Exercise-1

 \mathbf{x} Marked Questions are for Revision Questions.

ONLY ONE OPTION CORRECT TYPE

SECTION - A # NUCLEIC ACIDS (THE SEARCH FOR GENETIC MATERIAL, DNA, RNA)

| 1. | To prove that DNA is the genetic material, Griffith used | | | | | |
|------|--|---------------------------|--------------------------------|------------------------------------|--|--|
| | (1) Neurospora crassa | | (2) Drosophila melanogaster | | | |
| | (3) Diplococcus pneum | oniae | (4) Escherichia coli | | | |
| 2. | Who experimently prov | ed that DNA is the basic | genetic material? | | | |
| | (1) J. D Watson | (2) H.G. Khorana | (3) Alfred Griffith | (4) Hershey & Chase | | |
| 3.2a | Radioactive (35S) was d | letected in? | | | | |
| | (1) Supernatant | (2) Sediment | (3) Both 1 and 2 | (4) None of these | | |
| 4. | DNA was first discovered | ed by | | | | |
| | (1) Beadle and Tatum | (2) Watson and Crick | (3) Friedrich Miescher | (4) A. Kornberg | | |
| 5.2 | With respect to the bacteriophage, choose the correct sequence of Harshey-Chase experime (1) (a) Blending, (b) Infection, (c) Centrifugation (2) (a) Infection, (b) Centrifugation, (c) Blending (3) (a) Infection, (b) Blending, (c) Centrifugation (4) (a) Centrifugation, (b) Blending, (c) Infection | | | | | |
| 6. | A nucleoside is | | | | | |
| | (1) purine / pyrimidine | + phosphate | (2) purine / pyrimidine | + sugar | | |
| | (3) pyrimidine + purine + phosphate | | (4) Purine + sugar + phosphate | | | |
| 7.2 | A DNA molecule makes | s complete turn after eve | ery | | | |
| | (1) 3.4 Å | (2) 20Å | (3) 10 bases | (4) 12 bases | | |
| 8. | The two stands of DNA | are | | | | |
| | (1) Similar in nature and | | | (2) Antiparallel and complementary | | |
| | (3) Always single strand | ded | (4) Rarely double stranded | | | |
| 9. | The similarity between | DNA & RNA is that both | | | | |
| | (1) are double stranded | I | (2) have simillar sugars | | | |
| | (3) are polymers | | (4) have similar pyrimic | lines | | |
| 10. | In which of the following | g, double stranded RNA | is present? | | | |
| | (1) bacteria | (2) | (3) retrovirus | (4) reovirus | | |
| 11. | Why does cytosine make pair with guanine and not with adenine? (1) Polar nature of C and A (2) C - A pair would not reach across the double helix (3) C - A pair would be wider than double helix (4) Hydrogen bond forming functional groups are not complementary between C and A | | | | | |

| 12. | Regarding to features of double helix structure of DNA which of the following is wrong (1) Two polynucleotide chains have antiparallel polarity (2) The bases in two strands are paired through phosphodiester bonds (3) Adenine form two hydrogen bonds with thymine (4) The pitch of the helix is 3.4 nm | | | | |
|------|--|----------------------------------|---|----------------------------------|--|
| 13. | In the experiments on the chemistry of DNA Chargaff estimated the base composition of human sperms and found that adenine constituted 31% and guanine 19%. The quantity of cytosine in DNA of a human somatic cell is likely to be (1) 10% (2) 28% (3) 21% (4) 62% | | | | |
| | (1) 19% | (2) 38% | (3) 31% | (4) 62% | |
| 14. | In a given sample of nucleic acid G + A content is not equal to C + T. This indicates that sample is (1) GC rich (2) AT rich | | | | |
| | (3) single-stranded DN/ | | (4) double-stranded DN | IA | |
| 15. | | ially synthesized in vitro | • | | |
| | (1) Ochoa and Kornber(3) Nirenberg and Ocho | - | (2) Nirnberg and Ochoa(4) Kornberg and Niren | | |
| 16. | The haploid content of | | | berg | |
| 10. | (1) 3.3×10^{9} bp | (2) 3.3×10^{9} kbp | (3) 4·6 × 10 ⁶ bp | (4) 48502 bp | |
| 17.2 | Histone proteins are ric (1) Tryptophan, Lysine | | (3) Histidine, Arginine | (4) Histidine, Tryptophan | |
| 18. | Bacterial DNA is assoc (1) Few polyamines or (3) No proteins | | (2) Histone proteins (4) Non histone acidic p | proteins | |
| 19. | Which was first genetic | material? | | | |
| | (1) RNA | (2) DNA | (3) Protein | (4) Both (1) and (2) | |
| 20. | Which RNA occurs abu (1) r RNA | indantly in a cell? (2) t RNA | (4) m RNA | (3) Primer RNA | |
| 21.๖ | The length of DNA mol | | e dimensions of the nucl | eus in the eukaryotic cells. How | |
| | (1) Super coiling in nuc(3) Through elimination | | (2) DNase digestion(4) Deletion of non-ess | ential genes | |
| 22. | Which of the following is/are wrong regarding double helical structure of DNA (a) DNA is made up of two polynucleotide chains (b) Backbone of DNA is constituted by sugar & Nitrogenous base (c) The two chain have anti parallel polarity (d) The pitch of the helix is 3.4 A^o | | | | |
| | (1) b & c | (2) a & d | (3) b only | (4) b & d | |
| 23. | (1) b & c (2) a & d (3) b only (4) b & d (5) b only (6) b & d (7) b & d (8) b & d (9) b & d (9) b & d (1) Ability of the following is not a criteria for determination of genetic material (1) Ability of replication (2) Chemically and structurally stable (3) It should be non mutable (4) Ability to expres itself in form of Mendelian characters | | | | |

| 24. | Choose the incorrect one: (1) Nucleosomes in chromatin are seen as "beads on string structure" (2) Nucleosome in a histone octamer (3) Nucleosome is present in both prokaryotic & eukaryotic DNA (4) A typical nucleosome contains 200 bp. of DNA helix Number of Nucleosomes found in helical coil of 30 nm chromatin fibre is | | | | |
|-------|---|--------------------------------------|--|----------------------------------|--|
| 25. | Number of Nucleosom (1) 6 | es found in helical coil c (2) 10 | of 30 nm chromatin fibre i (3) 12 | is (4) 15 | |
| 26. 🕿 | Which is incorrect regarding nucleosome? (a) A typical nucleosome contain 200 bp of DNA helix (b) Histone are rich in the basic amino acid residue lysines & arginines (c) The packaging of chromatin at higher level require additional set of proteins that collectively are referred to as Non-histone chromosomal (NHC) protein | | | | |
| | (1) a only | (2) a & c both | (3) c only | (4) None | |
| 27. | Which is incorrect for t-RNA (1) t-RNA has an anticodon loop that has bases complementary to the codon of m-RNA (2) t-RNA are specific for each amino acid (3) Three t-RNA are present for stop codon (4) In actual structure, the t-RNA is a compact molecule which looks like inverted L. | | | | |
| 28. | Heat killed pathogenion The result would be | bacterial cells and live | e nonpathogenic cells a | re mixed and injected into mice. | |
| | (1) Mice develop disea(3) Mice remain health(5) All mice remain health | у | (2) Mice die without d (4) 50% mice develop | | |
| 29. | Chargaff's rules are ap (1) Single stranded RN (3) Single stranded DN | IA | (2) Single stranded D (4) Double stranded D | | |
| | | | | | |
| I | DNA REPLICATIO | | ION - B # N, GENETIC CODE | AND TRANSLATION | |
| 1. | The experimental syst | em used in the studies c | on the discovery of replic | ation of DNA has been | |
| | (1) Drosophila melano | gaster | (2) Pneumococcus | | |
| | (3) Escherichia coli | | (4) Neurospora crass | a | |
| 2.2 | DNA replication is | | | | |
| | (1) Semiconservative | and semi discontinous | (2) Semiconservative | | |
| | (3) Conservative | | (4) Conservative and | aiscontinous | |
| 3. | DNA replication is aide (1) DNA polymerase o | • | | | |
| | (3) Both DNA polymer | - | (2) DNA ligase only (4) RNA polymerase | | |
| 4. | | h new strand is produce | | | |
| | (1) complementary | | (2) template | | |
| | (3) primer | | (4) elongating | | |

| 5.24 | In DNA replication, primer strand is formed by (1) A small piece of deoxyribonucleotide polymer (2) A small piece of ribonucleotide polymer (3) Deoxyribonucleotides + pyrophosphates (4) DNA replicase + nucleotide + ATP | | | | |
|------|---|---|--|--|--|
| 6. | The enzyme which cata (1) Reverse transcripta (3) DNA polymerase | • | RNA from DNA template is known as (2) RNA polymerase (4) Nucleases | | |
| 7. | Ligase - an ezyme is u (1) joining bits of DNA (3) denaturation | sed for | (2) splitting DNA thread (4) none of the above | l into small bits | |
| 8. | The protein which helps to unwind DNA doubl (1) DNA polymerase (2) DNA gyrase | | helix during replication is (3) helicase | s (4) DNA topoisomerase | |
| 9. | Small fragments of DN (1) Nucleotides (3) Okazaki fragements | | lication of DNA are called (2) Genes (4) Single stranded DNA | | |
| 10. | The strand of DNA whi (1) leading strand | ch is synthesized continu (2) lagging strand | iously during replication i (3) sense strand | is called (4) antisense strand | |
| 11.2 | DNA polymerase enzy (1) Kornberg | me was discovered by (2) Nirenberg | (3) Khorana | (4) Ochoa | |
| 12. | The first codon discove (1) GGG | ered by Nirenberg and Ma (2) CCC | athaei was (3) UUU | (4) AAA | |
| 13. | A codon is said to be degenerate because (1) It degenerates soon after coding (2) more than one amino acid can be coded by a single codon (3) the same amino acid can have many codons (4) all the above | | | | |
| 14. | Which of the following (1) AUG | serves as a termination of (2) CGC | codon? (3) UAG | (4) GUG | |
| 15. | In the genetic code dic (1) 20 | tionary, how many codor (2) 64 | as are used to code for al (3) 61 | l the 20 essential amino acids? (4) 60 | |
| 16.๖ | There are 64 codons in genetic code dictionary because (1) There are 64 types of tRNA found in the cell (2) There are 44 meaningless and 20 codons for amino acids (3) There are 64 amino acids to be coded (4) Genetic code is triplet | | | | |
| 17. | The DNA chain acting What will be the order (1) TCGT AAGCT | - | synthesis has the followin (3) UCG UAG CT | ng order of bases AGCTTCGA (4) UCG AAG CU | |
| 18. | Which of the following (1) 5' AATAAT3' | is Pribnow box? (2) 5' ATATTA3' | (3) 5' TATAAT3' | (4) 5TAATTA3' | |

