Ultimate KCET Crash Course 2026

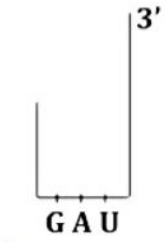
BOTANY

DPP: 1

Molecular Basis of Inheritance

Q1 tRNA with which of the following anticodon is not found?

(A) 

(B) 

(C) 

(D) 

Q2 Methyl guanosine triphosphate is added at 5′ end of hnRNA in a process of _____.

(A) Tailing (B) Splicing

(C) Capping (D) None of these

Q3 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 of the transcription unit

(D) the 3' (downstream) end of the transcription unit.

Q4 P^{32} was used to culture bacteriophages in Hershey and Chase experiments, that resulted in radioactive _____.

(A) Viral DNA

(B) Bacterial capsule

(C) Viral proteins

(D) Plasma membrane of bacteria

Q5 What is the function of DNA polymerase during DNA replication?

(A) To unwind the DNA helix

(B) To synthesize the RNA primer

(C) To synthesize the new strand of DNA

(D) To seal the nicks in the DNA strand

Q6 Nitrogenous base is linked to which carbon of pentose sugar _____.

(A) 1′C (B) 2'C

(C) 3'C (D) 5'C

Q7 During translation initiation in prokaryotes, a GTP molecule is needed in
(A) formation of formylmettRNA
(B) binding of 30S subunit of ribosome with mRNA
(C) association of 30S mRNA with formylmet tRNA
(D) association of 50S subunit of ribosome with initiation complex.

Q8 Minisatellites used in DNA fingerprinting are also called:
(A) VNTRs (B) SNPs
(C) STRs (D) Plasmids

Q9 Select the incorrect statement w.r.t. heterochromatin.
(A) This region synthesises non-histone chromosomal proteins
(B) It is darkly stained region
(C) This is the region where chromatin is densely packed
(D) This region is transcriptionally inactive

Q10 Genetic code determines _____.
(A) Sequence of amino acids in protein chain
(B) Variations
(C) Constancy of morphological traits
(D) Structural pattern

Q11 What would be the effect on histone proteins in the nucleus, on neutralisation of their positive charge?
(A) They would bind the DNA tighter.
(B) They would separate from DNA.
(C) They would no longer attract each other.
(D) They would cause supercoiling of DNA.

Q12 Watson and Crick proposed double helix model for the structure of DNA which was based on X-ray diffraction data produced by
(A) Erwin Chargaff
(B) Temin and Baltimore
(C) Wilkins and Franklin
(D) Oswald Avery

Q13 Which one is not a termination codon ?
(A) U A A (B) U A G
(C) A U G (D) U G A

Q14 Which of the following sequences of mRNA a required for translation process but are not translated ?
(A) Stop codons (B) Anticodons
(C) Sense codons (D) UTR

Q15 In which region of the tRNA molecule is the amino-acid binding site located ?
(A) 5' end
(B) anticodon loop
(C) 3' end
(D) None of the above

Q16 An octamer of 4 histones complexed with DNA forms
(A) endosome (B) nucleosome
(C) mesosome (D) centromere

Q17 In Griffith's experiment, what happened when mice were injected with a mixture of heat-killed S strain and live R strain?
(A) Mice remained healthy
(B) Mice died, and live S strain bacteria were recovered
(C) Mice showed partial infection but survived
(D) No bacteria were found in the mice

Q18 Expressed Sequence Tags (ESTs) refers to _____.
(A) all genes whether expressed or unexpressed
(B) certain important expressed genes
(C) all genes that are expressed as RNA
(D) all genes that are expressed as proteins

Q19 In which of the following steps in DNA fingerprinting technique are labelled VNTR probes used ?
(A) During isolation of DNA
(B) During digestion of DNA by REN
(C) During electrophoresis
(D) During hybridisation

Q20 A molecule that acts as genetic material should provide the scope for slow mutation. This is required for
(A) Quick duplication of genetic material
(B) Evolution of life forms
(C) Genetic recombination during sexual reproduction
(D) Replication with highest degree of accuracy

Q21 Match the following genes of the Lac operon with their respective products.

