is consistent with and accounts for Chargaff's rule.
- The bases in two strands are paired through hydrogen bond (H-bonds) forming base pairs (bp). Adenine forms two hydrogen bonds with thymine from opposite strand and *vice-versa*. Similarly, guanine is bonded with cytosine with three H-bonds. As a result, always a purine comes opposite to a pyrimidine.
- This generates approximately uniform distance between the two strands of the helix.
- Most DNA double helices are right-handed. (Only one type of DNA, called ZDNA, is left-handed.)
- The DNA double helix is anti-parallel, which means that the 5′ end of one strand is paired with the 3′ end of its complementary strand (and *vice versa*).

– Nucleotides are linked to each other by their phosphate groups, which bind the 3′ end of one sugar to the 5′ end of the next sugar.
– Not only are the DNA base pairs connected *via* hydrogen bonding, but the outer edges of the nitrogen-containing bases are exposed and available for potential hydrogen bonding as well. These hydrogen bonds provide easy access to the DNA for other molecules, including the proteins that play vital roles in the replication and expression of DNA.
– The pitch of the helix is 3.4 nm and there are roughly 10 bp in each turn.
– Consequently, the distance between a bp in a helix is approximately equal to 0.34 nm. The diameter of the double helix is 2nm.
– The plane of one base pair stacks over the other in double helix. This, in addition to H-bonds, confers stability of the helical structure.
– DNA, has two asymmetric grooves. One groove is smaller than the other. This asymmetry is a result of the geometrical configuration of the bonds between the phosphate, sugar, and base groups that forces the base groups to attach at 120-degree angles instead of 180 degrees.
– The larger groove is called the major groove, occurs when the backbones are far apart; while the smaller one is called the minor groove, and occurs when they are close together.

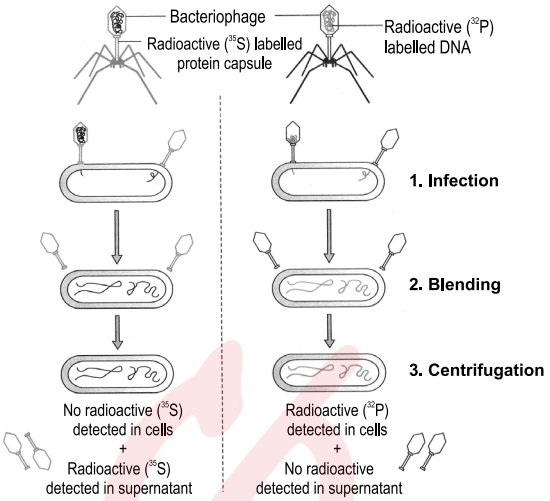
OR

(a) Alfred D. Hershey and Martha Chase, chose T_2 bacteriophage as their experimental material. They decided to see which of the bacteriophage components-protein or DNA-entered bacterial cells and directed reproduction of the virus.

Hershey and Chase experiment is based on the fact that DNA but not the protein contains phosphorus, and similarly sulphur is present in proteins (cysteine and methionine) but not in DNA. They incorporated radioactive isotope of phosphorus (^{32}P) into phage DNA and that of sulphur (^{35}S) into proteins of separate phage cultures. These phage types were used independently to infect the bacterium *Escherichia coli*. After sometime, the cultures were agitated in a blender to separate the empty phage capsids from the surface of bacterial cells and the two were separated by centrifugation. Hershey and Chase showed that in bacterial cells, infected with virus containing radioactive phosphorus (^{32}P), radioactivity was associated with bacterial cells and also, appeared in the progeny phage. However, in bacterial culture where radioactive sulphur (^{35}S) was used, all radioactive material was limited to phage 'ghosts' (empty viral protein coats).

These results indicated that the DNA of the bacteriophage and not the protein enters the host, where viral replication takes place. Therefore, DNA is the genetic material of T_2 bacteriophage. It directs protein coat synthesis and allows replication to occur.