| 19.১ | During elongation occuring in translation, the er (1) Peptidyl transferase (3) Protease | | nzyme which catalyses the synthesis of peptide bond is (2) Peptidyl synthetase (4) Amino acyl synthetase | | |
|-------|--|---|--|--|--|
| 20. | Identify the characterist (1) Non-Polar | tic which is not applicable (2) Non-overlapping | e to the genetic code (3) Commaless | (4) Universal | |
| 21. | (1) Activate the DNA te(2) Synthesize DNA nu | cleotides for the formatic n of new strand on the te | n of new strand | | |
| 22. | At the end of the proce the (1) Okazaki fragements | · | e newly formed lagging strand is also continuous due to (2) Semiconservative method of replication | | |
| | (3) DNA ligases | | (4) Double-stranded na | | |
| 23. | Find out the correct ma | itching | | | |
| | a Helicase b Gyrase c Primase d DNA polymerase (1) a - ii, b - iii, c - iv, c (3) a - iv, b - iii, c - i, d | i – i | NA | | |
| 24. 🕿 | Transcriptionally active chromatin is called as(a)and transcriptionally inactive chromatin is called as(b) One strand of DNA, replication is continuous & it is called as(c)while on another strand of DNA replication is discontinuous & it is called as(d) Here (a), (b), (c) & (d) respectively: (1) (a) Heterochromatin, (b) Euchromatin, (c) Lagging strand, (d) Leading strand (2) (a) Euchromatin, (b) Heterochromatin, (c) Leading strand, (d) Lagging strand (3) (a) Heterochromatin, (b) Euchromatin, (c) Leading strand, (d) Continuous strand (4) (a) Euchromatin, (b) Heterochromatin, (c) Discontinuous strand, (d) Leading strand | | | | |
| 25. | Termination of the trans (1) 5' end of the DNA to (3) 3' end of t-RNA | slation process occurs at emplate | the (2) 3' end of the mRNA (4) 5' end of mRNA | | |
| 26. | The amino acid valine i code is referred to as (1) Degeneracy | is recognised by the triple (2) Universality | ets GUU, GUC, GUA and (3) Non-ambiguity | d GUG and this character of the (4) Commalessness | |
| 27. | (1) Despected (1) (2) Watson and Crick (3) Nirenberg and Matthaei | | (2) Nirenberg and Lede (4) Crick | | |
| 28. | The m-RNA, AUGCAG as | GAUCGU recognises fo | ur amino acid and this c | haracter of the code referred to | |
| | (1) Degeneracy | (2) Universality | (3) Non-amibiguity | (4) Commalessness | |

| 29. | Sigma factor is component of (1) RNA polymerase (2) Dissociation factor (3) DNA ligase (4) DNA polymerase | | | | |
|-------|--|---|---|---------------------------------|--|
| 30. | After reaching into cyto (1) 40S particle | oplasm the m-RNA attach (2) ER | es itself to (3) 70 ribosomes | (4) 60S particle | |
| 31. | Functional unit of gene (1) Recon | that specifies synthesis ((2) Cistron | of one polypeptides is (3) Codon | (4) Muton | |
| 32. | Starting and stopping ((1) AUG and UGA | codons are (2) GUA and AAA | (3) UCA and UAA | (4) GUC and AUG | |
| 33.24 | The amino acids with a (1) Phenylalanine and (3) Glutamic acid and a | glycine | (2) Methionine and Tryp (4) Proline and Glycine | • | |
| 34. | 5'AUG CUA UACCUC this m-RNA- | of the processed m–RNA CUUUAUCUGUGA–3' H | ow many different t–RN | A molecule require to translate | |
| | (1) 8 | (2) 7 | (3) 6 | (4) 5 | |
| 35. | Which of the following (1) Initiation | is exclusive property of tr (2) Elongation | anscription found in RNA (3) Termination | A-polymerase (4) Processing | |
| 36. | Which of the following contiguous manner (1) Chromosomal struc (3) Substitutional muta | ctural mutations | tic basis of proof that codon is a triplet and it is read in a (2) Chromosomal numerical mutations (4) Frame shift insertion or deletion mutation | | |
| 37. | What is wroing about transcription? (1) RNA polymerase is associated with initiation factor (σ) & termination factor (2) There is only one RNA polymerase is present in eukaryotes. (3) In eukaryotes, hn-RNA undergoes additional processing called as capping & tailing. (4) Transcription is monocistronic in eukaryotes & polycistronic in prokaryotes. | | | | |
| 38. | Read the following statements. (a) During protein synthesis formation of a peptide bonds do not require energy (b) The UTRS are present at both 5' and at 3' end. (c) The structural gene in a transcription unit could be said as monocstronic mostly in eucaryotes. How many of above statement are correct. (1) One (2) Two (3) Three (4) All are correct | | | | |
| 39. | Enzyme required for p (1) Peptidase | () | | (4) Nitrate reductase | |
| 40. | cDNA is formed by (1) DNA dependent DI (3) DNA dependent RI | | (2) RNA dependent DN (4) DNA ligase | A polymerase | |
| 41. | Mode of DNA replication (1) Conservative and u (3) Conservative and b | | (2) Semiconservative a(4) Semiconservative a | | |

42. Match the columns Column I

Column II

| a. | Termination | 1. | Aminoacyl tRNA synthetase | | | |
|-------|----------------------|--------|--------------------------------|--|--|--|
| b. | Translation | 2. | Okazaki fragments | | | |
| c. | Transcription | 3. | GTP dependent release factor | | | |
| d. | DNA replication | 4. | RNA polymerase | | | |
| (1) a | - 2, b - 3, c - 1, c | l – 4 | (2) a − 1, b − 4, c − 2, d − 3 | | | |
| (3) a | - 3, b - 1, c - 4, c | l – 2 | (4) a − 2, b − 4, c − 1, d − 3 | | | |
| (5) a | - 2, b - 4, c - 1, c | l – 3. | | | | |
| | | | | | | |

43. In Rous sarcoma virus, the flow of information is

| (1) DNA \rightarrow RNA \rightarrow Proteins | | | | (2) DNA – | Proteins - | $\rightarrow RNA$ |
|--|--|--|--|-----------|------------|-------------------|
| | | | | | | |

- (3) $RNA \rightarrow DNA \rightarrow RNA \rightarrow proteins$ (4) RNA \rightarrow DNA \rightarrow proteins
- 44. While working on Neurospora crassa Beadle and Tatum proved
 - (1) Every gene is responsible for a specific enzyme
 - (2) Plant cells are totipotent
 - (3) DNA replication is semiconservative
 - (4) Viruses have genetic material.
- 45. The sequence of events mentioned below are symbolised by alphabets. Choose the correct answer where the alphabets are matched with the processes

RNA \xrightarrow{a} DNA \xrightarrow{b} DNA \xrightarrow{c} mRNA \xrightarrow{d} Polypeptide

- (1) a = Reverse transcription. b= Replication, c = Transcription, d = Translation
- (2) a = Replication, b = Transformation, c = Transcription, d = Translation
- (3) a = Reverse transcription, b = Transformation c= Transcription, d = Translation
- (4) a = Replication, b = Transduction. c = Translation, d = Transcription.
- 46. Match the column:

| | Column I | Column II | | |
|----|------------------------------|-----------|----------------|--|
| a. | Transforming principle | i. | Watson & Crick | |
| b. | Semiconservative replication | ii. | Gamow | |
| C. | Lac operon model | iii. | Griffith | |
| d. | Triplet codon | iv | Jacob & Monod | |

(1) $a \rightarrow iii$, $b \rightarrow i$, $c \rightarrow iv$, $d \rightarrow ii$

(3) $a \rightarrow i$, $b \rightarrow ii$, $c \rightarrow iii$, $d \rightarrow iv$

(2) $a \rightarrow iv$, $b \rightarrow ii$, $c \rightarrow iii$, $d \rightarrow i$

(4) $a \rightarrow iii$, $b \rightarrow iv$, $c \rightarrow i$, $d \rightarrow ii$

SECTION - C #

REGULATION OF GENE EXPRESSION, HGP AND DNA FINGERPRINTING

- 1. Which of the following is/are the level of regulating of gene expression in eukaryotes
 - (a) Translational level
 - (b) Transport of mRNA from nucleus to the cytoplasm
 - (c) Processing level
 - (d) Transcriptional level
 - (1) a, b only (2) d, c, b only (3) d, c, a only (4) d, c, b, a all

| 2. | Operon contains (1) Operator and regula (2) Operator and struct (3) Operator and regula | ural gene | | |
|----|--|--|--|----------------------------|
| | (4) Operator gene, reg | ulator gene repressor, s | tructural genes and prom | oter gene |
| 3. | Which one of the follow (1) z, a, y | ving is the correct seque (2) z, y, a | ence of structural gene in (3) a, z, y | lac operon? (4) y, a, z |
| 4. | According to Operon c (1) A general inhibitor (3) A repressor | oncept a regulator gene | forms (2) A small peptide (4) An inducer | |
| 5. | In lac operon, sturctura (1) β-galactosidase (3) Galactosidase trans | | (2) Galactosidase perr (4) None of the above. | |
| 6. | The function of promot (1) Bind to gyrase (3) Code for DNA polyr | | (2) Bind to RNA polym (4) Process mRNA. | erase |
| 7. | Due to high degree of ((1) 0.1—2kb (3) 0.01 — 20 kb | polymorphism, size of V | NTR varies from (2) 0.1—20 kb (4) 0.1 — 200 kb | |
| 8. | Crime scene sample | rou charge with the crim 1 Suspect 2 | e | |
| | - | | | |

- (1) Both suspect 1 and 2
- (3) Only suspect 2

- (2) Only suspect 1
- (4) Neither suspect 1 nor suspect 2

9. A Match the column:

10.