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

Select the correct option.
(A) (A) – (iii), (B) – (iv), (C) – (i), (D) – (ii)
(B) (A) – (i), (B) – (iii), (C) – (ii), (D) – (iv)
(C) (A) – (iii), (B) – (i), (C) – (ii), (D) – (iv)
(D) (A) – (iii), (B) – (i), (C) – (iv), (D) – (ii)

Q22 In prokaryotes like *E. coli* the DNA in the nucleoid region is organised as
(A) negatively charged DNA wrapped around histone
(B) densely packed chromatin with NHC proteins
(C) large loops held by the proteins
(D) many repeating units of nucleosomes.

Q23 If a geneticist uses the blind approach for sequencing the whole genome of an organism, followed by assignment of function to different segments, the methodology adopted by him is called as _____.
(A) Sequence annotation
(B) Gene mapping
(C) Expressed sequence tags
(D) Bioinformatics

Q24 According to Human Genome Project (HGP), the total number of genes in human genome is estimated at 30,000, the number of genes present on Y chromosome are _____.
(A) 2968 genes (B) 242 genes
(C) 231 genes (D) 2898 genes

Q25 The largest human gene discovered during HGP was:
(A) Insulin gene
(B) Hemoglobin gene
(C) Dystrophin gene
(D) Myosin gene

Q26 Given below is a list of steps Meselson and Stahl carried out in their experiment to prove that DNA replication is semi-conservative. Select the option that gives the correct sequence of steps followed by them.

(i) Bacteria transferred to a N^{14} medium and sampled every 20 minutes.

(ii) All bacteria contain hybrid DNA (N^{14} DNA and N^{15} DNA).

(iii) Bacteria grown in N^{15} medium for many generations.

(iv) All bacteria contain N^{15} DNA.

(v) Bacteria contain either all N^{14} DNA or all hybrid DNA

(A) (ii) (iv) (iii) (i) (v)
(B) (i) (ii) (v) (iv) (iii)
(C) (iii) (iv) (i) (ii) (v)
(D) (iv) (iii) (ii) (v) (i)

Q27 What would be happen if both the strands of DNA are copied during transcription ?

(A) The segment of DNA would be coding for two different proteins
(B) 2 RNA will be produced simultaneously, complementing to each other
(C) Formation of double helical RNA
(D) All of the above are correct

Q28 A nucleotide is composed of three components. Which of the following is NOT one of them?

(A) A nitrogenous base
(B) A pentose sugar
(C) A phosphate group
(D) An amino acid

Q29 For 50 amino acids in a polypeptide chain, what will be the minimum number of nucleotides in its cistron ?

(A) 50 (B) 153
(C) 306 (D) 300

Q30 In a crime investigation, the investigating officer collects different biological samples from the crime spot for DNA fingerprinting analysis. Which of the following samples is not helpful in this analysis ?

(A) Skin Shreds (B) Erythrocytes
(C) Semen sample (D) Hair follicle

Answer Key

Q1	A
Q2	C
Q3	B
Q4	A
Q5	C
Q6	A
Q7	C
Q8	A
Q9	A
Q10	A
Q11	B
Q12	C
Q13	C
Q14	D
Q15	C
Q16	B
Q17	B
Q18	C
Q19	D
Q20	B
Q21	D
Q22	C
Q23	A
Q24	C
Q25	C
Q26	C
Q27	D
Q28	D
Q29	B
Q30	B

Hints & Solutions

Note: scan the QR code to watch video solution

Q1 Text Solution:

(A)

Video Solution:

Q2 Text Solution:

C - Capping.

Methyl guanosine triphosphate (m^7G) addition at the 5′ end of hnRNA (heterogeneous nuclear RNA) is known as capping.

Process of Capping:

1. Initiation:

- Capping occurs shortly after transcription initiation, when the nascent RNA is about 20-30 nucleotides long.

2. Addition of 7-Methylguanosine:

- An enzyme called guanylyltransferase adds a guanosine triphosphate (GTP) molecule to the 5' end of the RNA via a 5'-5' triphosphate linkage.

- This guanosine is then methylated at the 7th position by another enzyme called methyltransferase, forming 7-methylguanosine (m^7G).

Purpose of Capping:

1. Protection:

- The 5' cap protects the nascent RNA from degradation by exonucleases.