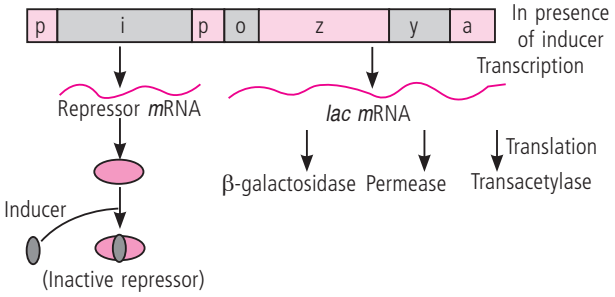
Diagrammatic representation of Hershey and Chase experiment is as follows:



(b) The aim was to determine the biochemical nature of the genetic material.

32. (a) Transfer ribonucleic acid (*t*RNA) is a type of RNA molecule that helps to decode a messenger RNA (*m*RNA) sequence into a protein. *t*RNAs function at specific sites in the ribosome during translation, which is a process that synthesises a protein from an *m*RNA molecule. Proteins are built from smaller units called amino acids, which are specified by three-nucleotide *m*RNA sequences called codons. Each codon represents a particular amino acid, and each codon is recognised by a specific *t*RNA. The *t*RNA molecule has a distinctive folded structure with three hairpin loops that form the shape of a three-leafed clover. One of these hairpin loops contains a sequence called the anticodon, which can recognise and decode an *m*RNA codon. Each *t*RNA has its corresponding amino acid attached to its end. When a *t*RNA recognises and binds to its corresponding codon in the ribosome, the *t*RNA transfers the appropriate amino acid to the end of the growing amino acid chain. Then the *t*RNAs and ribosome continue to decode the *m*RNA molecule until the entire sequence is translated into a protein.

(b) Schematic diagram of *lac* operon in 'switched on' position is as follows:



The operon gets switched 'off' in the absence of lactose (inducer). The repressor molecule binds with the operator

region of the operon and prevents RNA polymerase from transcribing the operon.

OR

(a) During the process of capping, an unusual nucleotide (methyl guanosine triphosphate) is added to the 5′- end of the hnRNA. It helps in *m*RNA recognition during translation or protein synthesis.

(b) The code is degenerate which means that the same amino acid is coded by more than one base triplet. Degeneracy does not imply lack of specificity in protein synthesis. It merely means that a particular amino acid can be directed to its place in the peptide chain by more than one base triplets. For example, the three amino acids arginine, alanine and leucine each have six synonymous codons.

The code degeneracy is basically of 2 types: partial and complete. In partial degeneracy, the first two nucleotides are identical but the third (*i.e.*, 3′ base) nucleotide of the degenerate codon differs; for example, CUU and CUC code for leucine. Complete degeneracy occurs when any of the 4 bases can take third position and still code for the same amino acid; for example, UCU, UCC, UCA and UCG all code for serine.

(c) Stop codons UAA, UGA, and UAG are called nonsense codons because they do not code for any amino acid and instead signal the end of protein synthesis. However, the so-called non-sense codons have now been found to be of "special sense".

(d) Helicases are enzymes that bind and may even remodel nucleic acid or nucleic acid protein complexes. There are DNA and RNA helicases. DNA helicases are essential during DNA replication because they separate double-stranded DNA into single strands allowing each strand to be copied.

These unzips the DNA strands by breaking the hydrogen bonds between them. Thus, it helps in the formation of the replication fork.

33. DNA fingerprinting (also called DNA profiling) is a technique employed by forensic scientists to assist in the identification of individuals or samples by their respective DNA profiles. DNA is the basis of life and the eukaryotic DNA contains the coding as well as non coding sequences which do not code for any protein. In eukaryotic DNA, there are stretches of repetitive DNA called satellite DNA regions which do not code for any specific protein. These non-coding sequences form a major chunk of the DNA profile of humans. They depict a high level of polymorphism and are the basis of DNA fingerprinting. As a result of they prove to be very useful in forensic studies. The steps involved in DNA fingerprinting are as follows:

Isolating the DNA from any cell
↓
Digestion of DNA molecule using restriction endonuclease enzymes.
↓
Separation of DNA fragments obtained through electrophoresis.
↓
Transferring the separated fragments to synthetic membranes like nitrocellulose or nylon.
↓
Hybridising the DNA fragments with labelled VNTR probes.
↓
Analysing the hybrid fragments using autoradiography.