| | | Column – I | | Column – II | | |
|---|----------------------------|-------------------|------|-------------------------------------|---|--|
| | a. | VNTR | i. | β-Galactosidase | | |
| | b. | Lac operon | ii. | DNA ligase | | |
| | c. | Genetic code | iii. | DNA finger printing | | |
| | d. | Okazaki fragments | iv. | Unambiguous | | |
| (| (1) a→iv, b→ii, c→iii, d→i | | | (2) a→iii, b→i, c→iv, d→ii | | |
| (| (3) a→i, b→ii, c→iii, d→iv | | | (4) a→iii, b→iv, c→i, d→ii | | |
| | | | | (2) Error in bas (4) DNA replica | • | |

| 11. | Which of the following (1) BAC & YAC cloning (3) VNTR | is not related with HGP g vector | (2) Bioinformatics(4) EST'S | | |
|-----|--|---|---|----------------------------|--|
| 12. | (b) Hybridisation using | NA finger printing was in I labelled VNTR probe is uence among human is t | nitially developed by Alec Jeffreys. one of the step utilize in DNA finger printing the same. | | |
| | (1) 'a' only | (2) 'b' only | (3) 'c' only | (4) None | |
| 13. | Best method to determine parternity is (1) Protein analysis (3) Gene counting | | (2) Chromosome counting(4) DNA finger printing | | |
| | | MISCELLANEC | US QUESTIONS | | |
| 1. | Which is true accordin | g to Chargaff's rule | | | |
| | (1) A + G = T + C | (2) A = C | (3) G = T | $(4) \frac{A+T}{C+G} = 1$ | |
| 2. | DNA element with abil (1) Cistron | ity to change its position (2) Transposon | is (3) Intron | (4) Recon. | |
| 3. | Intron is part of DNA which (1) Codes for protein synthesis (3) Does not code for protein synthesis | | (2) Helps in joining pieces of DNA(4) Initiates transcription. | | |
| 4. | In DNA replication, the | e leading strand is the on | e which replicates in | | |
| | (1) 5' \longrightarrow 3' direction of | continuously | (2) $3' \rightarrow 5'$ direction of | continuously | |
| | (3) 5' \longrightarrow 3' direction of | discontinuously | (4) $3' \rightarrow 5'$ direction of | discontinuously. | |
| 5. | Hargobind Khorana wa (1) Deciphering geneti (3) Nucleotide sequen | | for (2) Artificial gene synthesis (4) Discovery of transposons. | | |
| 6. | t-RNA has the function of (1) Transcription (2) Adapter for attaching amino acids over mRNA template (3) Transferring information to mRNA (4) Carry genetic code to cytoplasm. | | | | |
| 7. | Length of mRNA that o (1) Muton | carries information for co (2) Codon | mplete polypeptide synth (3) Operon | nesis is (4) Cistron. | |
| 8. | Codon AUG specifies (1) Methionine | (2) Valine | (3) Tyrosine | (4) Phenylalanine | |
| 9. | Which one codes for a (1) Cistron | n amino acid (2) Exon | (3) Intron | (4) Codon | |
| | | | | | |

| 10. | Okazaki fragments are (1) RNA primers (3) Short DNA frageme | nts on lagging strand | (2) Short DNA fragmer (4) DNA fragements fro | - | | | |
|-----|--|--|--|--|--|--|--|
| 11. | Repressor binds to ope (1) Lactose is unable to (3) Galactosidase does | remove the repressor | (2) RNA polymerase is (4) Structural genes z, | activated y and a fail to transcribe. | | | |
| 12. | Enzyme catalysing pep (1) Smaller subunit of ri (3) Central part of tRNA | | in (2) Larger subunit of rib (4) None of the above | posome | | | |
| 13. | Who was awarded Nob (1) Kornberg | el Prize for in vitro synth (2) Tatum | esis of polyribonucleotid (3) Ochoa | es? (4) Khorana | | | |
| 14. | What is correct (1) mRNA is polycistronic in eukaryotes and moncistronic in prokaryotes (2) mRNA is polycistronic in both eukaryotes and prokaryotes (3) mRNA is monocistronic in both eukaryotes and prokaryotes (4) mRNA is polycistronic in prokaryotes and monocistronic in eukaryotes | | | | | | |
| 15. | VNTR is employed for (1) Protoplasmic culture (3) Regulation of plant growth hormones | | (2) DNA finger printing (4) Enhancing photosynthesis in desert plant. | | | | |
| 16. | Smallest part of DNA th (1) Muton | nat can undergo recomb (2) Cistron | ination is (3) Replicon | (4) Recon | | | |
| 17. | DNA and RNA differs b (1) Nitrogen bases and (3) Number of C- atoms | sugars | (2) Nitrogen bases and phosphate groups (4) Sugar and phosphate groups. | | | | |
| 18. | DNA acts as a template (1) RNA | e for synthesis of (2) DNA | (3) Both (1) and (2) | (4) Protein | | | |
| 19. | Length of DNA with 23 (1) 78·4 Å | base pairs is (2) 78⋅2 Å | (3) 78 Å | (4) 74 ·8 Å | | | |
| 20. | Find the correct match (1) UUA – Valine | (2) AUG – Cysteine | (3) AAA – Lysine | (4) CCC- Alanine | | | |
| 21. | – CCA 3' end of t-RNA (1) Anticodon loop | is called (2) DHU loop | (3) TψC | (4) Amino acid binding site | | | |
| 22. | Portion of gene which is (1) Exon | s transcribed but not tran (2) Intron | nslated is (3) Cistron | (4) Codon | | | |
| 23. | The bond formed betwe (1) Sulphide bond (3) Hydrogen bond | een phosphate and pent | ose sugars of DNA is (2) Phosphodiester bor (4) Covalent bond | nd | | | |
| 24. | Unwinding due to releat (1) Gyrase | se of coiling tension ahe (2) Unwindase | ead of moving replication (3) Topoisomerase | fork is due to (4) All the above | | | |

| 25. | Synthesis of RNA mole (1) Alpha factor | ecule is terminated by (2) Gamma factor | (3) Delta factor | (4) rho factor | | |
|-----|--|--|--|---|--|--|
| 26. | (2) Starts at operator r(3) Starts at promoter | region and ends at stop egion and ends at telome region and ends are term and ends at TATA box. | eric end | | | |
| 27. | In ATG ACC AGG ACC CCA ACA sequence, the first base gets mutated. It will affect (1) Change in types and sequence of amino acids (2) Change in first amino acid only (3) No change (4) One amino acid less | | | | | |
| 28. | Hn-RNA is (1) Heteronuclear RNA (3) Heterogeneous RN | | (2) Homonuclear RNA (4) Useful RNA. | | | |
| 29. | Continuously functiona (1) House keeping ger (3) Mild genes | • • | ated on the tissue level are (2) Luxury genes (4) Gene battery. | | | |
| 30. | Which amino acid is sp (1) Leucine | Decified by genetic codes (2) Methionine | ACU, ACC, ACA, ACG (3) Glycine | showing degeneracy? (4) Threonine | | |
| 31. | Transfer of DNA bands (1) Southern transfer | s from agarose gel to nitr (2) Western transfer | ocellulose or nylon mem (3) Northern transfer | brane is (4) Eastern transfer | | |
| 32. | Complete turns in 450 (1) 45 | 00 bp DNA would (2) 450 | (3) 4500 | (4) 45, 000. | | |
| 33. | Teminious central dog (1) DNA \rightarrow DNA \rightarrow mI (3) gRNA \rightarrow DNA \rightarrow n | • | is (2) mRNA \rightarrow gRNA \rightarrow DNA \rightarrow Protein (4) DNA \rightarrow gRNA \rightarrow mRNA \rightarrow Protein | | | |
| 34. | DNA replication requir (1) DNA polymerase | es (2) DNA ligase | (3) RNA polymerase | (4) All the above | | |
| 35. | The RNA primer is use (1) Translation | ed in (2) Replication | (3) Conjugation | (4) Transformation | | |
| 36. | In a DNA, percentage (1) 20% | of thymine is 20% what i (2) 40% | s the percentage of guar (3) 30% | nine (4) 60% | | |
| 37. | • | -operon concept, which ssing the activity of the o (2) Regulator gene | | e bacterial genetic material is ence of lactose? (4) Promoter gene. | | |
| 38. | - | ukaryotes the anticodon t (2) 3' – UAC – 5' | - | | | |

| 39. | - | ving six coils, there are ses are found in that se | • | linked by two hydrogen bonds. | |
|-----|--|--|--|---|--|
| | (1) 22 | (2) 38 | (3) 44 | (4) 76 | |
| 40. | Identify the triplet codo | ns which code for aminc | acids serine and proline |). | |
| | (a) UCC The correct answer is | (b) CCA | (c) GGG | (d) AAG | |
| | (1) a and c | (2) b and d | (3) c and d | (4) a and b | |
| 41. | | ng as template for m-RN | | | |
| | (a) Coding strand The correct answer is | (b) Noncoding strand | (c) Sense strand | (d) Antisense strand | |
| | (1) a and c | (2) a and d | (3) b and c | (4) b and d | |
| 42. | | ntains two kinds of bas | e sequences. Which of | these plays an important role in | |
| | protein synthesis (1) Introns | (2) Exons | (3) Both (1) and (2) | (4) None of these | |
| | Exercise | 2 | | | |
| | | ·Z | | | |
| 1. | Restriction endonuclear of bond do they act on | • | eave DNA molecules int | o smaller fragments. Which type [KVPY_2010_SB] | |
| | N-glycosidic Bond Hydrogen bond | | (2) Phosphodiester bond(4) Disulfide bond | | |
| 2. | If the sequence of bas will be : | e in DNA is 5'- ATGTAT | CTCAAT- 3', then the se | quence of bases in its transcript [KVPY_2011_SB] | |
| | (1) 5' - TACATAGAGT (3) 5' - AUGUAUCUCA | | (2) 5' - UACAUAGAGL (4) 5' - AUUGAGAUAC | | |
| 3. | | | osed by Watson & Crick | | |
| | (1) left handed helix | | | [KVPY_2011_SB] | |
| | (2) helix that makes a f | ull turn every 70 nm. | | | |
| | | n of DNA contains 20 ba | • | | |
| | | where each strand has o | | | |
| 4. | - | plete turn of a DNA doub | | [KVPY_2011_SB] | |
| _ | (1) 34 Å | (2) 34 nm | (3) 3.4 Å | (4) 3.4 μm | |
| 5. | expect that the baby w | ould be | | io cones in his eyes. We would [KVPY_2012_SA] | |
| | (1) color blind | (2) night blind | (3) blind in both eyes | (4) blind in one eye | |
| 6. | Transfer RNA (tRNA) (1) is present in the rib (2) usually has clover b | osomes and provides str | uctural integrity | [KVPY_2012_SB] | |
| | ., . | rmation from DNA to ribo | osomes | | |
| 7. | DNA mutations that do | not cause any functiona | I change in the protein p | roduct are known as [KVPY_2012_SB] | |
| | (1) nonsense mutation | s (2) missense mutation | s (3) deletion mutations | (4) silent mutations | |