2. Translation Initiation:

- The cap structure is recognized by the cap-binding complex, which is necessary for the initiation of translation.

3. Splicing and Export:

- The cap also plays a role in RNA splicing and export from the nucleus to the cytoplasm.

Tailing:

- Tailing refers to the addition of a poly-A tail (a string of adenine nucleotides) to the 3' end of the mRNA.

Splicing:

- Splicing is the process by which introns (non-coding regions) are removed from hnRNA, and exons (coding regions) are joined together to form mature mRNA.

Video Solution:

Q3 Text Solution:

(B)

1. A **transcription unit** includes promoter, structural gene, and terminator.

2. **Promoter** lies at the **5′ (upstream)** end and initiates transcription.

3. **Terminator** lies at the **3′ (downstream)** end and stops transcription.

4. RNA polymerase binds at the promoter to start mRNA synthesis.

5. So the correct arrangement is 5′ (upstream) promoter 3′ (downstream) terminator.

Video Solution:

Q4 Text Solution:

In the Hershey and Chase experiments, bacteriophages were cultured with radioactive phosphorus (32P), which is incorporated into the DNA. This resulted in radioactive viral DNA. Since DNA contains phosphorus and proteins do not, the 32P specifically labeled the DNA of the bacteriophages. When these labeled phages infected bacteria, the radioactive DNA entered the bacterial cells, demonstrating that DNA is the genetic material.

Video Solution:

Q5 Text Solution:

(C)

DNA polymerase synthesizes the new DNA strand.

It adds nucleotides in the 5' 3' direction.

It uses the template strand for base pairing.

It also proofreads for errors.

This ensures accurate replication

Video Solution:

Q6 Text Solution:

A. 1'C

The nitrogenous base is linked to the **1'C** carbon of the pentose sugar.

In nucleotides, the nitrogenous base (either a pyrimidine or purine) is attached to the 1' carbon of the pentose sugar. This linkage occurs via a glycosidic bond between the base and the sugar molecule. The numbering convention (1', 2', 3', etc.) refers to the specific carbon atom in the sugar ring.

Video Solution:

Q7 Text Solution:

The initiation of polypeptide chain in prokaryotes is always brought about by the amino acid methionine but it has to be formylated to form tRNA f^{met}. Then methionine binds with tRNA f met to form f^{met} tRNA f^{met}. This f^{met}-tRNA f^{met} complex binds with the mRNA 30S subunit complex using initiation factors IF_2 and IF_1 and GTP.

Video Solution:

Q8 Text Solution:

VNTRs are tandem repeat sequences with variable lengths.

They differ among individuals and create unique patterns.

They are used for identity testing and parentage analysis.

They are inherited in Mendelian fashion.

Video Solution:

Q9 Text Solution:

A: This region synthesizes non-histone chromosomal proteins

- Heterochromatin is a tightly packed form of DNA, which is transcriptionally inactive, meaning that it is not typically involved in gene expression.
- A: is incorrect because heterochromatin is not specifically associated with the synthesis of non-histone chromosomal proteins. Non-histone proteins can be found in various regions of chromatin, not just heterochromatin. Heterochromatin is more associated with structural and regulatory roles rather than protein synthesis.
- B: is correct because heterochromatin is darkly stained due to its dense packing.
- C: is correct as heterochromatin is the region where chromatin is densely packed.
- D: is correct because heterochromatin is transcriptionally inactive.

Video Solution:

Q10 Text Solution:

A. Sequence of amino acids in protein chain

The genetic code is a set of rules used by living cells to translate information encoded within genetic material (DNA or RNA sequences) into proteins. Specifically, it determines the sequence of amino acids in a protein chain. Each set of three nucleotides, known as a codon, corresponds to a specific amino acid or a stop signal during protein synthesis.

Video Solution:

Q11 Text Solution:

(B)

Histones are positively charged and bind to negatively charged DNA.

Neutralising their charge causes separation from DNA.

This disrupts nucleosome formation and chromatin structure.

Hence, histone proteins would detach from DNA.

This supports DNA packaging and regulation of gene expression.

