NEET Important Questions with Solutions from Molecular Basis of Inheritance

Q.1. According to HGP, the longest gene consists of

A) $3,164,7$ million base pairs

B) 3000 base pairs

C) 2968 base pairs

D) 2.4 million base pairs

Answer: 2.4 million base pairs

Solution: Some of the salient observations drawn from the human genome project are as follows:

- 3164.7 million nucleotide bases are there in the human genome.
- The average gene consists of 3000 bases, but size varies greatly, with the largest known human gene being dystrophin as 2.4 million bases and TDF gene as the smallest gene with 14 bases.
- The total number of genes was estimated at about 30,000, which is much lower than previous estimates of 80,000 to 1,40,000 genes. Almost all (99.9 percent) nucleotide bases are exactly the same in all people.
- The functions are unknown for half of the discovered genes.
- Less than 2% of the whole genome codes for proteins.
- Repetitive sequences are stretches of DNA sequences that are repeated many times, sometimes a hundred to a thousand times.
- Chromosome I has the most genes (2968) - Largest, and the Y has the fewest (231) - smallest.

Q.2. Which one of the following pairs of nitrogenous bases of nucleic acids, is wrongly matched with the category mentioned against it?

A) Guanine, Adenine - Purines

B) Adenine, Thymine - Purines

C) Thymine, Uracil - Pyrimidines

D) Uracil, Cytosine - Pyrimidines

Answer: Adenine, Thymine - Purines

Solution: A nitrogenous base, a pentose sugar (ribose in the case of RNA and deoxyribose in the case of DNA), and a phosphate group constitute a nucleotide. Purines and pyrimidines are two forms of nitrogenous bases. Purines, such as adenine and guanine, are heterocyclic two-ring molecules.
Pyrimidines, such as thymine, cytosine, and uracil, are single-ring compounds.

Q.3. Locations on sites in the human DNA where single base DNA differences occurs are called:

A) Repetitive DNA

B) VNTR

C) SNP

D) SSCP

E) Expressed sequence tags

Answer: SNP

Solution: Scientists have identified about 1.4 million locations where single-base DNA differences present in the human genome. They are called SNPs or Single Nucleotide Polymorphism. Variations in DNA occur when a single nucleotide in the genome differs between members of a biological species or paired chromosomes called single nucleotide polymorphism.

- DNA polymorphism can be defined as a condition where more than one different nucleotide sequence can exist at the same locus in DNA.
- A single nucleotide polymorphism (SNP) is a variation in which a single nucleotide (A, T, C or G) differs between members of the same or different biological species.
- This type of polymorphism may be due to a single nucleotide mutation, like the substitution of the nucleotide base by another base.

Q.4. During DNA fingerprinting, separation of DNA fragments is done by

A) Autoradiography

B) Hybridisation

C) Denaturation

D) Electrophoresis

Answer: Electrophoresis

Solution: DNA fingerprinting is one of the techniques which is extensively used. This involves identifying differences in some specific regions in DNA sequence called as repetitive DNA.

The technique of DNA Fingerprinting was initially developed by Alec Jeffreys. He used a satellite DNA as probe that shows very high degree of polymorphism. It was called as Variable Number of Tandem Repeats (VNTR). The process is as follows:

- Isolation of DNA
- Digestion of DNA by restriction endonucleases
- Separation of DNA fragments by electrophoresis
- Transferring (blotting) of separated DNA fragments to synthetic membranes, such as nitrocellulose or nylon
- Hybridisation using labelled VNTR probe
- Detection of hybridised DNA fragments by autoradiography.

Q.5. Which of the following codons codes for methionine, and it also acts as an initiator codon?

A) GUU

B) AUG

C) UAA

D) UUU

Answer: AUG

Solution: A three-nucleotide codon in a nucleic acid sequence specifies a single amino acid.

AUG acts as a start codon for protein synthesis which is also known as the initiator codon. Subsequently, the first amino acid to bind to the ribosome during the synthesis of proteins is methionine.

UGA, **UAA**, and UAG are stop codons. They do not code for any amino acids.

UUU codes for phenylalanine.

GUU codes for valine.

Q.6. The force that holds DNA together in a double helix is _____.