| 8. | - | | IA is 5'-GTTCATCG-3, t | hen the sequence of bases in its | | |
|-----|--|--|--|---|--|--|
| | RNA transcript would be (1) 5'-GTTCATCG-3' | e (2) 5'GUUCAUCG-3 | (3) 5'CAAGTAGC-3' | [KVPY_2012_SB] (4) 5'CAAGUAGC -3 | | |
| 9. | roan (red and white colo will have phenotypic rati | our in equal proportion) io (red : roan : white) is | . If F ₁ progeny are self- - | express equally in F ₁ to produce bred, the resulting progeny in F ₂ [KVPY_2012_SB] | | |
| 10. | (1) 1 : 1 : 1 'a' person with blood gro | (2) 3 : 9 : 3 oun "A" can (a) donate t | (3) 1 : 2 : 1 | (4) 3 : 9 : 4 receive blood from | | |
| 10. | a person wan blood gre | | | [KVPY_2013_SA] | | |
| | (1) (a) persons with bloc (2) (a) person with blocc (3) (a) person with blocc (4) (a) person with any blocc | d group "A" or "AB", and d group "B" or "AB", and | l (b) "A" or "O" blood gro l (b) "B" or "O" blood gro | ups | | |
| 11. | The sequences of four E i. TATATATATATATA ATATATATATATATAT Which one of these DNA | ii. TTTCCCGGGAAA AAAGGGCCCTTT | iii. TTGCGTTGCC AACGCAACGG | G CGGCCTAGGCCG | | |
| | (1) i | (2) ii | (3) iii | (4) iv | | |
| 12. | If DNA codons are ATG (1) non-sense mutation | • | | esults in, [KVPY_2013_SB] tion (4) silent mutation | | |
| 13. | According to Mendel, | So | egregate and | assort independently. | | |
| | (1) alleles of a gene; alle(3) dominanat traits; rec | - | (2) alleles of difference(4) recessive traits | [KVPY_2013_SB] ent genes; alleles of a gene recessive traits | | |
| 14. | Watson and Crick mode | el of DNA is | | [KVPY_2013_SB] | | |
| | (1) B-form DNA with a spiral length of 34 Å and a diameter of 20 Å (2) A-form DNA with a spiral length of 15 Å and a diameter of 20 Å (3) Z-form DNA with a spiral length of 34 Å and a diameter of 20 Å (4) B-form DNA with a spiral length of 28 Å and a diameter of 14 Å | | | | | |
| 15. | In Griffith's experiments | mice died when injecte | d with: | [KVPY_2014_SB] | | |
| | (1) heat killed S-strain(3) heat killed R-strain | | (2) heat killed S-strain(4) live R-strain | combined with R-strain | | |
| 16. | Which of the following is (1) a polypeptide (3) either polypeptide or | | ene? (2) an RNA only (4) a nucleotide only | [KVPY_2014_SB] | | |
| 17. | Which one of the followi | ing is the complementar | y sequence for the DNA | | | |
| | (1) 5'-TAGTACG-3' | (2) 5'-ATCATGC-3' | (3) 5'-UTCUTGC-3' | [KVPY_2014_SB] (4) 5'-GCUAGCA-3' | | |

Exercise-3

PART - I: NEET / AIPMT QUESTION (PREVIOUS YEARS)

| 1. | Length of one coil of B- | | (2) 40 | (4) 00 | (AIPMT-2000) |
|-----|--|--|--|------------------|----------------|
| _ | (1) 0-34 nm | (2) 3·4 nm | (3) 10 nm | (4) 20 nm | |
| 2. | Three dimensional sha | | (2) V shared | (1) V shared | (AIPMT-2000) |
| | (1) L-shaped | (2) Clover leaf-like | (3) X-shaped | (4) Y- shaped | |
| 3. | • | A and RNA is that both ha | | lipption | (AIPMT-2000) |
| | (1) Similar sugars(3) Similar pyrimidines | | (2) Similar mode of repl(4) Polymers of nucleot | | |
| 4. | ., | union of DNA fragments | | | (AIPMT-2002) |
| 4. | (1) Ligase | (2) Polymerase | (3) Helicase | (4) Endonuclea | , |
| - | | | | | |
| 5. | (1) Four | ases operative in eukaryo (2) Three | otes are (3) Two | (4) One | (AIPMT-2001) |
| | | | (3) 1 WU | (4) One | |
| 6. | <i>Escherichia coli</i> is allo correct | wed to replicate once i | n medium having radioa | active thymidine | . Which one is |
| | (1) Both strands of DNA | A become radioactive | (2) One strand become | s radioactive | (AIPMT-2001) |
| | (3) Each strand is half i | radioactive | (4) None is redioactive. | | |
| 7. | Evolution was termed F | RNA world due to discove | ery of | | (AIPMT-2001) |
| | (1) Absence of RNAs in | n some cells | (2) Genomic RNA | | |
| | (3) RNA enzymes | | (4) Synthesis of proteins by mRNA, tRNA, and rRNA. | | |
| 8. | | oosed operon concept | on the basis of their s | tudy of lactose | |
| | Escherichia coli. The co | | (2) All prokenistes and | aama aukanyata | (AIPMT-2002) |
| | (1) All prokaryotes only(3) All prokaryotes and | | (2) All prokaryotes and some eukaryotes(4) All prokaryotes and some protozoans. | | |
| • | | - | | | |
| 9. | - | periment on bacteria was | | rium | (AIPMT-2002) |
| | (1) Escherichia coli(3) Pasteurella pestis | | (2) Salmonella typhimurium(4) Diplococcus pneumoniae. | | |
| 40 | | | | | |
| 10. | (1) Overlapping genes | odes are for 20 types of a | (AIPMI-200) (AIPMI-200) (AIPMI-200) (AIPMI-200) | | (AIPMT-2002) |
| | (3) Wobbling of codons | | (2) Degeneracy of generic code (4) Universality of codons | | |
| 11. | Exon segments are reu | | () | - | (AIPMT-2002) |
| ••• | (1) RNA primase | (2) RNA protease | (3) RNA polymerase | (4) RNA ligase | . , |
| 12. | | matched with its specifici | | ., . | |
| 12. | which one is correctly | | ty for an annino aciu, star | | (AIPMT-2002) |
| | (1) UCG – start | (2) UUU – stop | (3) UGU – Leucine | (4) UAC – Tyrc | . , |

| 13. | A gene encoding for polypeptide of 50 amino acids get mutated at 25 codon UAU becoming result would be (AII (1) Polypeptide of 24 amino acid (2) Two polypeptides one with 24 amino acids and second with 25 amino acids (3) A polypeptide with 49 amino acid (4) A polypeptide of 25 amino acids | | | | | | |
|-----|---|--|---|--------------------------|------------------------------|--|--|
| 14. | During transcription, R (1) Regulator | NA polymerase binds to I (2) Promoter | DNA site (3) Enhancer | (4) Receptor. | (AIPMT-2003) | | |
| 15. | Degeneration of geneti (1) First member of coo (3) Third member of co | | (2) Second member of(4) Entire codons. | codons | (AIPMT-2003) | | |
| 16. | What does lac refer to (1) Lactase | in lac operon (2) 1,00,000 | (3) Lac insect | (4) Lactose | (AIPMT-2003) | | |
| 17. | (1) Formation of formyl(2) Binding of 30 S sub(3) Association of 30S | ation in prokaryotes GTP met - tRNA punit of ribosome with mR - mRNA with formyl - me subunit of ribosome with | NA et - tRNA | | (AIPMT-2003) | | |
| 18. | In genetic code dictions (1) 20 | ary, codons used to code (2) 60 | for all the 20 essential a (3) 61 | mino acids are (4) 64 | (AIPMT-2003) | | |
| 19. | In gene mutation, ader (1) Frame-shift mutatio | nine is replaced by guanir n (2) Transcription | ne. It is (3) Transition | (4) Transversio | (AIPMT-2004) | | |
| 20. | The ratio constant for a (1) A + G/C + T | a species is (2) T + C/G + A | (3) A + C/T + G | (4) G + C/A + T | (AIPMT-2004) | | |
| 21. | In bacterial DNA replica (1) Involves RNA prime (3) Proceeds unidirecti | | rom the site of origin of r (2) Requires telomeras (4) Moves bidirectionall | e | (AIPMT-2004) | | |
| 22. | DNA finger printing is related to (1) Molecular analysis of profiles of DNA samples (2) Analysis of DNA samples using imprinting devices (3) Techniques used for molecular analysis of different specimens of DNA (4) Techniques used in identification of finger prints of different persons | | | | | | |
| 23. | On which organism Be | adle and Tatum worked t | o propose one gene-one | enzyme hypoth | esis (AIPMT-2007) | | |
| | (1) Drosophila (3) Neurospora crassa | | (2) Escherichia coli (4) Nostoc | | | | |
| 24. | saddle like structure at | that point. The sequence | e is called | | NA assumes a (AIPMT-2007) | | |
| | (1) AAAT box | (2) TATA box | (3) GGTT box | (4) CAAT box. | | | |
| 25. | Amino acid sequence i (1) rRNA | n protein synthesis is det (2) tRNA | ermined by sequence of (3) mRNA | (4) cDNA. | (AIPMT-2006) | | |

| 26. | Antiparallel strands of (1) One strand turns c (2) One strand turns a | | | (AIPMT-2006) |
|-----|--|---|--|---|
| | ., | | the same position their trands are in opposite po | |
| 27. | A sequential expression | on of a set of human gen | es occurs when a steroid | d molecule binds to |
| | | | | (AIPMT-2007) |
| | (1) mRNA | (2) DNA sequence | (3) tRNA | (4) Ribosome |
| 28. | The two polynucleotide (1) Discontinuous | e chains of DNA are (2) Antiparallel | (3) Parallel | (AIPMT-2007) (4) Semiconservative |
| 29. | In the DNA molecule | | | (AIPMT-2008) |
| | (2) There are two strait(3) The total amount of | nds which run antiparalle | mine varies with the organized one in 5' \rightarrow 3' direction pyrimidine nucleotides is the 5' \rightarrow 3' direction. | and other in $3' \rightarrow 5'$ |
| 30. | | • · | correctly matched with t | heir function or the signal for the |
| | particular amino acid? (1) AUG, ACG – start/ (3) GUU – Alanine | | (2) UUA, UCA – Leuc (4) UAG, UGA – stop | (AIPMT-2008) ne |
| 31. | gene (2) RNA polymerase p (3) A cell displaying a | RNA that is complement | synthesis of antigens | (AIPMT-2008) to stop expression of a specific |
| 32. | What is not for genetic (1) It is unambiguous (2) A codon in mRNA (3) It is nearly universa (4) It is degenerate | is read in a non-contigue | ous fashion | (АІРМТ-2009) |
| 33. | Semiconservative repl | lication of DNA was first | demonstrated in | (AIPMT-2009) |
| | (1) Salmonella typhim | urium | (2) Drosophila melang | |
| | (3) Escherichia coli | | (4) Streptococcus pne | |
| 34. | Removal of introns an (1) Looping | d joining of exons in a de (2) Inducing | efined order during transo (3) Slicing | cription is called: (AIPMT-2009) (4) Splicing |
| 35. | The one aspect which (1) Ambiguous | is not a salient feature c (2) Universal | f genetic code, is its beir (3) Specific | ng (AIPMT-2010) (4) Degenerate |

| 36. | (a) Glucose or galactor(b) In the absence of la(c) The z-gene codes f | se may bind with the rep actose the repressor bin for permease d by Francois Jacob and | ur (a-d) given below abou pressor and inactivate it ids with the operator regio d jacque Monod | |
|-----|---|---|---|--|
| | (1) (a) and (c) | (2) (b) and (d) | (3) (a) and (b) | (4) (b) and (c) |
| 37. | Satellite DNA is useful (1) Sex determination (3) Genetic engineerin | | (2) Forensic science (4) Organ transplantati | (AIPMT-2010) on |
| 38. | What are those structue electron microscope? | ures that appear as bea | ads - on - string in the ch | romosomes when viewed under (AIPMT-2011) |
| | (1) Genes | (2) Nucleotides | (3) Nucleosomes | (4) Base pairs |
| 39. | Removal of RNA polyn (1) t-RNA | nerase III from nucleopl (2) hn-RNA | asm will affect the synthes (3) m-RNA | sis of: (AIPMT Pre. 2012) (4) r-RNA |
| 40. | Which one of the follow (1) The inducer | wing is not a part of a tra (2) A terminator | anscription unit in DNA? (3) A promoter | (AIPMT Pre. 2012) (4) The structural gene |
| 41. | Which one of the follow (1) 5' - GAATTC - 3' 3' - CTTAAG - 5' (2) 5' - CCAATG - 3' 3' - GAATCC - 5' (3) 5' - CATTAG - 3' 3' - GATAAC - 5' (4) 5' - GATACC - 3' 3' - CCTAAG - 5' | wing represents a palinc | Iromic sequence in DNA? | (AIPMT Mains 2012) |
| 42. | (1) The relative propor(2) The relative difference(3) The relative amount | | imidines in DNA nce in blood, skin and sali nd grooves of the fingerpi | |
| 43. | (B) Regulation of <i>lac</i> o(C) The human genom(D) Haemophilia is a second se | enosine pairs with uraci | eferred to as positive regul 0,000 genes. | (AIPMT Mains 2012) ation. |

| 44. | The diagram shows an in | nportant concept i | n the genetic implication of | DNA. Fill in the blanks A to C. |
|-----|---|--------------------|-------------------------------|--|
| | O A A M M M A B $Protector B$ | • • | | (NEET- 2013 |
| | (1) A - translation B - trans | _ | n Chargaff | (NEE1-2013) |
| | (2) A -transcription B - tra | | - | |
| | (3) A - translation B - exte | | | |
| | (4) A - transcription B - re | plication C - Jame | es Watson | |
| 45. | Which one of the following | g is wrongly match | ned? | (AIPMT-2014) |
| | (1) Transscription - Writing | | | , , , , , , , , , , , , , , , , , , , |
| | (2) Transscription - Using | information in m - | RNA to make protein | |
| | (3) Repressor protein - Bi | nds to a operature | e to stop enzme synthes | |
| | (4) Operon - Structural ge | nes, operator and | promoter. | |
| 46. | Transformation was disco | vered by: | | (AIPMT-2014) |
| | (1) Meseson and stahl | | (2) Hershey and chas | se |
| | (3) Griffith | | (4) Waston and crick | |
| 47. | Select the correct option: | | | (AIPMT-2014) |
| | Directionof RNA | Direction of read | ling of the template | |
| | synthesis | DNA strand | ing of the template | |
| | (1) 5' - 3' | 3' - 5' | | |
| | (2) 3' - 5' | 5' - 3' | | |
| | (3) 5' - 3' | 5' - 3' | | |
| | (4) 3' - 5' | 3' - 5' | | |
| 48. | Commonly used vectors f | or human genome | e sequencing are: | (AIPMT-2014) |
| | (1) T - DNA | | (2) BAC and YAC | |
| | (3) Expression Vectors | | (4) T/A Cloning Vecto | ors |
| 49. | | | d, 17% of the bases were s | - |
| | | • | ted to be present in this D | · · · · · · · · · · · · · · · · · · · |
| | (1) G 17%, A 16.5%, T32. | | (2) G 17%, A 33%,T | |
| | (3) G8.5%,A50%, T24.5% |) | (4) G 34%,A 24.5%,T | 24.5% |
| 50. | A somatic cell that has jus species, has : | st completed the S | S-phase of its cell cycle, as | compared to gamete of the same (AIPMT-2015) |
| | (1) same number of chron | nosomes but twice | e the amount of DNA | , , , , , , , , , , , , , , , , , , , |
| | (2) twice the number of ch | nromosomes and f | four times the amount of DI | NA |
| | (3) four time the number of | of chromosomes a | nd twice the amount of DN | A |
| | (4) twice the number of ch | romosomes and t | twice the amount of DNA | |
| 51. | Satelliete DNA is importar | nt because it: | | (Re-AIPMT-2015) |
| | shows high degree of individual, which is heritat | | • • | me degree of polymorphism in ar |
| | | • | in all members of the popul | ation |
| | | eded for DNA repl | lication | |
| | (3) codes for enzymes ne | | lication | |

| 52. | Which of the following (1) lactose and galacto (3) galactose | is required as inducer(s) ose | for the expression of La (2) glucose (4) lactose | c operon? | (NEET-1-2016) |
|-----|--|--|---|----------------------|--|
| 53. | A complex of ribosome (1) Okazaki fragment | es attached to a single st (2) Polysome | rand of RNA is known as (3) Polymer | :: (4) Polypeptid | (NEET-1-2016) e |
| 54. | Which of the followin present? (1) DNA -DNA hybridiz (3) Zinc finger analysis | | y of the techniques of (2) Polymerase chain (4) Restriction enzyme | reaction | ting available at (NEET-1-2016) |
| 55. | Which one of the follow (1) UAG | wing is the starte codon? (2) AUG | (3) UGA | (4) UAA | (NEET-1-2016) |
| 56. | Taylor conducted the e | experiments to prove sen (2) <i>Vinca rosea</i> | niconservative mode of c (3) <i>Vicia faba</i> | | lication on (NEET-2-2016) melanogaster |
| 57. | | uctural gene is A true bre (2) Muton | | (4) Operon | (NEET-2-2016) |
| 58. | · | polymerase catalyzes tra | | | (NEET-2-2016) |
| 59. | | (2) Template strand in RNA that codes for a at the length of the RNA | • | | base at position |
| | (1) 1 | (2) 11 | (3) 33 | (4) 333 | (, |
| 60. | DNA fragments are: (1) Positively charged (2) Negatively charged (3) Neutral (4) Either positively or | l negatively charged depe | ending on their size | | (NEET-2017) |
| 61. | During DNA replication (1) The leading strand (2) The lagging strand (3) The leading strand (4) The lagging strand | (NEET-2017) | | | |
| 62. | Spliceosomes are not | | (2) Animala | (1) Postaria | (NEET-2017) |
| 63. | (1) PlantsThe final proof for DN/(1) Griffith(3) Avery, Mcleod and | (2) Fungi A as the genetic material McCarty | (3) Animalscame from the experime(2) Hershey and Chas(4) Hargobind Khorana | е | (NEET-2017) |

PRINCIPLES OF INHERITANCE & VARIATION

| 64 | seque (1) A | TATCGC ence of th GGUAUC CCUAUC | he trans CGCAU | - | | ding strand of a gene. (2) UCCAUAGCGUA (4) UGGTUTCGCAT | What will be the corresponding (NEET-2018) | - |
|-----|----------------------------------|--|---|------------------------------------|--|--|--|---|
| 65 | | the follo | - | • | an operon <i>excej</i> promoter | ot (3) an enhancer | (NEET-2018) (4) structural genes | |
| | . , | | | | | | | |
| 66 | | t the <i>cor</i> ibozyme | | | | (2) G. Mendel – Trans | (NEET-2018) | |
| | . , | H. Morga | | | n | (4) F ₂ x Recessive pa | | |
| 67 | | - | | | | | - | |
| 67 | | t the <i>col</i> cc Jeffre | | itch: | | – Streptococcus pne | (NEET-2018) | |
| | . , | | • | d Jacqu | es Monod | Lac operon | | |
| | . , | atthew M | | • | | – Pisum sativum | | |
| | (4) Al | fred Her | shey and | d Martha | a Chase | – TMV | | |
| 68 | (1) Fr (2) Tr (3) Sp | ansducti | tahl coin on was nes take | ed the te discover e part in | erm "linkage". ed by S. Altman translation. oped by a British | | (NEET-2018) | |
| 69 | The e | experime | ntal proc | of for sei | miconservative r | eplication of DNA was fir | st shown in a (NEET-2018) | |
| | (1) Fu | ungus | | (2) Vi | rus | (3) Plant | (4) Bacterium | |
| 70. | Match | h the follo | owing ge | enes of t | he Lac operon v | vith their respective produ | ucts (NEET-1-2019) | |
| | (a) i g | gene | | (i) β - g | galactosidase | | | |
| | (b) z | gene | | (ii) Pe | ermease | | | |
| | (c) a | gene | | (iii) R | epressor | | | |
| | (d) y | gene | | (iv) Ti | ransacetylase | | | |
| | Selec | t the cor | rect opti | on. | | | | |
| | | (a) | (b) | (c) | (d) | | | |
| | (1) | (iii) | (iv) | (i) | (ii) | | | |
| | (2) | (i) | (iii) | (ii) | (iv) | | | |
| | (3) | (iii) | (i) | (ii) | (iv) | | | |
| | (4) | (iii) | (i) | (iv) | (ii) | | | |
| 71. | mRN 5' AA (1) De (2) In | A? CAGCG | GUGCU ^f GGU fr f G at 5 ^t | AUU 3' om 7 th , 8 | 3 th and 9 th positio | | the reading frame of following (NEET-1-2019) | 3 |

(4) Insertion of A and G at 4^{th} and 5^{th} position respectively

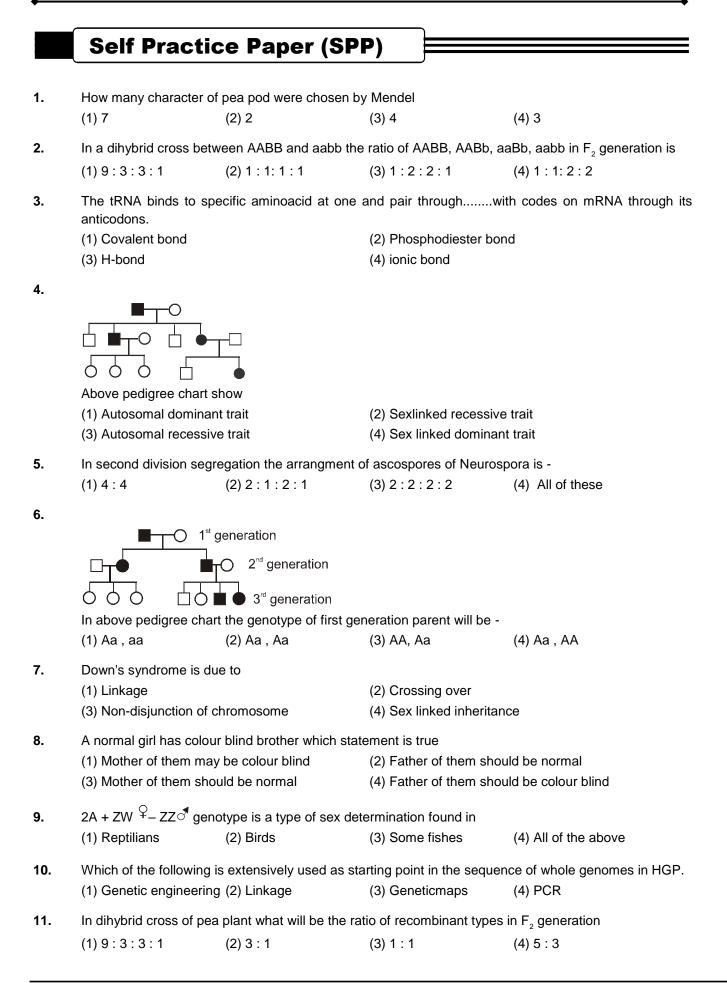
| (1) Novel DNAsequences (2) Genes expressed as RNA (3) Polypeptide expression (4) DNA polymorphism 73. What will be the sequence of mRNA produced by the following stretch of DNA? (NEET-2-2019) 3' ATGCATGCATGATG 5' TEMPLATE STRAND 5' TACGATGCATGAC 5' CODING STRAND (1) 3' AUGCAUGCAUGCAUG 5' (2) 5' UACGUACGUACGUAC 3' (3) 3' UACGUACGUACGUAC 5' (4) 5' AUGCAUGCAUGCAUG 3' 74. From the following, identify the correct combination of salient features of Genetic Code (NEET-2-2019) (1) Universal, Non-ambiguous, Overlapping (2) Degenerate, Overlapping, Commaless (3) Universal, Ambiguous, Degenerate (4) Degenerate, Non-overlapping, Non ambiguous 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes - (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) RNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot' is used to confirm the structure of (NEET-2-2019) (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) do _ RNA (2) ss _ DNA (3) ss _ RNA (4) ds _ DNA 79. What initiation and termination factors are involved in transcription in EUkaryotes? (NEET-2-2019) (1) do _ respectively (2) a and p, respectively (3) β and γ, respectively (4) a and α, respectively (3) β and γ, respectively | 72. | Expressed Sequence | Tags (ESfs) refers to : | | (NEET-1-2019 |) |
|--|-----|---|--|--|------------------------------|---------|
| 73. What will be the sequence of mRNA produced by the following stretch of DNA? (NEET-2-2019) 3' ATGCATGCATGCATG 5' TEMPLATE STRAND 5' TACGTACGTACGTAC 3' CODING STRAND (1) 3' AUGCAUGCAUGCAUG 5' (2) 5' UACGUACGUACGUAC 3' (3) 3' UACGUACGUACGUAC 5' (4) 5' AUGCAUGCAUGCAUG 3' 74. From the following, identify the correct combination of salient features of Genetic Code (NEET-2-2019) (1) Universal, Non-ambiguous, Overlapping (2) Degenerate, Overlapping, Commaless (3) Universal, Ambiguous, Degenerate (4) Degenerate, Non-overlapping, Non ambiguous 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) IRNA, 5 S rNA and anRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds = RNA (2) ss = DNA (3) ss = RNA (4) ds = DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) ds = RNA < | | (1) Novel DNAsequen | ces | (2) Genes expressed a | as RNA | |
| 3' ATGCATGCATG GATG 5' TEMPLATE STRAND 5' TACGTACGTACGTAC 3' CODING STRAND (1) 3' AUGCAUGCAUGCAUG 5' (2) 5' UACGUACGUAGCAUG 3' (3) 3' UACGUACGUACGUAC 5' (4) 5' AUGCAUGCAUGCAUG 3' 74. From the following, identify the correct combination of salient features of Genetic Code (NEET-2-2019) (1) Universal, Non-ambiguous, Overlapping (2) Degenerate, Overlapping, Commaless (3) Universal, Ambiguous, Degenerate (4) Degenerate, Non-overlapping, Non ambiguous 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) ss – DNA (3) ss – RNA (4) ds – DNA 79. | | (3) Polypeptide expres | ssion | (4) DNA polymorphism | 1 | |
| (1) 3' AUGCAUGCAUGCAUG 5' (2) 5' UACGUACGUAC 3' (3) 3' UACGUACGUAC 5' (4) 5' AUGCAUGCAUGCAUG 3' 74. From the following, identify the correct combination of salient features of Genetic Code (NEET-2-2019) (1) Universal, Non-ambiguous, Overlapping (2) Degenerate, Overlapping, Commaless (3) Universal, Ambiguous, Degenerate (4) Degenerate, Non-overlapping, Non ambiguous 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes - (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, InRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds - RNA (2) ss - DNA (3) ss - RNA (4) ds - DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively (3) β and γ, respectively (4) α and σ, respectively (1) πanscription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, DNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2022) | 73. | 3' ATGCATGCATGCA | TG 5' TEMPLATE STRA | ND | of DNA? (NEET-2-2019) |) |
| (3) 3' UACGUACGUAC 5' (4) 5' AUGCAUGCAUGCAUG 3' 74. From the following, identify the correct combination of salient features of Genetic Code (NEET-2-2019) (1) Universal, Ambiguous, Overlapping (2) Degenerate, Overlapping, Commaless (3) Universal, Ambiguous, Degenerate (4) Degenerate, Non-overlapping, Non ambiguous 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) ss – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) a and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively (3) β and γ, respectively (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA, DNA and amino acids (2) DNA, tRNA, DNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2022) | | | | | CGUAC 3' | |
| (1) Universal, Non-ambiguous, Overlapping (2) Degenerate, Overlapping, Commaless (3) Universal, Ambiguous, Degenerate (4) Degenerate, Non-overlapping, Non ambiguous 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) s s – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ , respectively (2) α and β , respectively (3) β and γ , respectively (4) α and σ , respectively (3) β and γ , respectively (2) α and β , respectively (3) β and γ , respectively (4) α and σ , | | | | . , | | |
| (1) Universal, Non-ambiguous, Overlapping (2) Degenerate, Overlapping, Commaless (3) Universal, Ambiguous, Degenerate (4) Degenerate, Non-overlapping, Non ambiguous 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) s s – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ , respectively (2) α and β , respectively (3) β and γ , respectively (4) α and σ , respectively (3) β and γ , respectively (2) α and β , respectively (3) β and γ , respectively (4) α and σ , | 74. | From the following, ide | entify the correct combina | ation of salient features o | f Genetic Code (NEET-2 | -2019) |
| 75. Which scientist experimentally proved that DNA is the sole genetic material in bacteriophage? (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (1) ds – RNA (2) S s – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (2) α and β, respectively (3) β and γ, respectively (3) α and σ, respectively (1) σ rand ρ, respectively (2) Translation (3) Transduction (4) Translocation (AIIMS QUESTION (PREVIOUS YEARS) 1. Proteins are synthesised by the process </th <th></th> <th>_</th> <th>-</th> <th></th> <th>-</th> <th>,</th> | | _ | - | | - | , |
| (NEET-2-2019) (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) ss – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ , respectively (2) α and β , respectively (3) β and γ , respectively (4) α and σ , respectively (1) σ and ρ , respectively (2) α and β , respectively (3) β and γ , respectively (4) α and σ , respectively (1) Transcription (2) Translation (3) Transduction (4) Translocation Correct sequence of code transfer during polypeptide formation is (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA </th <th></th> <th></th> <th></th> <th>., .</th> <th></th> <th>ous</th> | | | | ., . | | ous |
| (1) Beadle and Tautum (2) Messelson and Stahl (3) Hershey and Chase (4) Jacob and Monod 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds - RNA (2) ss - DNA (3) ss - RNA (4) ds - DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | 75. | Which scientist experi | mentally proved that DNA | A is the sole genetic mate | |) |
| 76. In the process of transcription in Eukaryotes, the RNA polymerase I transcribes – (NEET-2-2019) (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) ss – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (2) α and β, respectively (1) σ and ρ, respectively (2) α and σ, respectively (3) Transduction (4) Translocation (AlIMS OUESTION (PREVIOUS YEARS) 1. PART - II : AlIIMS QUESTION (PREVIOUS YEARS) 1. Proteins are synthesised by the process (AlIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AlIMS-1999) (1) DNA, mRNA, tRNA and amino acids < | | (1) Beadle and Tautun | n | (2) Messelson and Sta | • | • |
| (1) mRNA with additional processing, capping and tailing (2) tRNA, 5 S rRNA and snRNAs (3) rRNAs - 28 S, 18 S and 5.8 S (4) Precursor of mRNA, hnRNA 77. "Ramachandran plot" is used to confirm the structure of (NEET-2-2019) (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA (2) Proteins (3) Triacylglycerides 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds - RNA (2) ss - DNA (3) ss - RNA (4) ds - DNA (2) ss - DNA (3) ss - RNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively (1) Transcription (2) Translation (3) Transduction (1) Transcription (2) Translation (3) Transduction (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, rDNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | | | | (4) Jacob and Monod | | |
| (1) RNA (2) Proteins (3) Triacylglycerides (4) DNA 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) ss – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively (3) Froteins are synthesised by the process (AIIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | 70. | (1) mRNA with addition (2) tRNA, 5 S rRNA ar (3) rRNAs - 28 S, 18 S | nal processing, capping and snRNAs and 5.8 S | | | 3) |
| 78. In RNAi, the genes are silenced using: (NEET-2-2019) (1) ds – RNA (2) ss – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively (3) β and γ, respectively (1) σ and σ, respectively PART - II : AIIMS QUESTION (PREVIOUS YEARS) 1. Proteins are synthesised by the process (AIIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | 77. | "Ramachandran plot" | is used to confirm the stru | ucture of | (NEET-2-2019) |) |
| (1) ds – RNA (2) ss – DNA (3) ss – RNA (4) ds – DNA 79. What initiation and termination factors are involved in transcription in Eukaryotes? (NEET-2-2019) (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively (3) β and γ, respectively (4) α and σ, respectively (5) β and γ, respectively (4) α and σ, respectively (7) α and β, respectively (8) β and γ, respectively (9) α and β, respectively (1) σ and γ, respectively (1) α and γ, respectively (1) α and γ, respectively (1) Transcription (2) Translation (3) Transduction (4) Translocation (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. (AIIMS-2002) | | (1) RNA | (2) Proteins | (3) Triacylglycerides | (4) DNA | |
| (1) σ and ρ, respectively (2) α and β, respectively (3) β and γ, respectively (4) α and σ, respectively PART - II : AIIMS QUESTION (PREVIOUS YEARS) Proteins are synthesised by the process (AIIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. A point mutation comprising substitution of purine with pyrimidine is | 78. | - | - | (3) ss – RNA | • |) |
| (3) β and γ, respectively (4) α and σ, respectively PART - II : AIIMS QUESTION (PREVIOUS YEARS) 1. Proteins are synthesised by the process (AIIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | 79. | What initiation and terr | mination factors are invol | ved in transcription in Eu | Ikaryotes? (NEET-2-201 | 9) |
| PART - II : AIIMS QUESTION (PREVIOUS YEARS) 1. Proteins are synthesised by the process (AIIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | | (1) σ and ρ , respective | ely | (2) α and β , respective | ły | |
| 1. Proteins are synthesised by the process (AIIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | | (3) β and γ , respective | ly | (4) α and σ , respective | łly | |
| 1. Proteins are synthesised by the process (AIIMS-1999) (1) Transcription (2) Translation (3) Transduction (4) Translocation 2. Correct sequence of code transfer during polypeptide formation is (AIIMS-1999) (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | | PART - | II : AIIMS QUEST | ION (PREVIOUS | YEARS) | |
| (1) Transcription (2) Translation (3) Transduction (4) Translocation Correct sequence of code transfer during polypeptide formation is (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA and tRNA. A point mutation comprising substitution of purity with pyrimidine is (AIIMS-2002) | 4 | Drotaina ara avethasia | ad by the process | • | , / A IIMG | S 1000) |
| (1) DNA, mRNA, tRNA and amino acids (2) DNA, tRNA, rDNA and mRNA (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | 1. | - | | (3) Transduction | • | 5-1999) |
| (3) mRNA, tRNA, DNA and amino acids (4) rRNA, DNA, mRNA and tRNA. 3. A point mutation comprising substitution of purine with pyrimidine is (AIIMS-2002) | 2. | Correct sequence of c | ode transfer during polyp | eptide formation is | (AIIMS | S-1999) |
| | | | | | | |
| | 3. | A point mutation comp (1) Transition | orising substitution of puri (2) Transversion | ne with pyrimidine is (3) Deletion | (AIIMS (4) Translocation. | S-2002) |

| 4. | Frame shift mutation of (1) Base is deleted or a (3) Base is deleted | | (2) Base is added (4) Anticodons are n | ot present. | (AIIMS-2002) |
|-----|--|--|--|---------------------------------|--------------|
| 5. | Which is important for (1) CAAT Box (3) DNA polymerase | ranscription | (2) Promoter (4) DNA methylase | | (AIIMS-2002) |
| 6. | | | | | (AIIMS-2003) |
| 7. | Which one represents (1) $3'_{5'}$ | the correct manner of D (2) $3^{5'}$ | NA replication (3) ^{5'} / _{3'} / _{5'} | (4) ⁵ / ₃ | (AIIMS-2003) |
| 8. | Which one of the follow (1) UGU | ving codons codes for th (2) UGA | e same information as (3) UAG | UGC (4) UGG | (AIIMS-2003) |
| 9. | cDNA is copied from m (1) Restriction enzyme (3) DNA polymerase | RNA molecule with the | help of (2) Reverse transcrip (4) Adenosine deam | | (AIIMS-2005) |
| 10. | it was made to replicate (1) Each strand half rac | DNA will be radioactive | • | • | |
| 11. | (1) Association of 50 S(2) Formation of formyl(3) Association of 30S | tion in prokaryotes, a G subunit of ribosome wit -met-RNA m-RNA with formyl-met uit of ribosome with mRI | h initiation complex tRNA | in | (AIIMS-2007) |
| 12. | The telomeres of euka (1) Cytosine rich repea (3) Adenine rich repeat | | nsists of short sequence (2) Thymine rich rep (4) Guanine rich rep | eats | (AIIMS-2007) |
| 13. | Match the following (a) tRNA (b) mRNA (c) rRNA (d) Peptidyl transferse (1) $a - 4$, $b - 2$, $c - 3$, d (3) $a - 1$, $b - 2$, $c - 3$, d | | nformation g region | , d –2 | (AIIMS-2007) |

| 14. | The total number of nitr (1) 3⋅5 million | ogenous bases in huma (2) 35 million | n genome is estimated to (3) 35 thousand | b be about (4) 3⋅1 billion | (AIIMS-2008) |
|-----|--|---|--|----------------------------------|--------------------------------|
| 15. | Which one of the follo coded by it? (1) UUA-valine | wing pairs is correctly r (2) AUG-cysteine | matched with regard to (3) CCC-alanine | the codon and (4) AAA-lysine | the amino acid (AIIMS-2008) |
| 16. | Which one of the follow (1) 5'-GAATTC-3' 3'-CTTAAG-5' (2) 5'- CCAATG - 3' 3' - GAATCC - 5' (3) 5' - CATTAG - 3' 3'-GATAAC - 5' (4) 5' - GATACC - 3' 3' - CCTAAG - 5' | ing represents palindron | nic sequence in DNA? | | (AIIMS-2012) |
| 17. | Human Genome Proje biology called as (1) biotechnology | ct (HGP) is closely ass (2) bioinformatics | sociated with the rapid | development of (4) bioscience | a new area in (AIIMS-2013) |
| 18. | DNA and RNA compris (1) sugar, phosphate, b (3) base, phosphate | e of | (2) sugar, phosphate (4) sugar, base. | | (AIIMS-2014) |
| 19. | Select the correct optio Direction of RNA synthesis (1) 5'-3' (2) 3'-5' (3) 5'-3' (4) 3'-5' | n: Direction of reading of the template DNA strar 3'-5' 5'-3' 5'-3' 3'-5' | nd | | (AIIMS-2014) |
| 20. | • • | ses in a sample of DNA osine is present in this D (2) 20% | extracted from eukaryoti NA? (3) 30% | c cells is adenine (4) 40% | e. (AIIMS-2015) |
| 21. | Which one of the follow (1) UAA, UAG and UGA (3) UUC,UUU, CCU,CA | A | alled as nonsense codor (2) GUA, GUU GCA, G (4) UUA, UUU, CUU, C | CG and GAA | (AIIMS-2016) UG |
| 22. | Select the wrong pair (1) RNA polymerase I – (2) RNA polymerase I – (3) RNA polymerase II (4) RNA polymerase III | – hnRNA | IA | | (AIIMS-2018-I) |

| 23. | In the Diagram given figure of | (AIIMS-2018-I) | | | |
|-----|---|---|--|-------------|-----------------------------------|
| | p i p o | | | | |
| | (1) i – Repressor, z – β-galacto (2) i – Inhibitor, z – Repressor, (3) i – Inducer, z – β-galactosio (4) i – β-galactosidase, z – Repression | y– Transacetyl dase, y– Perme | ase, a– Permease ase, a– Repressor | | |
| 24. | Which of the following is codo | ns codes for pro | | | (AIIMS-2018-I) |
| | (1) CCC, CCU, CCG (3) CUG, CUU, CUA | | (2) UCC, UGU, CCU (4) CGC, CGG, CCA | | |
| 05 | | II I I (d | | | |
| 25. | Match column-I to the column- | | e option naving correct | matching – | (AIIMS-2018-II) |
| | Column-I A Bacteriophage λ | i 5386 nu | ucleotides | | |
| | B E. coli | ii 3.3 × 10 | | | |
| | C Human genome | iii 4.6 × 10 | | | |
| | D | iv 48502 k | pp | | |
| | (1) A - (iv), B - (iii), C- (ii), D - (3) A - (iv), B - (iii), C- (i), D - (| () | (2) A - (iii), B - (ii), ((4) A - (iv), B - (i), (| | |
| 26. | Which of the following correctl (1) GGG, GGC, GGA (2) AA | | odons for glycine? (3) AUG, AUA, AUC | (4) CCC, CC | (AIIMS-2018-II) CG, CGA |
| 27. | Which of the following stateme (1) Splicing is not required (2) Single RNA polymerase co (3) This process required more (4) None | ontrols all DNA p | · | eria. | (AIIMS-2018-III) |
| 28. | Which among the following is (1) It involves all the three type (2) It involves 3 types of RNA (3) It involves single type of RI (4) It involves RNA processing | es of RNAs (m-F polymerases NA polymerase | • |) | (AIIMS-2018-III) |
| 29. | Codons of alanine (1) CUC, CUA, CUG (3) GUG, GUC, GUA | | (2) GGG, GGU, GG (4) GCU, GCC, GC | | (AIIMS-2018-IV) |
| 30. | Which of the following can syn (1) r-RNA (2) t-F | • • | s of RNA (3) m-RNA | (4) DNA | (AIIMS-2018-IV) |

| | | neu | vers | | | | | | | | | | |
|--|---|--|---|---|---|---|---|--|---|--|---|---|---|
| | | | | | | | | 4 | | | | | |
| SECT | ION - A | | | | | EXER | CISE - | - 1 | | | | | |
| 1. 8. 15. 22. 29. | (3) (2) (1) (4) (4) | 2. 9. 16. 23. | (4) (3) (1) (3) | 3. 10. 17. 24. | (1) (4) (2) (3) | 4. 11. 18. 25. | (3) (4) (1) (1) | 5. 12. 19. 26. | (3) (2) (1) (4) | 6. 13. 20. 27. | (2) (1) (1) (3) | 7. 14. 21. 28. | (3) (3) (1) (1) |
| SECT | ION - B | | | | | | | | | | | | |
| | (3) (3) (3) (1) (4) (3) TION - C | 2. 9. 16. 23. 30. 37. 44. | (1) (3) (4) (1) (1) (2) (1) | 3. 10. 17. 24. 31. 38. 45. | (3) (1) (4) (2) (2) (2) (1) | 4. 11. 18. 25. 32. 39. 46. | (2) (1) (3) (2) (1) (2) (1) | 5. 12. 19. 26. 33. 40. | (2) (3) (1) (1) (2) (2) | 6. 13. 20. 27. 34. 41. | (2) (3) (1) (4) (2) (4) | 7. 14. 21. 28. 35. 42. | (1) (3) (3) (2) (3) |
| 1. 8. | (4) (2) | 2. 9. | (4) (2) | 3. 10. | (2) (3) | 4. 11. | (3) (3) | 5. 12. | (1) (4) | 6. 13. | (2) (4) | 7. | (2) |
| _ | <u>\</u> | | _/ | | · · / | ellaneo | | | () | | () | | |
| 1. 8. 15. 22. 29. 36. | (1) (1) (2) (2) (1) (3) | 2. 9. 16. 23. 30. 37. | (2) (4) (4) (2) (4) (2) | 3. 10. 17. 24. 31. 38. | (3) (3) (1) (3) (1) (2) | 4. 11. 18. 25. 32. 39. | (1) (4) (3) (4) (3) (2) | 5. 12. 19. 26. 33. 40. | (2) (2) (3) (3) (4) | 6. 13. 20. 27. 34. 41. | (2) (3) (3) (2) (4) (4) | 7. 14. 21. 28. 35. 42. | (4) (4) (3) (2) (2) |
| | | | | | | | CISE - | | | | | | |
| 1. 8. 15. | (2) (2) (2) | 2. 9. 16. | (3) (3) (3) | 3. 10. 17. | (4) (2) (1) | 4. 11. | (1) (4) | 5. 12. | (1) (3) | 6. 13. | (2) (1) | 7. 14. | (4) (1) |
| | | | | | | | CISE - | 3 | | | | | |
| | (-) | | | - | | | RT-I | _ | (-) | - | (-) | _ | (-) |
| 1. 8. 15. 22. 29. 36. 43. 50. 57. 64. 71. 78. | (2) (2) (3) (1) (2) (1) (2) (3) (1) (1) (1) | 2. 9. 16. 23. 30. 37. 44. 51. 58. 65. 72. 79. | (1) (4) (3) (4) (2) (1) (2) (1) (2) (3) (2) (1/bot | 3. 10. 17. 24. 31. 38. 45. 59. 66. 73. nus) | (4) (2) (3) (2) (1) (3) (1) (4) (3) (1) (2) | 4. 11. 25. 32. 39. 46. 53. 60. 67. 74. | (1) (4) (3) (2) (1) (3) (2) (2) (2) (2) (4) | 5. 12. 19. 26. 33. 40. 47. 54. 61. 68. 75. | (2) (4) (3) (1) (1) (3) (4) (4) (3) | 6. 13. 20. 27. 34. 41. 48. 55. 62. 69. 76. | (2) (1) (4) (2) (4) (1) (2) (2) (4) (4) (3) | 7. 14. 21. 35. 42. 49. 56. 63. 70. 77. | (3) (2) (4) (2) (1) (4) (2) (3) (2) (4) (2) |
| 1. | (2) | 2. | (1) | 3. | (2) | 4. | (1) | 5. | (2) | 6. | (1) | 7. | (4) |
| 8. 15. 22. 29. | (2) (1) (4) (1) (4) | 9. 16. 23. 30. | (1) (2) (1) (1) (4) | 3. 10. 17. 24. | (2) (3) (2) (1) | 4. 11. 18. 25. | (1) (3) (1) (1) | 5. 12. 19. 26. | (2) (4) (1) (1) | 0. 13. 20. 27. | (1) (2) (2) | 14. 21. 28. | (4) (4) (1) (3) |



| 12. | | | | s in blue birds in F_1 ger | neration and then cross between | |
|-----|---|---|--|---|--|--|
| | blue in F_1 generation v (1) 3 blue : 1 white | | | (2) 1 blue · 1 block · 1 | white | |
| | (1) 3 blue : 1 white (3) 9 blue : 3 back : 3 | white | | (2) 1 blue : 1 black : 1(4) 1 black : 1 white : 2 | | |
| | | | | | | |
| 13. | In monohybrid cross with F_2 - generation | what is the | e ratio of homo | zygous dominant and he | omozyguos recessive individuals | |
| | (1) 1 : 2 : 1 | (2) 2 : 1 | /1:2 | (3) 3:1/1:3 | (4) 1 : 1 | |
| 14. | A normal man marries the following statemer (1) 50% dayghters nor (2) All the daughters a (3) 50% daughters ma (4) All the daughters a | nt is correc rmal & 509 are normal ay haemop | ct about their of % son are haen & 50% sons ar philic & 50% soi | fsprings nophilic re haemophilic ns are normal. | them were haemophilic which of | |
| 15. | Which of the following | has mono | osomic conditio | n | | |
| | (1) Klinefelter syndron | ne | | (2) Down's syndrome | | |
| | (3) Turner syndrome | | | (4) Cry-du-chat syndro | ome | |
| 16. | Match the column | | | | | |
| | Column I | | Column II | | | |
| | (a) Grasshopper | | (i) Palmer crea | ase in hand | | |
| | (b) Turner's syndrome | ; | (ii) Mental reta | rdation & accumulation | of phenylpyruvic acid | |
| | (c) Phenylketonuria | | (iii) Barr body | absent | | |
| | (d) Sickle cell anaemia | a | (iv) XX ^Q – XC |) ් | | |
| | (e) Down's syndrome Select the correct opti | on | (v) Pleiotropic | gene | | |
| | (1) a – iv, b – iii, c – ii, | | ·i | (2) a – iii, b – iv, c – ii, | d – v, e – i | |
| | (3) a – iii, b – ii, c − v, | d – i, e – i | iv (4) a – iv, b – iii, c – ii, d – i, e – v | | | |
| 17. | | - | • | d by three alleles I ^A , I ^B espective by these allele | and i or lº . How many possible s in humans. | |
| | (1) 4, 6 | (2) 3, 4 | | (3) 9, 3 | (4) 6, 4 | |
| 18. | If one parent has blo blood group | od group | A and the othe | er parent has blood gro | up B. The offspring have which | |
| | (1) AB | (2) O | | (3) BO | (4) A, B, AB, O | |
| 19. | produced bearing pink ratio of pink and red fl | k- flowered owered pla | d plants on self ants will be. | ing of F_1 generation F_2 g | owered plant (rr) F_1 generation generation obtained. In which the | |
| | (1) 1 : 2 | (2) 1 : 1 | | (3) 2:1 | (4) 3 :1 | |
| 20. | In dihybrid cross of person seeded plants in F_2 ge | - | - | heterozygous for both | yellow round and green wrinkled | |
| | (1) $\frac{1}{16}$ | (2) $\frac{1}{4}$ | | (3) $\frac{1}{8}$ | (4) $\frac{3}{16}$ | |
| | 16 | 4 | | 8 | 16 | |

| 21. | Most cell organelle duplication occur during whic (1) G_1 (2) G_2 | ch phase of cell cycle (3) S-phase | (4) M-phase |
|-----|---|--|--|
| 22. | Find out the incorrect statement about RNA mole (1) It shows high rate of mutation than DNA (3) Some reactions are catalyzed by RNA | ecule (2) It is genetic materia (4) RNA follows charga | |
| 23. | Exon segments are reunited after splicing by (1) DNA ligase (2) RNA primase | (3) RNA polymerase | (4) RNA ligase |
| 24. | During elongation of polypeptide chain sigma fac (1) Functionless (3) Released for re-use | ctor is (2) Retained for specifi (4) Required during clo | |
| 25. | Deletion or insertion of base pairs produces f inserted base pairs is | rame shift mutation un (3) Two | less the number of deleted or (4) Three |
| 26. | Which type of DNA is found in bacteria. (1) Straight DNA (3) Membrane bound DNA | (2) Helical DNA(4) Circular free DNA | |
| 27. | DNA segment ,3'TAC ATG GGT CCG 5' transcr (a) AUG (b) UAC (c) CCG and (D) GGU are requ (1) abdc (2) badc | | |
| 28. | A variety of pea plant with round yellow seeds a having wrinkled green seeds and white flowers (in the F_2 generation would be: | (<i>rryycc</i>). The frequency | of plants with genotype <i>RrYyCc</i> |
| 29. | (1) 1/2 (2) 1/8 | (3) 27/64 | (4) 9/64 |
| 23. | Transcriptional unit consists of (1) Template strand, α- factor & ρ-factor (2) Promoter, structural gene, Terminator (3) Regulator gene, promoter gene, operator gere (4) DNA template, RNA polymerase, Nitrogenous | - | |
| 30. | Triplet codon concept can be proved by (1) Wobble hypothesis (3) Transversion | (2) Transition(4) Frame shift mutatio | n |
| 31. | If the length of E. coli DNA is 1.36 mm. the no. o (1) 48502 bp (2) 6.6× 10 ⁶ bp | f Base pairs in E.coli ma (3) 4 × 10º bp | ay be (4) 3.3 ×10 ⁶ bp |
| 32. | Which of the following also confers additional sta | • | |
| 33. | (1) Adenine (2) Guanine The RNA is more reactive and also known to be (1) 3' - OH group at every nucleotide (3) 2' - C = O group at every nucleotide | (3) Thyminecatalytic due to presend(2) 3' - CCA group at e(4) 2'- OH group at eve | very nucleotide |
| 34. | If E.coli labelled by N ¹⁵ allowed to grow for 60 m the proportion of light and hybrid densities DNA (1) 12 \cdot 5% N ¹⁴ N ¹⁴ , 87 \cdot 5% N ¹⁵ N ¹⁴ (3) 50% N ¹⁴ N ¹⁴ , 50% N ¹⁵ N ¹⁴ | | N ¹⁵ N ¹⁴ |
| 35. | Which of the following difference between S-stratis not correct (1) S-Strain is virulent while R- strain is non virule (2) R-strain bears mucous (polysacharide) coat v (3) S- strain bears smooth surface while R-strain (4) None of the above | ent while S-strain does not | ptococcus pneumoniae bacteria |

| 36. | The negative charge of | DNA is due to | | |
|-----|---|--|---|---------------------------------|
| | (1) Nitrogen bases | (2) Pentose sugar | (3) Phosphate group | (4) All of the above |
| 37. | (2) Bidrectional, semidia(3) Unidirectional, disco | Bidirectional, discontinuo scontinuous, conservativ | e | |
| 38. | Who proposed central ((1) Crick | dogma? (2) Watson and Crick | (3) Klug | (4) Beadle and Tatum |
| 39. | (1) Strong Hydrogen bo | the two strands of DNA o nds bet ⁿ Nitrogenous ba ster bonds between nucle quirement | ses | s entire length due to |
| 40. | The length of DNA with (1) 156⋅8A⁰ | 46 base pairs is (2) 156·4Aº | (3) 156Aº | (4) 149·6Aº |
| 41. | In DNA genetic informa (1) Nitrogenous bases | • | (3) phosphoric acid | (4) all of them |
| 42. | The distance between 2 (1) 3.4 Å | 2 strands of DNA is (2) 34 Å | (3) 20Å | (4) 10 Å |
| 43. | A segment of DNA that (1) palindromic DNA (3) complementary DN/ | reads the same in forwa | rd and backward is calle (2) plasminic DNA (4) copy DNA | d |
| 44. | m-RNA directs the build (1) Exons | ling of proteins through a (2) Codons | a sequenc of (3) anticodons | (4) Introns |
| 45. | Addition of adenylate re (1) Splicing | esidues (200-300) at 3'-e (2) Capping | nd in a template of hnRN (3) Tailing | IA is called (4) Termination |

| | SP | P A | nsv | /ers | | | | | | | | | |
|-----|-----|-----|-----|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1. | (4) | 2. | (3) | 3. | (3) | 4. | (3) | 5. | (3) | 6. | (1) | 7. | (3) |
| 8. | (1) | 9. | (4) | 10. | (3) | 11. | (3) | 12. | (4) | 13. | (4) | 14. | (2) |
| 15. | (3) | 16. | (1) | 17. | (4) | 18. | (4) | 19. | (3) | 20. | (2) | 21. | (1) |
| 22. | (4) | 23. | (4) | 24. | (1) | 25. | (4) | 26. | (4) | 27. | (2) | 28. | (2) |
| 29. | (2) | 30. | (4) | 31. | (3) | 32. | (3) | 33. | (4) | 34. | (2) | 35. | (2) |
| 36. | (3) | 37. | (4) | 38. | (1) | 39. | (3) | 40. | (2) | 41. | (1) | 42. | (3) |
| 43. | (1) | 44. | (1) | 45. | (3) | | | | | | | | |