Video Solution:

Q12 Text Solution:

C: Wilkins and Franklin

- Watson and Crick's double helix model of DNA was based on X-ray diffraction data produced by Rosalind Franklin and Maurice Wilkins.
- Franklin's X-ray crystallography images of DNA were critical in determining the helical structure of DNA, and Wilkins also contributed to this research.

This data was crucial in enabling Watson and Crick to propose the correct double helix structure of DNA in 1953.

Video Solution:

Q13 Text Solution:

C. A U G

- AUG is not a termination codon. Instead, it is the start codon, which codes for the amino acid methionine and signals the beginning of protein synthesis.
- UAA: Termination codon
- UAG: Termination codon
- UGA: Termination codon

Video Solution:

Q14 Text Solution:

D. UTR

The sequences of mRNA required for the translation process but are not translated are UTR (Untranslated Regions).

- Stop Codons: These are codons (UAA, UAG, UGA) that signal the termination of translation. They are translated into signals that end protein synthesis, but they are not part of the actual amino acid sequence.

- Anticodons: These are found on tRNA molecules and pair with the codons on the mRNA during translation. They are not part of the mRNA sequence itself.

- Sense Codons: These are codons on the mRNA that are translated into amino acids during the protein synthesis process.

- UTR (Untranslated Regions): These are regions at the 5' and 3' ends of the mRNA molecule. They are crucial for the regulation of translation and stability of the mRNA but do not encode for proteins themselves.

Video Solution:

Q15 Text Solution:

C. 3' end

The amino acid binding site of the tRNA molecule is located at the 3' end.

tRNA molecules have a specific structure that allows them to transport amino acids to the ribosome during protein synthesis. This structure includes several key regions:

1. 5' End: This end of the tRNA is not involved in binding amino acids.

2. Anticodon Loop: This region contains the anticodon, a sequence of three nucleotides that is complementary to the mRNA codon. It is responsible for recognizing the specific codon on the mRNA during translation.

3. 3' End: This end of the tRNA molecule has a conserved sequence of CCA. The terminal adenine (A) at the 3' end is the site where the amino acid is covalently attached by an enzyme called aminoacyl-tRNA synthetase.

Video Solution:

Q16 Text Solution:

An octamer of 4 histones complexed with DNA forms nucleosome. The association of histones with DNA is very characteristic. It involves the formation of linear array of spherial structures called nucleosomes. These structures contains four pairs of histones (H_2A, H_2B, H_3 and H_4) in a ball; around which is wrapped a stretch of about 150 base pairs of DNA.

Video Solution:

Q17 Text Solution:

(b) Mice died, and live S strain bacteria were recovered

Key Concept: Bacterial Transformation

1. Frederick Griffi th's experiment (1928) demonstrated the transforming principle in bacteria.
2. The heat-killed virulent S strain transferred genetic material to the live non-virulent R strain.
3. This made the R strain acquire the ability to cause disease.
4. It provided evidence that DNA is the genetic material, later confi rmed by Avery, MacLeod, and McCarty.
5. This process is called bacterial transformation.

Video Solution:

Q18 Text Solution:

C. all genes that are expressed as RNA

Expressed Sequence Tags (ESTs) are short DNA sequences generated from mRNA, representing the portions of genes that are actively transcribed into RNA. Therefore, ESTs correspond to all genes that are expressed as RNA, helping researchers identify gene transcripts and their functions.

Video Solution:

Q19 Text Solution:

D. During hybridization

In DNA fingerprinting, labelled VNTR (Variable Number Tandem Repeats) probes are used during the hybridization step. After the DNA has been digested by restriction enzymes and separated by gel electrophoresis, the DNA fragments are transferred onto a membrane in a process called Southern blotting. The membrane is then exposed to labelled VNTR probes, which bind to the complementary VNTR sequences in the DNA fragments. This allows the visualization of the specific patterns of VNTRs, which are used to create a DNA fingerprint.

Video Solution:

Q20 Text Solution:

B: Evolution of life forms

A molecule that acts as genetic material must allow for slow mutations, which are essential for the evolution of life forms. Mutations introduce variations in the genetic material, which can lead to new traits and, over time, contribute to the evolutionary process. Without the ability to mutate, the genetic material would be static, and evolution would not occur.