A) hydrogen bonds

B) the force of the twist

C) N–glycosidic linkage

D) ionic interactions

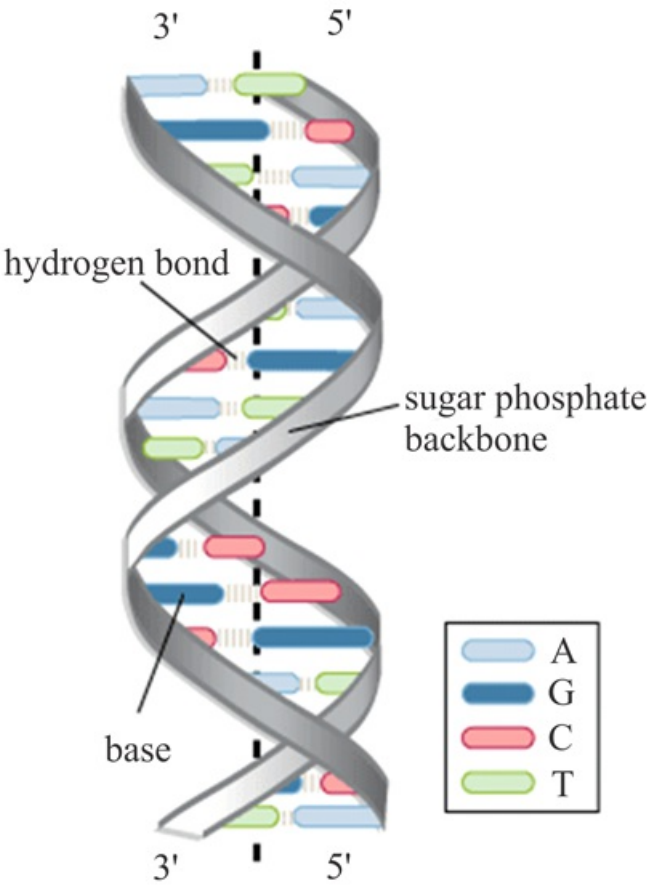
Answer: hydrogen bonds

Solution: In a DNA molecule, two strands of polynucleotide chains are present.

In each nucleotide, nitrogen base is attached to pentose sugar with the help of N-glycosidic linkage and the phosphate group is attached to pentose sugar with the help of phosphodiester bond.

In two opposite strands, complementary bases are paired with hydrogen bonds.

DNA double-helix:



Q.7. The lac operator is present only in lac operon, and it interacts specifically with___.

A. Lac repressor

B. Lactose

C. Promoter

D. Co–repressor inducer complex

Choose the correct option to fill in the blank given above.

A) A and B

B) A and C

C) Only A

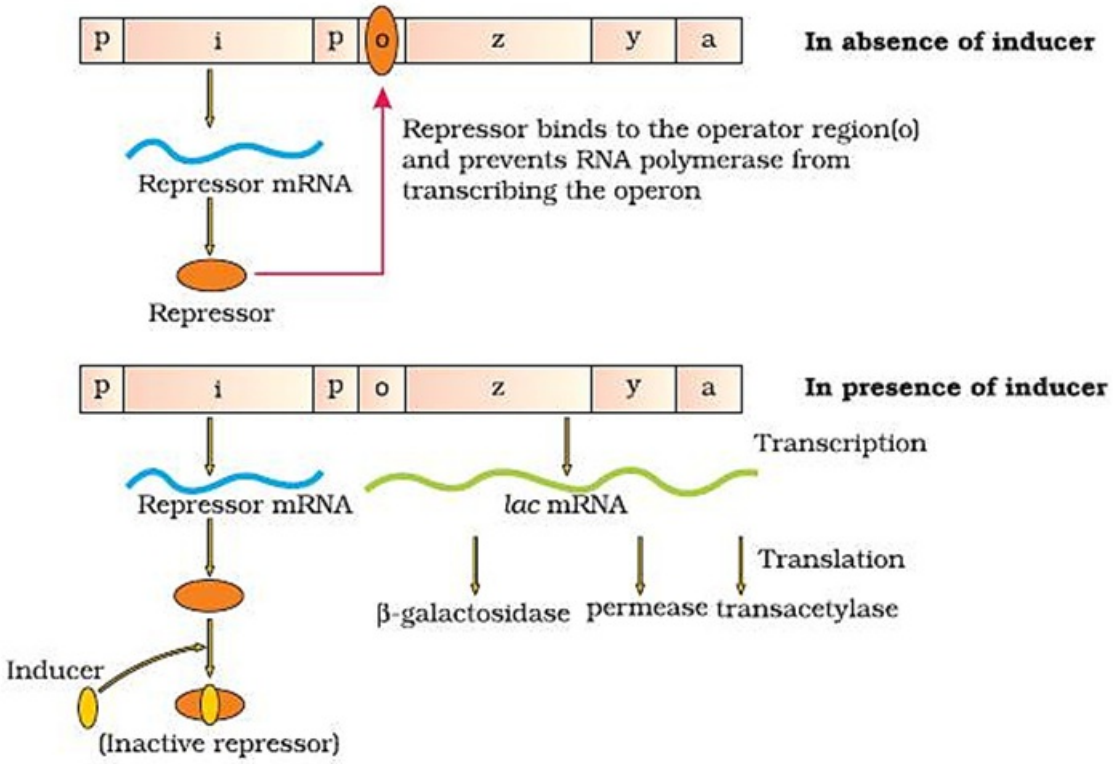
D) C and D

Answer: Only A

Solution: The operon model of prokaryotic gene regulation was proposed by Jacob and Monod. Operons are groups of genes, coding for related proteins, and are arranged in units.

It is the part of the DNA which act as a single regulated unit having one or more structural gene, an operator, a promoter, and a regulator gene.

The regulator or i-gene synthesizes a repressor protein to regulate the functioning of the structural gene. To control the regulation of structural genes in lac operon, repressor protein binds to the operator region and prevents the movement of RNA polymerase. However, the repressor protein in lac-operon gets deactivated by an inducer that is lactose.



Q.8. The fully processed hnRNA is called as __(i)__ and is transported out of the __(ii)__ into the __(iii)__ for translation.

A) (i) (ii) (iii)
mRNA nucleus cytoplasm

B) (i) (ii) (iii)
mRNA cytoplasm nucleus

C) (i) (ii) (iii)
iRNA cytoplasm nucleus

D) (i) (ii) (iii)
iRNA nucleus cytoplasm

Answer: (i) (ii) (iii)
mRNA nucleus cytoplasm

Solution: The nascent RNA synthesised by RNA polymerase II is called the primary transcript or hnRNA (heterogeneous nuclear RNA). hnRNA is a large molecule that undergoes modification like capping, tailing and splicing to produce mature mRNA. In order to prevent RNA from any damage, it is processed initially and then transferred to the cytoplasm. RNA polymerase II enzyme is present in the nucleoplasm (the fluid found inside the nucleus).

Q.9. According to Watson and Crick, DNA

A) is a double helical structure

B) consists of two antiparallel strands

C) consists of two complementary strands

D) all of these

Answer: all of these

Solution: Watson and Crick had proposed the double helix structure of DNA (1953-1954) and according to their model DNA is:

- A double-stranded DNA contains two polynucleotide chains.
- The backbone of the DNA double helix is formed by sugars and phosphates where nitrogenous bases are projecting inwards.
- The two strands of DNA possess anti-parallel polarity, which means one chain has polarity 5'-3' and the other has 3'-5'.
- The two strands of DNA are complementary and joined together by hydrogen bonds between purines and pyrimidines.
- The two chains are coiled around each other where the pitch of the helix is 3.4 nm and the distance between two base pairs is 3.4 A°.

Q.10. Mark the odd one with respect to Chargaff's rule.

A) A + G = T + C

B) $\frac{\mathrm{A+T}}{\mathrm{G+C}}$ ratio is more than one for prokaryotes

C) It is applicable for double-stranded only

D) Sugar deoxyribose and phosphate occur in equimolar proportions

Answer: $\frac{\mathrm{A+T}}{\mathrm{G+C}}$ ratio is more than one for prokaryotes

Solution: Erwin Chargaff's rule: Chargaff's along with his colleagues, performed base composition studies and put forward certain generalizations for double-stranded DNA, called 'Chargaff's rule' (not applicable for single-stranded DNA).

i) Purines and pyrimidines occur in equal amounts.
ii) Purines found in DNA are adenine and guanine. Pyrimidines of DNA are thymine and cytosine.
A + G = T + C
iii) $\frac{A+T}{G+C}$, this value is constant for all species.
iv) The base ratio is specific for a species. It is used to identify the species. It is less than one in prokaryotes, e.g., *E. coli* it is 0.92 while in eukaryotes it is more than one, e.g., Human = 1.52.
v) Sugar deoxyribose and phosphate residues occur in equal numbers.
vi) Purine adenine is equimolar with pyrimidine thymine.
vii) Purine guanine is equimolar with pyrimidine cytosine.

Q.11. The amino acid serine (Ser) is coded by four codons. This shows:

A) Ambiguous nature of codons

B) Degeneracy of codons

C) Universal nature of codons

D) Dual nature of codons

Answer: Degeneracy of codons

Solution: Genetic codes are degenerate, i.e., one amino acid is coded by several codons. UCU, UCC, UCU, UGC these are coded for one amino acid serine.

There are in all 64 codons, out of which 61 codons code for amino acids and 3 codons code for nothing.

Non-coding codons (UAA, UGA, and UAG) are also known as stop codons.

Following are the properties exhibited by codons :

- Triplet in nature
- Degeneracy
- Non-overlapping
- Comma Less
- Unambiguous
- Universal
- Co-linearity
- Gene-polypeptide Parity

Q.12. In operon concept, regulator gene functions as:

A) Repressor

B) Inducer

C) Activator

D) All of these

Answer: Repressor

Solution: Regulator gene produces a repressor protein that binds to the operator gene and regulates the transcription of the functional genes or structural genes.

Q.13. Which RNA picks up a specific amino acid from amino acid pool in the cytoplasm during protein synthesis?

A) rRNA

B) mRNA

C) tRNA

D) hnRNA

Answer: tRNA

Solution: Within our cells there are specific types of tRNA (because of anticodon) for specific amino acid. These tRNA transport the amino acids from the cytoplasm to the site of protein synthesis, i.e. towards the ribosomes.

Q.14. The process of formation of mRNA is known as

A) translation.

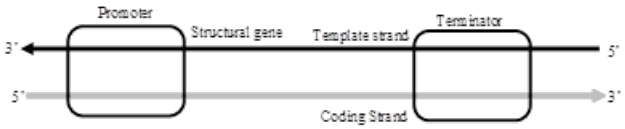
B) transcription.

C) gene expression.

D) replication.

Answer: transcription.

Solution:



Transcription or the formation of RNA on template DNA in prokaryotic and eukaryotic, has three main events.

- Initiation - Binding of RNA polymerase to double-stranded DNA; this step involves a transition to single strand in the region of binding; RNA polymerase binds at 5' end on a sequence of DNA called the promoter. Initiation is the most important step in gene expression.
- Elongation - The covalent addition of nucleotides to the 3' end of the growing polynucleotide chain. This involves the development of a short stretch of DNA that is transiently single-stranded.
- Termination - The recognition of the transcription termination sequence and the release of RNA polymerase. The promoter and terminator flank the structural gene in a transcription unit.

Q.15. During the translation process, the ATP molecule is required for

A) Association of 50S subunit of the ribosome with the initiation complex.

B) Binding of 30S subunit of the ribosome with mRNA

C) Association of 30S-mRNA with formyl-met-tRNA.

D) Charging of tRNA

Answer: Charging of tRNA

Solution: In the first phase of translation, the amino acids are activated in the presence of ATP and linked to their cognate tRNA. This process is commonly called as charging of tRNA or aminoacylation of tRNA to be more specific.

Q.16. The nitrogenous bases in DNA are

A) AUGC

B) UTGC

C) ATGC

D) ATUC

Answer: ATGC

Solution: The nitrogenous bases in DNA are purines (A and G) that pair with pyrimidines (C and T). A purine is always complementary with a pyrimidine.

Q.17. Length of DNA in human diploid cell is

A) 2.2 m

B) 2.3 m

C) 2.5 m

D) 2.6 m

Answer: 2.2 m

Solution: There are total 6.6×10^9 base pairs in our DNA. The distance between two bases in a typical DNA is 0.34 nm.

That means:

$$\text{Length of DNA in a diploid cell is :}$$
$$6.6 \times 10^9 \times 0.34 \times 10^{-9}\,\text{m} = 2.24\,\text{m}$$

Q.18. What is the sequence of structural genes in lac operon?

A) $Lac\ A, Lac\ Y, Lac\ Z$

B) $Lac\ A, Lac\ Z, Lac\ Y$

C) $Lac\ Y, Lac\ Z, Lac\ A$

D) $Lac\ Z, Lac\ Y, Lac\ A$

Answer: $Lac\ Z, Lac\ Y, Lac\ A$

Solution: Operons are groups of genes coding for related proteins and are arranged in units. Jacob and Monod proposed the operon model of prokaryotic gene regulation.

Operon is the part of the DNA which act as a single regulated unit having one or more structural gene, an operator, a promoter and a regulator gene. The lac operon consists of three structural genes-lac Z, lac Y and lac A gene. Lac Z codes for the beta-galactosidase enzyme which hydrolyses lactose to glucose and galactose. Lac Y codes for the enzyme lactose permease, a membrane-bound protein constituent of the lactose transport system which increases the permeability of the cell to lactose. Lac A codes for the enzyme thiogalactoside transacetylase, which converts galactose to the non-toxic form.

Q.19. Chemically, RNA is __(i)__ reactive and __(ii)__ stable as compared to DNA.

A) (i) equally, (ii) equally

B) (i) less, (ii) more

C) (i) more, (ii) less

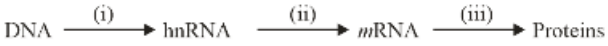
D) (i) more, (ii) equally

Answer: (i) more, (ii) less

Solution: DNA and RNA are the two types of nucleic acids that act as genetic material in organisms. All the organisms have DNA as their genetic material, but few viruses contain RNA as their genetic material. RNA is not a suitable genetic material and is not observed as genetic material in many organisms because:

- The $2' - \text{OH}$ group in the ribose sugar is a highly reactive group, that makes RNA highly reactive, labile and easily degradable.
- RNA acts as enzymes and this also denotes its reactive and unstable nature.
- The uracil present is RNA is less stable when compared to thymine (methyl uracil).
- RNA mutates much faster without any repair system and hence have a shorter life span.

Q.20. Refer to the given sequence of steps and select the correct option.



A)

(i)	(ii)	(iii)
Replication	Transcription	Translation

B)

(i)	(ii)	(iii)
Replication	Processing	Translation

C)

(i)	(ii)	(iii)
Transcription	Splicing	Translation

D)

(i)	(ii)	(iii)
Transcription	Replication	Translation

Answer:

(i)	(ii)	(iii)
Transcription	Splicing	Translation

Solution: The RNA polymerase enzyme catalyses the process of transcription which synthesises the nascent RNA from the DNA molecule. This nascent RNA is called the heteronuclear (hnRNA) RNA or primary RNA transcript. Post-transcriptional modification converts hnRNA to fully functional mature RNA before its translation into a protein. These modifications are 5' capping, 3' polyadenylation and RNA splicing to make the mature mRNA.

In capping a nucleotide (methyl guanosine triphosphate) is added to the 5' end of hnRNA. In tailing (3' polyadenylation) adenine is added. It is added to the 3' end of hnRNA. The process of capping aids the recognition of mRNA by the ribosomes and protects it from RNases. The poly-A tail plays a role in the stability of the mRNA. The stable mRNA comes to the cytoplasm and gets attached to the ribosomes to perform protein synthesis (translation).

Q.21. The three codons which result in the termination of polypeptide chain synthesis are

A) UAA, UAG, GUA

B) UAA, UAG, UGA

C) UAA, UGA, UUA

D) UGU, UAG, UGA

Answer: UAA, UAG, UGA

Solution: A sequence of three nucleotides present on the DNA or RNA is known as the codon. 64 codons are there out of which 61 codons code for amino acids and 3 codons code for nothing. Each codon codes for a specific amino acid. However, there are three codons, i.e., UAA, UAG and UGA, which do not code for any amino acid (non-sense codons). These are also called stop codons or terminator codons. The RNA polymerase when encounters any of these codons the process of translation stops.

Q.22. What is incorrect for DNA?

A) The pitch of the helix is 3.4 nm.

B) Phosphate moiety is at 5' end of deoxyribose sugar.

C) Diameter of the DNA is 2 nm.

D) The charge on the DNA is positive.

Answer: The charge on the DNA is positive.

Solution: Some features of the double-helix model of DNA:
1. Pitch of the helix = 3.4 nm. Pitch means the length of 1 coil.

2. Diameter of B- DNA = 20 Å.

3. The phosphate group is attached at 5^{th} carbon of deoxyribonucleotide with the help of phosphoester linkage.

4. Nitrogen base is attached on 1^{st} carbon of deoxyribonucleotide with the help of N-glycosidic bond.

5. In the strand of DNA, deoxyribose sugar and phosphate form the backbone and nitrogen bases are present on the inner side.

Q.23. The mutations that involve addition, deletion or substitution of a single base pair in a gene are referred to as

A) point mutations

B) lethal mutations

C) silent mutations

D) retrogressive mutations

Answer: point mutations

Solution: A mutation is a sudden change that occurs in the genomic sequence of an organism. Mutations are caused by various factors either physical, chemical, or biological (UV radiation, Gamma rays, acridine orange, ethidium bromide, excess of hormones, error during DNA replication, etc.). Some gene mutations involve single nucleotide changes and these gene mutations are called point mutations. For example, sickle cell anemia in which polypeptide chain coding for hemoglobin contains valine instead of glutamic acid due to substitution of T by A in the second position of triplet codon.

Q.24. Which RNA carries the amino acids from the amino acid pool to mRNA during protein synthesis?

A) rRNA

B) mRNA

C) tRNA

D) hnRNA

Answer: tRNA

Solution: tRNA is the adapter molecule involved in transferring the amino acids from the cytoplasm to the site of protein synthesis. These tRNA molecules are also known as soluble RNA (sRNA) molecules, constituting 7-15% of the total RNA. Francis Crick was the first to propose to explain the presence of an adapter molecule that performs two major functions of decoding the code present in the mRNA by bringing the suitable amino acids during protein synthesis. The tRNA molecules have unpaired (single stranded) CCA-OH sequence at the 3' end. This is called an amino acid binding site or acceptor arm because the amino acid becomes covalently attached to adenylic acid or A of CCA sequence during polypeptide synthesis. The amino acids according to the codon of the mRNA will be brought by the tRNA with respect to its anticodon nucleotides.

Q.25. The DNA fingerprinting technique is easier and rapidly done by the use of _____.

A) PCR

B) RAPD

C) SSR

D) SNP

Answer: PCR

Solution: Polymerase Chain Reaction (PCR) is a technique to make many copies of a specific DNA segment *in vitro*. PCR depends on a thermostable DNA polymerase enzyme, called 'Taq polymerase'. It requires DNA primers explicitly designed for the DNA region of interest. PCR is widely used to rapidly make billions of copies of a specific DNA segment, that allows scientists to take a tiny sample of DNA and amplify it to a large amount.

A Single-nucleotide Polymorphism (SNP, pronounced as "snips") is a DNA segment variation. It occurs when a single nucleotide Adenine (A), Thymine (T), Cytosine (C), or Guanine (G) in the genome (or another shared sequence) differs between members of a species or paired chromosomes in an individual.

Microsatellites or Simple Sequence Repeats (SSRs) represent the variation in the repetitive number of sequences. These are 1 to 6 base pair long (VNTRs can be as long as 1 kbp). As they are smaller in size, SSRs are more common. Recently, more than 300 loci representing microsatellites, were mapped each in human genomes. Similar efforts are also being made in several crop plants.

RAPD (pronounced as "rapid") stands for 'Random Amplification of Polymorphic DNA'. It is a type of PCR, but the segments of DNA that are amplified are random.

Practice more on Molecular Basis of Inheritance