OR

The Human Genome Project was an international research effort to determine the sequence of the human genome and identify the genes that it contains. The Project was coordinated by the National Institute of Health and the U.S. Department of Energy with international partners in the United Kingdom, France, Germany, Japan and China. The Human Genome Project formally began in 1990 and was completed in 2003, 2 years ahead of its original schedule.

The Human Genome Project was initiated with an objective to discover all the estimated 20,000-25,000 human genes and make them accessible for further biological study. The other goals included :

(i) The determination of the sequences of base pairs of human DNA;
(ii) Storage of the genetic information in databases;
(iii) Improvement in tools for data analysis;
(iv) Transfer of related technologies to other sectors, such as industries;
(v) To address the different ethical, legal, and social issues (ELSI) that may arise from the project.

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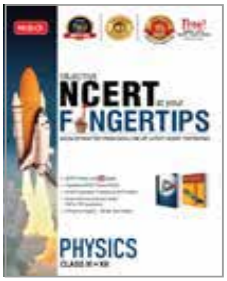

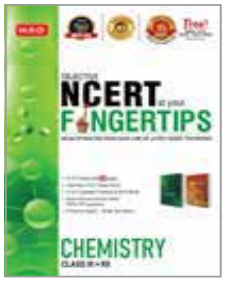

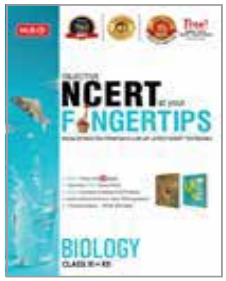

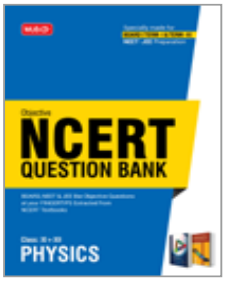

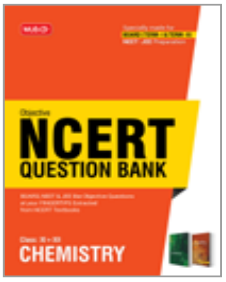

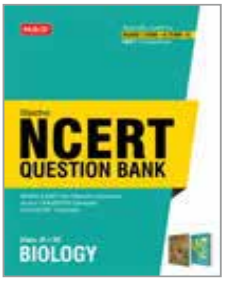

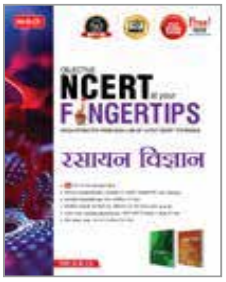

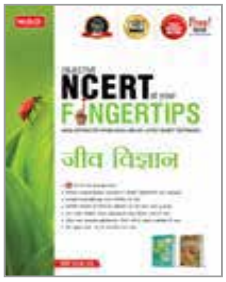

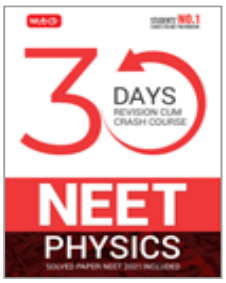

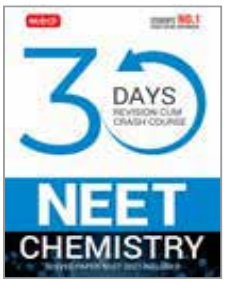

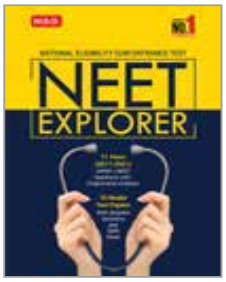

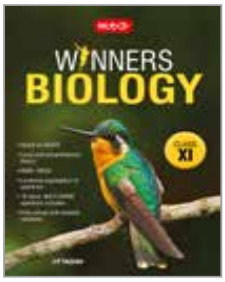

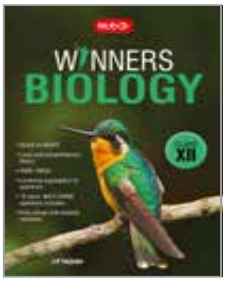

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