Video Solution:

Q21 Text Solution:

D. (A) – (iii), (B) – (i), (C) – (iv), (D) – (ii)

- i gene produces the repressor protein (iii).
- z gene encodes β-galactosidase (i), which breaks down lactose into glucose and galactose.
- a gene encodes transacetylase (iv), which is involved in the transfer of an acetyl group.
- y gene encodes permease (ii), which facilitates the entry of lactose into the cell.

Video Solution:

Q22 Text Solution:

(C)

Prokaryotes lack a well-defined nucleus.

DNA is organized into loops in the nucleoid region.

These loops are held by non-histone basic proteins.

This structure helps in DNA packaging inside small cells.

E. coli genome is tightly packed into this form.

Video Solution:

Q23 Text Solution:

A. Sequence annotation

Sequence annotation refers to the process where, after sequencing the whole genome, scientists identify and assign functions to different segments of DNA. This approach involves "blind" sequencing first, without prior knowledge of the functions, and then annotating the sequence by predicting or experimentally determining the function of each segment.

Video Solution:

Q24 Text Solution:

C. 231 genes

The Human Genome Project, an ambitious effort to sequence the human genome, provided valuable insights into chromosomes and their unique characteristics.

Chromosome 1, with 2,968 genes, has the highest number of genes among all chromosomes.

In contrast, the Y chromosome has the fewest genes, with only 231 identified.

Video Solution:

Q25 Text Solution:

(C) Dystrophin gene.

The dystrophin gene is the largest human gene known, spanning approximately 2.4 million base pairs. Its enormous size makes it susceptible to mutations, which are responsible for Duchenne muscular dystrophy. This gene was one of the major discoveries during the Human Genome Project (HGP) and exemplifi es the complexity of our genome.

Video Solution:

Q26 Text Solution:

C - (iii) (iv) (i) (ii) (v)

First, bacteria were grown in heavy (15N) medium.

Then, they were shifted to normal (14N) medium.

Samples were taken every 20 mins for generations.

Hybrid and light DNA were observed as replication occurred.

This confirmed DNA replicates semi-conservatively.

Video Solution:

Q27 Text Solution:

Option D: All of the above are correct

If both strands of DNA were copied during transcription, the consequences would be significant. Here's a detailed look at each option provided:

The segment of DNA would be coding for two different proteins

- If both strands were transcribed, each RNA strand would code for a different protein, provided that both strands contain coding sequences. This is because the two strands are complementary and usually have different sequences that could code for different proteins.

Two RNA molecules will be produced simultaneously, complementing each other

- This is accurate because each RNA molecule would be complementary to the other, just like the original DNA strands are complementary to each other.

Formation of double helical RNA

- Explanation: If two complementary RNA molecules were produced simultaneously, they could hybridize and form a double helical structure similar to DNA. However, RNA typically does not form long double helices like DNA because it is usually single-stranded and may fold into complex secondary structures.

Video Solution:

Q28 Text Solution:

(d) An amino acid

A nucleotide consists of three components: a nitrogenous base, a pentose sugar (either ribose or deoxyribose), and a phosphate group. Amino acids, however, are the building blocks of proteins and are not part of the nucleotide structure. Thus, amino acids are not components of nucleotides.

Video Solution:

Q29 Text Solution:

B. 153

A cistron is a segment of DNA that encodes for a single polypeptide chain. For a polypeptide consisting of 50 amino acids, the corresponding cistron must include at least 51 codons. This accounts for 50 codons encoding each amino acid and 1 codon serving as the stop signal. Since each codon is composed of three nucleotides, the minimum length of the cistron required would be:

$$51 \text{ codons} \times 3 \text{ nucleotides/codon}$$
$$= 153 \text{ base pairs (bp)}$$

Therefore, the cistron for a polypeptide chain of 50 amino acids would need to be at least 153 base pairs long to accommodate the necessary codons.

Video Solution:

Q30 Text Solution:

B. Erythrocytes

Erythrocytes (red blood cells) do not contain a nucleus and, therefore, lack DNA. This makes them unhelpful for DNA fingerprinting analysis. On the other hand, skin shreds, semen samples, and hair follicles all contain cells with nuclei, which contain DNA that can be analyzed for DNA fingerprinting.

Video Solution: