Unit 3_Fundamental Process

1. What percentage of the DNA is expected to be labelled with light nitrogen after three generations of multiplication, in the Meselson and Stahl experiment, If the *E. coli* cells that were grown on heavy nitrogen were transferred to light nitrogen?

a. 25

b. 50

c. 75

d. 100

Correct Answer: C

Meselson and Stahl experiment supported the hypothesis that DNA replication was semi-conservative. Semi-conservative replication means when the double stranded DNA helix was replicated, each of the two double stranded DNA helices consisted of one strand coming from the original helix and one newly synthesized. According to the semi-conservative theory, after one replication of DNA, we should obtain 2 hybrid (part N^{14} part N^{15}) molecules from each original strand of DNA. This would appear as a single line in the test tube. This result would be the same for the dispersive theory.

Core Concept:

Topic:

Difficulty Level:

Complexity:

2. During the one round of replication of H. *coil,* approximately how many Okazaki fragments are synthesized?

a. 5000 to 10000

b. 4×10^5

c. 2500 to 5000

d. 2

Correct Answer: C

Due to the anti-parallel structure of duplex DNA, one strand, referred to as leading, is in theory elongated in a continuous manner (but not in practice, due to frequent perturbations in the DNA template), while the other, termed lagging, is synthesized discontinuously in $\square 1$ kb pieces known as Okazaki fragments. As there are only $-300-600$ clamps/cell, and a new clamp is required for replication of each of the $2500-5,000$. Okazaki fragments synthesized during one round of replication, it is postulated that the clamp must be actively unloaded from DNA during replication.

Core Concept:

Topic:

Difficulty Level:

Complexity:

3. Regarding the initiation of the replication of DNA in eukaryotes which among the following statement is correct?

a. Replication can be initiated from the one end of chromatid extending to the other end.

b. Replication can be initiated from both ends of the chromatid simultaneously.

c. Replication can be initiated from the centromere to either of the ends of chromatids.

d. Replication can be initiated from several sites of the DNA of the chromatid simultaneously.

Correct Answer: D

Replication can be initiated from several sites of the DNA of the chromatid simultaneously.

Eukaryotic DNA is bound to proteins known as histories to form structures called nucleosomes. During initiation, the DNA is made accessible to the proteins and enzymes involved in the replication process. There are specific chromosomal locations called origins of replication where replication begins. In some eukaryotes, like yeast, these locations are defined by having a specific sequence of base pairs to which the replication initiation proteins bind. In other eukaryotes, like humans, there does not appear to be a consensus sequence for their origins of replication.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

4. Which among the following statement is true regarding the Okazaki fragments?

a. They require only RNA polymerase activity.

b. They are made when DNA is exposed to UV radiation.

c. They are composed of both DNA and RNA.

d. Both B and C

Correct Answer: C

They are composed of both DNA and RNA.

The synthesis of each Okazaki fragment requires a new initiation event. This is accomplished by making short pieces of RNA at the replication fork. These RNA primers are complementary to the lagging strand template. Each primer is extended from its $3'$ end by DNA polymerase 1 to form an Okazaki fragment. (Synthesis of the leading strand also begins with an RNA primer, but only one primer is required to initiate synthesis of the entire strand). The use of short RNA primers gets around-the limitation imposed by the mechanism of DNA polymerase, namely, that it cannot initiate DNA synthesis *de nova.* The primers are synthesized by a DNA dependent RNA polymerase enzyme called primase the product of the *dnaG* gene in *E. coil.*

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

5. _____can inhibit the eukaryotic DNA synthesis.

a. Aphidicoline

b. Cyclohexamide

c. Chloramphenicol

d. All of the above

Correct Answer: B

Epigenetic factors such as DNA methylation play an important role in regulating gene expression. DNA methylation involves the covelent transfer of methyl group to the $\mathrm{C}-5$ position of the cytosine ring of DNA.

Core Concept:

Topic:

Difficulty Level:

Complexity:

6. _____ is an epigenetic factor for gene expression in eukaryotes.

a. Genetic recombination

b. DNA methylation

c. Protein phosphorylation\

d. DNA protein interaction

Correct Answer: B

Helix-turn-helix motif is one of the common motifs observed in DNA-binding proteins. The motif interacts with DNA double helix and recognizes specific base sequences. It is assumed that the helix-turn-helix motif appears only once in seven prokaryotic transcriptional repressors of which $3-\mathrm{D}$ structures have been determined by X-ray crystallographic studies.

Core Concept:

Topic:

Difficulty Level:

Complexity:

7. The structural motif that is common in prokaryotic DNA binding protein is

a. homeodomain

b helix-turn-helix

c. helix-loop-helix

d. All of the above

Correct Answer: A

Aphidicolin is a selective inhibitor of DNA polymerase α In contrast to earlier reports, the drug was found to inhibit DNA synthesis catalyzed by DNA polymerase a .and isolated HeLa cell nuclei by a similar mechanism. For both systems aphidicolin primarily competed with dCTP incorporation.

Core Concept:

Topic:

Difficulty Level:

Complexity:

8. What are the Zinc finger and helix-turn-helix proteins?

a. Types of DNA-binding proteins

b. Involved in the control of translation

c. Both a and b

d. None of the above

Correct Answer: A

Basically, some of the structural motifs found in DNA binding proteins have been well characterized. They are characterized as zinc finger proteins. leucine zipper proteins, helix turn and helix loop helix proteins and there are few more other modules. They have the said motifs perhaps with certain structural combination of motifs. All the said types of proteins contain a region to interact with DNA in sequence specific manner (DNA binding domain), which is most important for identifying the site; then they have domains for protein-protein interaction by which they dimerizes or produce Aphidicolin is a selective inhibitor of DNA polymerase alpha.

Core Concept:

Topic:

Difficulty Level:

Complexity:

9. The migration in case of a Holliday junction, that is necessary for extending the repair/ recombination segment into homoduplex regions of the Interacting double stands, is achieved by

a. ATP-hydrolysis-dependent activity of the RecA protein.

b. ATP-hydrolytic action of the RuvAB helicase complex.

c. activity of the RecBCD protein complex.

d. tension in the DNA molecule caused by coiling.

Correct Answer: B

The RuvA, RuvB, and RuvC proteins in *Escherichia coli* play important role in the late stages of homologous genetic recombination and the recombinational repair of damaged DNA. Two proteins. RuvA and RuvB, form a complex that promotes ATP-dependent branch migration of Holiday junctions, a process that is important for the formation of heteroduplex DNA. Individual roles for each protein have been defined, with RuvA acting as a specificity factor that targets RuvB, the branch migration motor to the junction. Hexameric rings of RuvB face each other across the junction and promote a novel dual helicase action that "pumps" DNA through the RuvAB complex, using the free energy provided by ATP hydrolysis. Genetic and biochemical studies indicate that branch migration and resolution are coupled by direct interactions between the three proteins, possibly by the formation of a RuvABC complex.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

10.In case of Lambda phage, intergrations into the bacterial genome is accomplished by

a. restricting the bacterial genome with LamRl facilitated by integrase

b. site-specific recombination between the phage *attP* and the bacterial *attB* sequences.

c. single-strand assembly.

d. homologous recombination.

Correct Answer: B

Bacteriophage λ has long served as a model system for studies of regulated site-specific recombination, In conditions favorable for bacterial growth, the phage genome is inserted into the *Escherichia coli* genome by an 'integrative' recombination reaction, which takes place between DNA attachment sites called *attP* and *attB* in the phage and bacterial genomes, respectively. As a result, the integrated λ DNA is bounded by hybrid attachment sites, termed *attL* and *attR.* In response to the physiological state of the bacterial host or to DNA damage, λ phage DNA excises itself from the host chromosome. This excision reaction recombines attL with *attR* to precisely restore the *attP* and *attB* sites on the circular λ and E *. coli* DNAs.

Core Concept:

Topic:

Difficulty Level:

Complexity:

11. Which among the following repair systems is most error-prone, In the case of *Escherichia coli?*

a. Photoactivation

b. Excision repair

c. SOS repair

d. All of the above

Correct Answer: C

SOS repair or inducible error-prone repair is induced by single-stranded gaps and/or the presence of DNA degradation products. This system is capable of replication opposite thymine dimers or apurinic sites and apparently does so by putting in any base. It therefore causes a very broad spectrum of mutations, including duplications and deletions and hence most error proves. This system is often the cause of mutations following either

chemical or UV mutagenesis. In the E . *coli* SOS response, the expression of approximately forty-three SOS genes is induced after the cell is exposed to DNA damaging agents.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

12. What is a recessive mutation?

a. Mutation that is never expressed.

b. Mutation that is expressed only when heterozygous.

c. Mutation that is expressed only when homozygous or hemizygous.

d. Mutation that is expressed only under certain conditions.

Correct Answer: C

Recessive conditions are only manifest in individuals who have two copies of the mutant allele (homozygous). X-linked recessive traits are not clinically manifest when there is a normal copy of the gene. All X-linked recessive traits are fully evident in males because they only have one copy of the X chromosome, thus do not have a normal copy of the gene to compensate for the mutant copy.

Core Concept:

Topic:

Difficulty Level:

Complexity:

13. _____ could be termed as intergenic suppression of a mutation in a coding sequence.

a. Non-sense mutation in the codon leading to lack of interaction

b. The amber mutation in the codon recognized by the altered anticodon of a tRNA

c. A stop codon that can be recognized by the ribosomes

d. None of the above

Correct Answer: B

Sup-1 and *sup*-2 are both amber suppressors. due to a mutation in the gene encoding a tRNA which allows recognition of the UAG codon. However these two mutations affect two different tRNA genes such that, although both mutant tRNAs recognise amber codons, they insert different amino acids (because they are charged with the amino acid that charges each of the two different wild-type tRNAs). For example, *sup*-1 might be a mutated tRNA-*leu* gene whereas *sup*-2 might be a mutated tRNA-leu gene. Thus, the supression in *sup*-1 would insert either leucine and the suppression in *sup*-2 would insert a tyrosine at the position in the protein corresponding to the amber codon. If the inserted amino acid is not similar in size and/or charge to the amino acid at that position in the wild type protein, the resulting amino acid substitution may interfer with the structure and function of the resulting protein.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

14. Dideoxy DNA sequencing exclusively depends on

a. termination

b. plasmid vector

c. Both a and b

d. None of the above

Correct Answer: A

Di-deoxynucleotide sequencing represents only one method of sequencing DNA. It is commonly called Sanger sequencing since Sanger devised the method. This technique utilizes 2', 3'– dideoxynucleotide triphospates (ddNTPs), molecules that

differ from deoxynucleotides by the having a hydrogen atom attached to the $3'$ carbon rather than an OH group. These molecules terminate DNA chain elongation because they cannot form a phosphodiester bond with the next deoxynucleotide.

Core Concept:

Topic:

Difficulty Level:

Complexity:

15. The suppression of the mutant phenotype, that results in restoration of the wild type phenotype, is usually brought about by the

a. misreading of mutant codon and incorporation of a correct amino, acid.

b. insertion of normal copy of the gene.

c. reversion of mutation to wild type.

d. deletion of the mutant gene.

Correct Answer: A

The term "suppressor" is used because the mutant tRNA 'suppresses" the phenotypic effect of the coding mutation. Most suppressor tRNAs contain a mutation in either the anticodon, changing codon specificity or at some position that alters the aminoacylation identity of the tRNA. Suppressor tRNAs have been isolated that decode each of the three termination (non-sense) codons. Suppressors of missense and frameshift mutations are also known. Suppressor tRNAs have been used extensively to study tRNA functions Suppressors have also been used to insert specific amino acids at particular positions within proteins to study effects of specific amino acid substitutions.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

16. A silent mutant will have _____ as compared to the wild type strain.

a. same genotype and phenotype

b. same genotype but different phenotype

c. different genotype but same phenotype

d. different genotype and different phenotype

Correct Answer: C

"Phenotype" is the visible or quantifiable effect of the expression of a gene, whereas the specific genetic constitution responsible for a phenotype is called "genotype'. A silent mutationis a type of mutation in the coding region of a gene that doesn't actually change the amino acid sequence of the protein that is made. The changes

takes place only in the non-coading region of gene that change the genotype but not the phenotype.

Core Concept:

Topic:

Difficulty Level:

Complexity:

17. What is the mode of action of Ethidium bromide that acts as a mutagen?

a. By substituting adenine with its structural analogue.

b. By chemical modification of guanine and cytosine.

c. By the production of inter-strand cross-links in DNA.

d. By intercalating between DNA bases and hence interfering with proper base stacking.

Correct Answer: D

Ethidium is a large planar molecule that binds tightly to DNA. It is often used in biochemistry laboratories to visualize fragments of DNA that have been separated on gels. The ethidium molecule is fluorescent when illuminated with ultraviolet light; it shines in the visible range. Ethidium binds by inserting itself between the stacked bases in double stranded DNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

18._____ will get changed by the action of topoisomerase.

a. Linking number of ss linear DNA

b. Linking number of ds linear DNA

C. Linking number of closed circular ss DNA

d. Linking number of closed circular ds DNA

Correct Answer: D

When the double helix of DNA, which is composed of two strands, separates, helicase makes these two strands rotate around each other. But there is a problem due to the topological reason that the unreplicated part ahead of the replication fork will rotate around its helical axis when the two strands separate at the replication fork. It causes, strong strain in the helix. Thus it is impossible to unlink the double helical structure of DNA without disrupting the continuity of the strands. In order to perform unraveling of a "compensating winding up ' DNA, enzymes are required. Topoisomerase changes the linking number as well as catalyzes the interconversionn of other kinds of topological isomers of DNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

19. The sequence that is most likely to be a restriction enzyme recognition site is

a. CGGCTT

b. CGCCGC

c. GTCGAC

d. All of the above

Correct Answer: C

Restriction enzyme recognition sequence are usually four, five, six or occasionally eight base pairs in length. They typically exhibit two fold rotational (dyad) symmetry and are Palindromic. Although the sequences CGGC and GTAATG are symmetrical, they are not palindromes. The sequences of their complementary strands are GCCG and CATTAC, respectively. Both strands of GTCGAC are the same sequence when read in the $5'$ to $3'$ direction.

Core Concept:

Topic:

Difficulty Level:

Complexity:

20. What are the elements required for a plasmid to become a cloning vector?

a. Ori, multiple cloning site and marker gene.

b. Ori, multiple cloning site, marker and promoter,

c. Ori, multiple cloning site, marker and translation start site.

d. Ori, multiple cloning site and promoter.

Correct Answer: A

Plasmids are double-stranded, generally circular DNA sequences capable of automatically replicating in a host cell. Plasmid vectors minimally consist of the transgene insert and an origin of replication, which allows for semi-independent replication of the plasmid in the host. Modem plasmids generally have many more features, notably a "multiple cloning site"-with nucleotide overhangs for insertion of an insert and multiple restriction enzyme consensus sites on either side of the insert. Vectors with antibiotic-resistance allow for survival of cells that have taken up the vector in growth media containing antibiotics through antibiotic selection.

Core Concept:

Topic:

Difficulty Level:

Complexity:

21. Which among the following Is incorrect for the *model, plant Arabidopsisthaliana?*

a. Its mutants can be easily produced and characterized.

b. Its genome sequence is known.

c. All genes encompassing its genome have already been identified.

d. The molecular genetic of its flowering has been extensively studied.

Correct Answer: C

Arabidopsis thaliana is a popular model plant species, partially as a result of its short generation time and compact size. The genome of *Arabidopsis* was also the first plant genome to be published back in 2000 The *Arabidopsis* genome is $\square 120$ megabases of sequence spread across five chromosomes. The 1001 genomes project plans to sequence the genomes of 1001 different varieties of *Arabidopsis.* Currently 88 are available with more in progress. An analysis of the first 80 genomes was published in Nature Genetics in September 2011.

Core Concept:

Topic:

Difficulty Level:

Complexity:

22. What could be predicted from the statement that the synthesis of DNA is template dependent and semi-conservative'?

a. All single stranded genomes would be synthesized *via* a double-stranded intermediate.

b. Template independent DNA polymerase do not exist in nature.

c. Both A and B

d. None of the above

Correct Answer: A

The genomes are non-segmented, circular, positive-sense, single-stranded DNA, $4.4-8.5$ kilobases in length. They encode 4 to 11 proteins. Replication of the

genome occurs via a dsDNA intermediate and the rolling circle mechanism. Gene transcription is by the host's cellular machinery, as each gene has a specific promoter.

Core Concept:

Topic:

Difficulty Level:

Complexity:

23. _____ is the replicative polymerase in E . *coil*

a. DNA polymerase I

b. DNA polymerase II

c. DNA polymerase III

d. DNA polymerase lV

Correct Answer: C

Pot Ill is a multi subunit enzyme. It lacks a $5'$ to $3'$ exonucleolytic activity, although a subunit of the enzyme carries out the editing ($3'$ to $5'$) function during replication. Finally, only about 10 molecules of Pol III reside in each cell. This remains consistent with the function of Pol III in replication, because the chromosome only needs to be copied once per generation. Therefore, the cell only requires a few molecules of the enzyme. Pol III synthesizes DNA at least a hundred times more rapidly than the other polymerases. It can synthesize half of the bacterial chromosome in a little more than 20 minutes, which is the fastest that the bacterium can replicate.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

24. In the cell, what is the function of *E. coli* DNA polymerase II?

a. To initiate replication at the origins.

b. To carry out 'fill in' reaction at the Okazaki fragments after RNA primer removal.

c. To synthesis of leading strand only.

d. To restart replication at the stalled replication fork.

Correct Answer: D

Polymerase II plays a pivotal role in resuming DNA replication in cells exposed to UV irradiation. Although replication restart appears normal in $\Delta umuDC$ strains containing poll!, the restart process is delayed for $>90\,\mathrm{min}$ in cells lacking both pot., It and $\mathrm{UmuD'2C}$. Because of the presence of pot II, a transient replication-restart burst is observed in a "quick-stop" temperature-sensitive pol III mutant $(dnaE486)$ at non-permissive temperature.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

25. What would be the result of propagation of *Tetrahymena* chromosomes In yeast if the telomeric repeat sequence of *Tetrahymena* is TTCGGG and thetelomeric repeat sequence of yeast is GTGTGT?

a. TTGGGG TTGGGG TTGGGG

b. GTGTGT GTGTGT GTGTGT

c. GTOTGT TTGGGG GTGTGT

d. None of the above

Correct Answer: B

The telomerase from Tetrahymena can be much more processive in vitro, synthesizing many telomere repeats from 'a single binding event. The hypothesis that yeast telomerase follows a distributive or non-processive, mode of synthesis in vivo is consistent with the in vitro data and the irregular $\mathrm{GTI}-3$ repeat and has not relied on the existence of hybridization and template regions.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

26. In certain bacterial strains, when non-sense mutations occur in the reading frame of mRNA the protein synthesis do not get terminated, as It usually happen in the normal cases, rather these bacterial cells are able to synthesize full-length polypeptide. What is the reason?

a. Compensatory frame-shift mutation that occurs elsewhere in the mRNA.

b. Involvement of suppressor tRNAs.

c. Alternate splicing.

d. Post-transcriptional editing.

Correct Answer: A

A frameshift mutation is caused by either insertions or deletions of a number of nucleotides in a DNA sequence. Such kind of insertion or deletion can change the reading frame (the grouping of the cottons), due to the triplet nature of gene expression by coders. This will result in a completely different translation from the original. In such case the non-sense mutation will not be able to show its effect because the reading frame gets shifted, and the sequence of the stop codon will get distorted due to changes in the position of cotton. Hence, a full length polypeptide will be synthesized.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

27. How do the nonsense mutations differ from deletion mutations?

a. Nonsense mutations are non-reversible in nature.

b. Nonsense mutations can be suppressed easily.

c. Protein chain termination does not take place in nonsense mutations.

d. No transcription takes place in nonsense mutation.

Correct Answer: B

Nonsense mutations can be suppressed easily by a tRNA with a mutant anticodon, which inserts an amino acid at the mutant cotton, producing a fill length protein.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

28. What can be inferred from the fact that DNA polymerase I from E *.coli* has a $5'-3'$ exonuclease activity?

a. The enzyme has multiple subunits.

b. DNA polymerase I can use primers from both DNA and RNA.

c. It makes the enzyme able to detect thymine dimers in double - stranded DNA.

d. It enables the enzyme to play an important role in DNA replication.

Correct Answer: D

E *. coli* DNA replication in which polymerase I plays a critical role. In addition to its DNA polymerase activity, pol I acts as an exonuclease that can hydrolyze DNA (or RNA) in either the $3'$ to $5'$ or $5'$ to $3'$ direction. The action of polymerase I as a $5'$ to $3'$ exonuclease removes ribonucleotides from the $5'$ ends of Okazaki fragments, allowing them to be replaced with deoxyribonucleotides to yield fragments consisting entirely of DNA. Hence this enzyme has an important role in DNA replication.

Core Concept:

Topic:

Difficulty Level:

Complexity:

29. At what site do the okazaki fragments are formed during the replication of E *.coli* chromosome?

a. Only one of the strands of the circular genome.

b. On both the strands of the circular genome.

c. On one of the strands in one generation and the other strand in the next generation.

d. None of the above

Correct Answer: B

The joining of okazaki fragments requires an enzyme that catalyzes the joining of the ends of two DNA chains. The existence of circular DNA molecules also points to the existence of such an enzyme. DNA Pol III uses one set of its core subunits to synthesize the leading strand continuously, while the other set of core subunits cycles from one Okazaki fragment to the next on the looped lagging strand. Okazaki fragments are formed during the replication process.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

30. Which feature of transcription is similar to that of replication?

a. No primer is required for polymerization.

b. Polymerization does not have proofreading activity.

c. Newly synthesized strand stars falling off the template before complete RNA is synthesized.

d. RNA synthesis requires DNA topoisomerase action.

Correct Answer: D

In yeast, simultaneous inactivation of DNA topoisomerase I (topo I) and topoisomerase II (topo II) reduces rRNA synthesis, and to a lesser extent mRNA

synthesis is reduced. This reduction in RNA synthesis in yeast cells can be attributed to changes in the topology of the DNA template. Topoisomerase have been shown to be required for transcription in cells. Moreover, transcription on chromatin templates results in the accumulation of superhelical tension; making the relaxation activity of topoisomerase II essential for productive RNA synthesis on nucleosomal DNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

31. DNA replication in eukaryotes can start from

a. centromere to other end.

b. both ends of a chromosome simultaneously.

c. only the one end of chromosome.

d. several sites along DNA of chromosome simultaneously.

Correct Answer: D

Eukaryotic replication begins at different origins. Replication takes place simultaneously at many sites along the entire length of chromosomes ensures DNA synthesis. Eukaryotic polymerases insert nucleotide growth of chain at much lower rates.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

32. How do the eukaryotes differ from prokaryotes in mechanism or DNA replication?

a. Semi-discontinuous rather than continuous

b. DNA primers instead of RNA primers

c. Unidirectional rather than bidirectional

d. All of the above

Correct Answer: A

DNA replication in eukaryotes is semiconservative, semi-discontinuous and bidirectional as compared to semiconservative, bidirectional and continuous in prokaryotes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

33. How many number of DNA molecules shall be labelled with radioactive thymidine after three generations, if the DNA having labeled thymidine is allowed to replicate in medium having non-radioactive thymidine?

a. One molecule

b. Two molecules

c. Four molecules

d. Eight molecules

Correct Answer: B

It was found that found that, one generation after the heavy cells were moved to $^{14}\mathrm{N}$ medium, the DNA formed a single band of an intermediate density between the densities of the heavy and light controls. After two generations in $^{14}\mathrm{N}$ medium, the DNA formed two bands one at the intermediate position, the other at the light position. This result would be expected from the semiconservative mode of replication.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

34. Which statement is true regarding the double helical molecule?

a. Each strand is identical.

b. Bases are perpendicular to the axis.

c. All hydroxyl groups of pentose sugars are involved in linkages.

d. Each strand replicates itself.

Correct Answer: B

The bases are oriented perpendicular to the helix axis and are hydrophobic, therefore the energy interaction between two bases forming a hydrogen-bonding combination while the hydrophobic stacks of neighbouring base-pairs even in the single-stranded state which allows the chain to form regions of helical conformation.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

35. What will be the correct order of procedure to be followed by the forensic experts in order to identify the person who committed a crime, If the forensic experts need to extract DNA from the tissue sample collected from the crime scene?

a. Cut the DNA and hybridize with specific micro-satellite probes.

b. Cut the DNA and subclone the fragments.

c. Determine the sequence of the subclones.

d. Option B followed by C

Correct Answer: A

When the chromosomal DNA from a sample of actual cells is digested with a restriction enzyme, this would yield too many DNA fragments to analyze. Like minisatellites, microsatellites are found in multiple site of the genome of humans and other species and are variable among different individuals. As in automated DNA

sequencing, the amplified microsatellite fragments are fluorescently labeled. A laser excites the fluorescent molecule within a microsatellite. This type of DNA fingerprint yields a series of peaks, each peak having a characteristic molecular mass.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

36. DNA molecule that has the ability to replicate autonomously is known/called as _____.

a. Plasmid

b. Chromosome

c. Phagemid

d. Replicon

Correct Answer: D

The origin of replication (ori) confers on the DNA strand an ability to replicate autonomously. This property can be used to isolate the ori. A DNA molecule replicating from an ori is called a replicon.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

37. What is the chemical that resembles on the bases can mistakenly get incorporated into DNA/RNA?

a. Deoxyribonucleotide

b. Interchalating molecule

c. Base analog

d. Nitrogen base

Correct Answer: C

Base analogs are chemicals that are structurally very similar to the bases normally found in DNA. Base analogs can get incorporated into DNA during replication because of their structural similarity to normal bases. One base analog, $5-$ bromouracil, is almost identical to the base thymine.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

38. Approximately, _____ of DNA, between two cos sites, can be packaged by lambda packaging extract.

a. $10\,\text{kb}$

b. $15\,\text{kb}$

c. $25\,\text{kb}$

d. $45\,\text{kb}$

Correct Answer: D

Phage lambda packages DNA by a mechanism which involves the recognition of the *cos* sites on concatemeric DNA molecules, thus two adjacent *cos* sites are required for packaging of lambda DNA molecules. However, phage lambda also requires the amount of DNA between *cos* sites fall within a range of size centered on the normal wild type content $(45\,\text{kb})$.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

39. After two rounds of replication, _____ will be observed in a cesium chloride gradient.

a. one light, one medium and one heavy band

b. one light and one medium band

c. one medium band

d. one medium and one heavy band

Correct Answer: B

Meselson and Stahl found that, one generation after the heavy cells were moved to ^{14}N medium, the DNA formed a single band of an intermediate density between the densities of the heavy and light controls. After two generations in ^{14}N medium, the DNA formed two bands; one at the intermediate position, the other at the light position. This result would be expected from the semiconservative mode of replication; in fact, the result is compatible with only this mode if the experiment begins with chromosomes composed of individual double helices.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

40. What Is the principle behind, the yeast two-hybrid system?

a. Detection of protein and DNA interaction from two yeast hybrid strains.

b. Detection of protein-protein interactions by assembling a functional transcription factor from two fusion proteins.

c. Detection of protein-protein interactions by studying the hybridization of two cDNA sequences.

d. Detection of protein-protein interactions in a pair of hybrid yeast strains.

Correct Answer: B

The yeast two-hybrid system addresses the problems of the *in-vitro* assay format by testing for protein interactions within the yeast cell. The principle of the system is

the assembly of an active transcription factor from two fusion proteins and the detection of this assembly by the activation of a marker gene.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

41. What is the Characteristic of Dispersive replication?

a. Each daughter molecule contains either two parent polynucleotide or two newly synthesized polynucleotide.

b. Each daughter molecule is composed partly of original polynucleotide and partly of newly synthesized polynucleotide.

C. Each daughter molecule contains one polynucleotide from the original molecule and one newly synthesized polynucleotide.

d. None of the above

Correct Answer: B

In dispersive replication model, the parental double helix is broken into double-stranded DNA segments that, as for the Conservative Model, act as templates for the synthesis of new double helix molecules. The segments then reassemble into complete DNA double helices, each with parental and progeny DNA segments interspersed.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

42. The enzyme that catalyzes the synthesis of a new strand for a DNA molecule by linking nucleotides to the developing strand is

a. DNA ligase

b. DNA polymerase

C. Topoisomerase

d. ss binding protein

Correct Answer: B

DNA polymerase (the enzyme that carries out DNA synthesis) uses one strand of DNA as a template and adds a new nucleotide to the $3'$ end of the new elongating strand. DNA polymerase utilizes a deoxyribonucleotide, cleaves the two terminal phosphates from the $5'$ end of the nucleotide and uses the free energy to form a phosphodiester bond between the $5'$ phosphate of the incoming nucleotide and the $3'$ hydroxyl end of the last nucleotide in the strand. Therefore, the newly synthesized DNA strand can only elongate in one direction, $5'$ to $3'$.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

43. What is the attachment point between the phosphate group, in the carbon skeleton of the pentose-sugar in DNA?

a. $\mathrm{C1, C5}$

b. $\mathrm{C2, C5}$

c $\mathrm{C3, C5}$

d. $\mathrm{C4, C5}$

Correct Answer: C

The deoxyribose sugar of the DNA backbone has 5 carbons and 3 oxygens. The carbon atoms are numbered $1', 2', 3', 4$ and $5'$ to distinguish from the numbering of the atoms of the purine and pyrmidine rings. The hydroxyl groups on the $5'-$ and $3'-$ link to the phosphate groups to form the DNA backbone. Deoxyribose lacks a hydroxyl group at the $2'-$ position when compared to ribose, the sugar component of RNA.

Core Concept:

Topic:

Difficulty Level:

Complexity:

44. During DNA replication, the sequence $5'-TpApCpAp-3'$ would produce which of the following complementary structure?

a. $5'-ApTpCpTp-3'$

b. $5'-UpCpUpAp-3'$

c. $5'-GpCpGpAp-3'$

d. $5'-TpCpTpAp-3'$

Correct Answer: A

The base components of nucleic acids are heterocyclic compounds with the rings containing nitrogen and carbon. Adenine and guanine are purities, which contain a pair of fused rings; cytosine, thymine and uracil are pyrimidines. The strands are held in precise register by a regular base-pairing between the two strands A is paired with T through two hydrogen bonds; 0 is paired with C through three hydrogen bonds.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

45. Which enzyme is involved in relaxing the super coils in DNA?

a. Topoisomerase I

b. Primase

c. Helicase

d. DNA polymerase Ill

Correct Answer: A

Type I enzymes catalyze the relaxation of closed circular, negatively supercoiled DNA. But E. *coil* topoisomerase I can partially remove the negative turns and binds to ssDNA and catalyzes the knotting of single-stranded circles E. *Coli* topoisomerase I does not relax positive supercoils under normal circumstances.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

46. Choose the incorrect statement.

a. The helical dimer of A-DNA is 23Å.

b. Rotation per bp in Z-DNA is $36°$.

c. There are twelve bp per turn in Z-DNA.

d. None of the above.

Correct Answer: B

Within a region of Z-DNA the bases flip over $180°$. This flipping is accompanied by the rotation of the glycosidic bond of the purities from anti to syn and the sugar pucker change. For the pvrimidine nucleotides in Z-DNA, the sugar accompanies the base in its $180°$ rotation.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

47. Which among the following equation is correct about Chargaff's rule?

a. $\text{A}+\text{T}=\text{G}+\text{C}$

b. $\frac{\text{A}+\text{G}}{\text{C}+\text{T}}=1$

c. $A+G+T=C$

d. None of the above

Correct Answer: B

According to Chargaff's rule, the concentration of guanine always equalled the concentration of cytosine.

In other words,

The amount of purine $=$ The amount of pyrimidine in a DNA molecule.

$[A]+[G]=[C]+[T]$

Adenine (A) is paired to Thymine (T) by 2 hydrogen bonds $(A=T)$.

Cytosine (C) is paired to Guanine (G) by 3 hydrogen bonds $(G\equiv C)$

Core Concept:

Topic:

Difficulty Level:

Complexity:

48. Which among the following statement is correct about genome?

a. Genes on nuclear DNA

b. Nuclear DNA $+$ Mitochondrial DNA

c. Nuclear DNA $+$ Chloroplast DNA

d. Nuclear DNA $+$ Mitochondrial DNA $+$ Chloroplast A. DNA

Correct Answer: D

The multiple copies of mitochondrial and chloroplast DNA contained within the matrix or stroma of these organdies is usually distributed in several clusters, called nucleoids. In mammalian cells, mitochondrial DNA makes up less than 1% of the total cellular DNA. In other cells, however, such as the leaves of higher plants or the very large egg cells of amphibians, a much larger fraction of the cellular DNA may be

present in mitochondria or chloroplasts and a large fraction of RNA and protein synthesis takes place there.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

49. Lagging strand is formed by _____ in the ease of eukaryotic DNA replication

a. okazaki fragments

b. DNA fragments

c. nucleotide fragments

4. None of the above

Correct Answer: A

DNA polymerases, replication proceeds by continuous synthesis on the leading strand growing in the some direction as the opening of the parental strands and discontinuous synthesis on the lagging strand growing in the opposite direction. The lagging strand is first made as short fragments of DNA, which are initiated by RNA/DNA primers. These fragments, $100-150$ nucleotides (nt) in length, are known as Okazaki fragments.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

50. Which among the following enzyme Is required removing RNA primer during DNA replication?

a. DNA helicase

b. DNA topoisomerase

C. DNA polymerase I

d. DNA polymerase II

Correct Answer: C

DNA polymerase I has nucleolytic (depolymerizing) activities, which are an intimate part of their function. The $5'$ to $3'$ exonuclease activity removes base-paired sequences ahead of the polymerizing activity. During replication, this can remove primers ahead of the polymerizing function of the polymerase.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

51. The reunion or recolling of separated DNA strand, during DNA replication, is prevented by

a. Helix destabilizing protein

b. Single strand binding protein

c. Both A and B

d. None of the above

Correct Answer: C

The major function of SSBP is to prevent recoiling of DNA strands after it's unwinding by helicases. Thus, SSBP plays vital role in replication. It bind with single strand and prevent coiling. Helix destabilizing protein is a group of proteins that bind to single-stranded regions of duplex deoxyribonucleic acid and cause unwinding of the helix.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

52. In E . *coli,* recA gene is involved in recombination as well as repair and dnaB gene is involved in unwinding of DNA double strands during replication. Which of the following statements Is/are correct about Rec A and DNA B?

A. Mutation in E . *coli* recA gene is lethal.

B. E . *coil* with mutated dnaB gene does not survive.

C. Dna B after uncoiling DNA double strands prevents further reannealing at the separated strands.

D. Rec A gene is Involved in SOS response and helps DNA repair.

The correct options are;

a. B and C

b. A and B

c. B and D

d. A and C

Correct Answer: C

The SOS response is a global response to DNA damage in which the cell cycle is arrested and DNA repair and mutagenesis are induced. The system involves the RecA protein (Rad 51 in eukaryotes). The RecA protein, stimulated by single-stranded DNA, is involved in the inactivation of the LexA repressor thereby inducing the response. It is an error-prone repair system that is attributed to mutagenesis.

The E .coli are further modified in order to have a number of mutations including a uvrA mutation which renders the strain deficient in excision repair, increasing the response to certain DNA-damaging agents, as well as an rfa mutation, which renders the bacteria lipopolysaccharide-deficient, allowing better diffusion of certain chemicals into the cell in order to induce the SOS response. Commercial kits which measures the primary response of the E .*coli* cell to genetic damage are available and may be highly correlated with the Ames Test for certain materials. In E .*coli* dnaB gene is involved in unwinding of DNA double strands during replication. It is found that the dnaB protein is a DNA helicase that is capable of unwinding extensive stretches of double-stranded DNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

53. In a DNA replication, the telomerase RNA act as a/an

a. primer

b. template

c. enzyme

d. cofactor

Correct Answer: C

The telomerase enzyme attaches to the end of a chromosome and contains a catalytic part and a built-in RNA template. Telomerase adds complementary RNA bases to the $3'$ end of the DNA strand. Once the $3'$ end of the lagging stand template is sufficiently elongated, DNA polymerase adds the complementary nucleotides to the ends of the chromosomes; thus, the ends of the chromosomes are replicated.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

54. Which among the following enzyme helps in the removal of Okazaki fragments and gap filling?

a. DNA polymerase II and DNA ligase

b. DNA polymerase III and DNA ligase

c. DNA polymerase I and DNA ligase

d. RNA polymerase and DNA ligase

Correct Answer: C

To form a continuous lagging strand of DNA, the RNA primers must eventually be removed from the Okazaki fragments and replaced with DNA. The action of polymerase I as a $5'$ to $3'$ exonuclease removes ribonucleotides from the $5'$ ends of Okazaki fragments, allowing them to be replaced with deoxyribonucleotides to yield fragments consisting entirely of DNA. The segment of DNA is removed and replaced with the correctly-paired nucleotides by the action of DNA pol. Once the bases are filled in, the remaining gap is sealed with a phosphodiester linkage catalyzed by DNA ligase.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

55. What is true about eukaryotic DNA replication?

a; Only one replisome forms because there is a single origin of replication.

b. The Okazaki fragments are 1000 to 2000 nucleotides in length.

c. FEN1 (flap endonuclease 1) is involved in removing the primer.

d. None of the above.

Correct Answer: C

In eukaryotic primer removal, DNA polymerase & extends the Okazaki fragment in $5'$ to $3'$ direction and when it encounters the RNA primer from the previous Okazaki fragment, displacing the $5'$ end of the primer into a single stranded RNA flap, which is removed by nuclease cleavage. Cleavage of the RNA flaps involves either endonuclease I(FEN1) cleavage of short flaps or coating of long flaps by the single-stranded DNA binding protein replication protein A(RPA) and sequential cleavage by Dna2 nuclease and FEN1.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

56. Which among the following statement is true about DNA helicase in E. Coli?

a. It moves in the direction opposite of replication fork.

b. It binds with template of the leading strand.

c. It is a hexameric protein with ATPase activity.

d. It catalyzes the formation of primer.

Correct Answer: C

The separation of the two strands of the DNA duplex is a prerequisite in the propagation or transfer of genetic information during replication. Transcription, and repair. Helicase play an active role in catalysing strand separation using the energy generated in ATP hydrolysis. It acts comparably to an active motor, unwinding and translocating along its substrate as a direct result of its ATPase activity. DnaB is the hexameric replicative helicase of prokaryotes. Cells of E. Coli contain at least 12 DNA- dependent ATPases that cause unwinding of DNA at the expense of hydrolysis of ATP.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

57. All among the following statements are true about DNA pol I of E .coli, except

a. It belongs to $\gamma -$ family of DNA polymerase

b. It catalyzes translesion DNA synthesis

c. It has $5' \rightarrow 3'$ exonuclease activity

d. It catalyzes error-prone replication

Correct Answer: C

DNA polymerase I (E. *Coli*) is a DNA-dependent DNA polymerase with inherent $3' \rightarrow 5'$ and $5' \rightarrow 3'$ exonuclease activities. The $5' \rightarrow 3'$ exonuclease activity removes nucleotides ahead of the growing DNA chain, allowing nick-translation.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

58. Choose the incorrect statement.

a. Most of the eukaryotic mRNAs have a $7-$ methyguanosine cap at their $5'$ end.

b. Histones have no other function except in chromatin organization.

c. Eukaryotic RNA polymerase II consists of more than 4 subunits.

d. Both A and B

Correct Answer: B

Organization of the eukaryotic genome into chromatin enables its compaction inside the cell nucleus and concomitant regulation of DNA-related processes. Several mechanisms including histone modifications and ATP- dependent chromatin-remodeling culminate into an altered chromatin structure, which renders the *cis*-acting sites on the DNA accessible to the *trans*-acting factors. They often involve localized chromatin assembly/disassembly via eviction/deposition of the histones by specific histone chaperones, which bind dimers of canonical or variant histones $\mathrm{H2A/H2B}$ or $\mathrm{H3/H4}$. Histone chaperones also assist DNA transactions by exchanging old histones with new ones and play important roles in replication and repair processes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

59. The effect of nonsense mutation could be nullified by reversion as well as suppression. Which of the following processes will help to distinguish between the two kinds of

a. Complementation

b. Transgenesis

c. Test for allelism

d. Recombination

Correct Answer: D

Genetic recombination is the production of offspring with combinations of traits that differ from those found in either parent. In eukaryotes, genetic recombination during meiosis can lead, through sexual reproduction, to a novel set of genetic information that can be passed on through heredity from the parents to the offspring. Most recombination is naturally occurring. During meiosis in eukaryotes, genetic recombination involves the pairing of homologous chromosomes. This may be followed by information exchange between the chromosomes. The information exchange may occur without physical exchange (a section of genetic material is copied from one chromosome to another, without the donating chromosome being changed) or by the breaking and rejoining of DNA strands, which forms new molecules of DNA. Recombination may also occur during mitosis in eukaryotes where it ordinarily involves the two sister chromosomes formed after chromosomal replication. In this case, new combinations of alleles are not produced since the sister chromosomes are usually identical. Genetic recombination is catalyzed by many different enzymes. Recombinases are key enzymes that catalyse the strand transfer step during recombination.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

60. What is the mode of action of hydroxyurea in DNA replication?

a. It inhibits DNA polymerase.

b. It inhibits ribonucleotide reductase.

c. It inhibits lagging strand DNA synthesis.

d. It inhibits replicative helicase.

Correct Answer: B

Hydroxyurea (HU) is a potent inhibitor of the enzyme ribonucleotide reductase (RNR) and inhibits DNA replication in a wide variety of cells, including *Saccharomyces cerevisiae*. The simplest explanation for HU inhibition of DNA synthesis is that it starves the DNA polymerase at the replication forks for dNTPs. HU treatment has been shown to reduce the purine dNTP pools in a variety of mammalian cells; however, conflicting data exist concerning its modulation of pyrimidine dNTP pool levels.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

61. Double chained DNA strand is made radioactive in both Its chains. It Is allowed to replicate twice in non-radioactive medium. What would be the result?

a. All strands have radioactivity.

b. Half the strands have radioactivity.

c. Three strands have radioactivity.

d. Radioactivity is absent in all strands.

Correct Answer: B

Half of the strands will show radioactivity as its is allowed to replicate just twice so over all 4molecules will be formed from which 2 will show the presence of radio labelled nucleotides courtesy semi-conservation nature of DNA replication. Semi-conservative replication would result in double-stranded DNA with one strand of $15\mathrm{N}$ DNA and one of $14\mathrm{N}$ DNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

62. Which among the following Is required for DNA replication in prokaryotes?

a. Primase to make small primers containing deoxyribonucleotides.

b. DNA polymerase III to join Okazaki fragments.

c. DNA polymerase alpha to synthesize DNA.

d. DNA polymerase Ito cut out primers and fill in gaps in the lagging strand.

Correct Answer: D

Three DNA polymerases (I, II and III) have been purified from E . *Coli*. In addition to its role in filling the gaps between Okazaki fragments, DNA polymerase I probably is the most important enzyme for gap filling during DNA repair. This repair polymerase is involved in excision repair with $3'-5'$ and $5'-3'$ exonuclease activity and processing of Okazaki fragments generated during lagging strand synthesis. Pol I is the most abundant polymerase accounting for $> 95\%$ of polymerase activity in E . Coli, yet cells lacking Pol I have been found suggesting Pol I activity can be replaced by the other four polymerases.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

63. What is the function of the $3'$ to $5'$ exonuclease activity of DNA polymerase?

a. Removal of $5'$ end of the polynucleotide strand that is attached to the template strand that is being copied.

b. Removal of damaged nucleotide from the template strand during DNA synthesis.

c. Removal of nucleotides from ends of DNA molecules to ensure the generation of blunt ends

d. Removal of incorrect nucleotides from the newly synthesized strand of DNA.

Correct Answer: D

The $3' \rightarrow 5'$ exonuclease activity intrinsic to several DNA polymerases plays a primary role in genetic stability; it acts as a first line of defense in correcting DNA polymerase errors. A mismatched basepair at the primer terminus is the preferred substrate for the exonuclease activity over a correct basepair. The efficiency of the

exonuclease as a proofreading activity for mispairs containing a DNA lesion varies, however, being dependent upon both the DNA polymerase/exonuclease and the type of DNA lesion.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

64. Which among the following match is Incorrect?

a. Pal I - Primer removal and DNA repair

b. Pol Ill - DNA replication

c. Poll $\mathrm{V}-$ Translesion replication

d. Poly $\gamma-$ Nuclear DNA replication

Correct Answer: D

DNA polymerase subunit gamma is an enzyme in humans is encoded by the *POLG* gene. DNA polymerase (pol) gamma is the sole DNA polymerase in animal mitochondria. *POLG* (alias, *POLGJ* or *POLGa)* is the gene that codes for the catalytic subunit of the mitochondrial DNA polymerase, called DNA polymerase gamma.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

65. _____ helps in the repair of pyrimidine dimers that are formed by UV-B Induced damage of DNA.

a. $\mathrm{UV}-\mathrm{C}$ light

b. Green light

c. Blue light

d. Infrared

Correct Answer: C

Photolyasesare DNA repair enzymes that repair damage caused by exposure to ultraviolet light. This enzyme mechanism requires visible light, preferentially from the violet/blue end of the spectrum and is known as photoreactivation.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

66. How is the parental strand recognized during the mismatch repair in E *.coli?*

a. Via single-stranded breaks.

b. Via glycosylaled adenines.

c. Via methylated adenines.

d. Via the methylation of 6^{th} position of guanine residues.

Correct Answer: C

DNA. adenine methylase (darn methylase) to create $6-$ methyladenine in the sequence GATC. In wildtype E . *coli* cells, the DNA is normally filly methylated (both strands are methylated). Newly synthesized strands during DNA replication are temporarily (that is; for a shod period of time) unmethylated and DNA with one strand methylated and the other strand unmethylated is called hemi-methylated.

Core Concept:

Topic:

Difficulty Level:

Complexity:

67. A repressor of gene X , whose product is cytosolic protein, expression Is over expressed in a cell line using R-DNA technology and after the over expression, the

cell line Is observed to be susceptible to UV lights and higher mortality rates are observed upon even short exposures to the UV. What Is the probable function of the gene X?

a. Photosynthesis

b. DNA repair

c. DNA replication

d. X-chromosome assembly

Correct Answer: B

DNA repairs a collection of processes by which a cell identifies and corrects damage to the DNA molecules that encode its genome.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

68. How many expected number of limes do a given. $8-$ base-pair DNA site should be present In the E. *coli* genome if all four bases are equally probable?

a. 30 times

b. 40 times

C. 50 times

d. 70 times

Correct Answer: D

The number of possible $8-$ bp sites is $4^8 = 65,536$. In a genome of 4.6×10^6 base pairs, the average site should appear $4.6\times10^6/65,536 = 70$ times.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

69. Which among the following activity is associated with the large (klenow) fragment of E. *coil* DNA polymerase I?

a. Reverse transcriptase activity and nick-translation activity.

b. Polymerase activity and $3'-5'$ exonuclease activity.

e. Polymerase activity and nick-translation activity.

d. Both A and B

Correct Answer: B

The Klenow fragment of DNA polymerase I from E. *ccli* has two enzymatic activities DNA polymerase and $3'-5'$ exonuclease. In addition to generating Kienow fragment by proteolysis, it can be expressed in bacteria from a truncated form of the DNA polymerase I gene.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

70. What is the cause of formation of Okazaki fragments during DNA synthesis?

P. DNA synthesis extends from $5'$ to $3'$ direction.

Q. Their synthesis are opposite to the direction of replication fork.

R.DNA ahead of replication fork Is positively supercoiled.

S. DNA synthesis is semi-conservative.

a. Q and R

b. P and Q

c. R and S

d. S and P

Correct Answer: B

The "lagging strand" is synthesized in the direction away from the replication fork and away from the DNA helicase unwinds. This lagging strand is synthesized in pieces because the DNA polymerase can only synthesize in the $5'$ to $3'$ direction and so it constantly encounters the previously-synthesized new strand. The pieces are called Okazaki fragments and each fragment begins with its own RNA primer. DNA is synthesized in a continuous manner in the direction of overall DNA replication; the other is formed from small, discontinuous pieces of DNA that are synthesized backward with respect to the direction of movement of the replication fork.

Core Concept:

Topic:

Difficulty Level:

Complexity:

71. Which among the following would serve as a template for DNA synthesis, when added to a solution that contain DNA polymerase $\mathrm{I}, \mathrm{mg}^{2+}$ salts of dATP, dGTP, dCTP, dTTP and an appropriate buffer?

a. A single-stranded closed circle with linear strand.

b. A single-stranded closed circle base-paired to a shorter linear strand with a 3-terminal hydroxyl.

c. A single-stranded closed circle base-paired to a shorter linear strand.

d. A double-stranded closed circle.

Correct Answer: B

DNA polymerase adds nucleotides to an existing strand at the $3'$(hydroxyl) end. DNA polymerase does not initiate, which eliminates choice A - there's no primer there to elongate.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

72. The statement(s) incorrect about DNA ligase

P. It forms a phosphodiester bond between a $5'-$ hydroxyl and a $3'-$ phosphate in duplex DNA.

Q. it requires a cofactor, either NAD^+ or ATP depending on the source of the enzyme, to provide the energy to from the phosphodiester bond.

R. it catalyzed its reaction by mechanism that involves the formation of a covalently linked enzyme adenylate.

S. it catalyzed its reaction by a mechanism that Involves the activation of DNA phosphate through the formation of a phosphoanhydride bond with AMP.

a. P and S

b. P and R

C. S

d. P

Correct Answer: D

The DNA ligases requires two termini- 5' termini (phosphate group) and 3'termini (hydroxyl group) to act as a substrate. These termini must reside on a double-stranded molecule (DNA:DNA or DNA:RNA). The strands of the duplex (staggered end or blunt end) are joined together or sealed by the enzyme ligase requiring a second similar double-stranded terminus to till the reccess.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

73. An enzyme that is not required in the events at the replication fork, during the DNA replication is

a. DNA gyarase

b. DNA polymerase

C. DNA glycosylase

d. DNA ligase

Correct Answer: C

DNA glycosylase cleave the N-glycosylic bond between the target base and deoxyribose, thus releasing a free base and leaving an apurinic/apyrimidinic (AP) site. In addition, several DNA glycosylases are bifunctional, since they also display a lyase activity that cleaves the phosphodiester backbone $3'$ to the AP site generated by the glycosylase activity.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

74. What is the role of promoter site on DNA?

a. It codes for TWA.

b. It regulates termination.

c. It helps to initiate transcription.

d. It helps to transcribe the repressor region.

Correct Answer: C

Promoters are DNA sequences located in the $5'$ region adjacent to the transcriptional start site RNA polymerase and accessory. proteins (transcription factors) bind to the promoter to initiate production of an mRNA transcript. Interactions of proteins at the promoter regulate gene activity by activating or repressing transcription.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

75. Which among the following Is used to bind together the nucleotides In DNA strand?

a. Peptide bonds

b. Hydrogen bonds

c. Phosphodiester bonds

d. Glycosidic bonds

Correct Answer: C

DNA polymerase proceeds along a single-stranded molecule of DNA, recruiting free dNTP's (deoxy-nucleotide-triphosphates) to hydrogen bond with their appropriate complementary dNTP on the single strand (A with T and G with C) and to form a covalent phosphodiester bond with the previous nucleotide of the same strand. The energy stored in the triphosphate is used to covalently bind each new nucleotide to the growing second strand.

Core Concept:

Topic:

Difficulty Level:

Complexity:

76. Which pair of enzyme is responsible for site specific recombination?

a. DNA polymerase III and DNA ligase

b. DNA polymerase II and DNA ligase

c. DNA polymerase I and DNA ligase

d. Restriction endonuclease and DNA ligase

Correct Answer: D

Site-specific recombination is a process that is functionally (but not mechanistically) equivalent to a combination of restriction endonuclease and DNA ligase activities. The recombinases that mediate these recombination events recognize specific DNA

sequences and the recombinase-bound sites interact in a nucleoprotein intermediate called the synaptic complex.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

77. What will be the radioactive status of the four double stranded molecules, if the completely radioactive dsDNA undergo two rounds of replication in the solution that Is free of radioactive table?

a. All the strands will get radioactive.

b. Half contain radioactivity in both the strands.

c. Half contains no radioactivity.

d. One contains radioactivity in both the strands.

Correct Answer: C

According to the semi-conservative theory, after one replication of DNA, we should obtain 2 hybrid (part N^{14} part N^{15}) molecules from each original strand of DNA. This would appear as a single line in the test tube. After the two rounds of replication dsDNA contains half radioactive strands.

Core Concept:

Topic:

Difficulty Level:

Complexity:

78. A particular mutation was found by the geneticist that does not have any effect on the polypeptide encoded by the gene. What is this kind of mutation?

a. Non-sence mutation

b. Silent mutation

c. Missense mutation

d. Deletion

Correct Answer: B

A silent mutation is a type of mutation in the coding region of a gene that doesn't actually change the amino acid sequence of the protein that is made. Thus, asilent mutation alters DNA sequence, but has no apparent detectable effect on a phenotype or a function.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

79. Which among the following leads to frame shift mutation?

a. Deamination of cytosine to uracil

b. Formation of thymine dimers

c. Both A and B

d. None of the above

Correct Answer: D

A frameshift mutation is a genetic mutation caused by a deletion or insertion in a DNA sequence that shifts the way the sequence is read. Frameshift mutations arise when the normal sequence of codons is disrupted by the insertion or deletion of one or more nucleotides, provided that the number of nucleotides added or removed is not multiple of three. For instance, if just one nucleotide is deleted from the sequence, then all of the codons including and after the mutation will have a disrupted reading frame. This can result in the incorporation of many incorrect amino acids into the protein.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

80. Which among the following statement is correct regarding the proofreading activity that is required to maintain the fidelity of DNA synthesis?

a. It occurs only in prokaryotes and not in eukaryotes.

b. It is a function of the $3'-5'$ exonuclease activity of the DNA polymerases.

c. It occurs after the synthesis has been completed.

d. It requires the presence of an enzyme other than DNA polymerase.

Correct Answer: B

The $3' \rightarrow 5'$ exonuclease activity intrinsic to several DNA polymerases plays a primary role in genetic stability; it acts as a first line of defense in correcting DNA polymerase errors. A mismatched basepair at the primer terminus is the preferred substrate for the exonuclease activity over a correct basepair. The efficiency of the exonuclease as a proofreading activity for mispairs containing a DNA lesion varies, however, being dependent upon both the DNA polymerase/exonuclease and the type of DNA lesion.

Core Concept:

Topic:

Difficulty Level:

Complexity:

81. An enzyme that possesses both the $5'-3'$ and $3'-5'$ exonuclease activity Is

a. DNA polymerase Ill

b. Taq DNA polymerase

c. Komberg enzyme

d. RNA polymerase

Correct Answer: C

Several of the template -dependent DNA polymerase that are used in molecular biology are versions of the E *.coli* DNA polymerase I enzyme, which plays a central

role in replication of this bacterium's genome. This enzyme, sometimes called the Kornberg polymerase, has both the $3'-5'$ and $5'-3'$ exonuclease activities, which limits its usefulness in DNA manipulation.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

82. Which among the following chemical inhibit the activity of DNA gyrase?

a. Nalidixic acid

b. Tetracyclin

c. Cephalosporin

d. All of the above

Correct Answer: A

ATP dependent DNA supercoiling catalyzed by *Escherichia* coli. DNA gyrase was inhibited by oxolinic acid, a compound similar to but more potent than nalidixic acid and a known inhibitor of DNA replication in E *. coil.*

Core Concept:

Topic:

Difficulty Level:

Complexity:

83. What kind of mutation not affect the length of protein?

a. Non-sense mutation

b. Frameshift mutation

c. Missense mutation

d. None of the above

Correct Answer: C

This type of mutation is a change in one DNA base pair that results in the substitution of one amino acid for another in the protein made by a gene thus does not affect the protein length.

Core Concept:

Topic:

Difficulty Level:

Complexity:

84. What is the composition of chromosomal DNA?

a. Three types of histone as $\mathrm{H1}$, $\mathrm{H2A}$ and $\mathrm{H4}$.

b. Five types of historic as $\mathrm{H1}, \mathrm{H2A}, \mathrm{H2B}, \mathrm{H3}$ and $\mathrm{H4}$.

C. Two types of histone as $\mathrm{H1}$ and $\mathrm{H4}$.

d. None of the above

Correct Answer: B

The proteins that build the scaffold of the nucleosome arc called histories. They form a family of five major classes of historic proteins called $\mathrm{H1}(\mathrm{H5}), \mathrm{H2A}, \mathrm{H2B}, \mathrm{H3}$ and $\mathrm{H4}$. The amino acid sequences of histories are highly conserved during evolution indicating their critical function for the chromosome organization and control of gene expression with the highest frequency of mutations found in $\mathrm{H1}(\mathrm{H5})$. This historic type has a special function in the nucleosomal complex at the nucleosome surface.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

85. What is the other name of Messelsen and Stahl model of reputation?

a. Dispersive replication

b. Semi-conservative replication

c. Both A and B

d. None of the above

Correct Answer: B

The semi-conservative model seemed most reasonable since it would allow each daughter strand to remain associated with its template strand. The semi-conservative model was confirmed by the Meselson-Stahl experiment and other even more revealing experiments that allowed for autoradiographic visualization of the distribution of old and new strands within replicated chromosomes.
Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

86. _____ is synthesized discontinuously in the $3'$ to $5'$ direction.

a. Lagging strand

b. Leading strand

c. Both A and B

d. None of the above

Correct Answer: A

The strand on which Okazaki fragments are formed called lagging strand, whereas the one which synthesized without interruption, is the leading strand. Both the Okazaki fragments and the leading strand, are synthesized in the $5' \rightarrow 3'$ direction. The discontinuous assembly of the lagging strand enables $5' \rightarrow 3'$ polymerization at the nucleotide level to give rise to overall growth in the $3' \rightarrow 5'$ direction.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

87. _____ does not require primer in order to function.

a. RNA polymerase

b. DNA pol I

c. DNA pol II

d. DNA pot III

Correct Answer: A

RNA polymerase requires DNA as a 'template. In duplex DNA, the template strand of DNA is copied into RNA by RNA polymerase. The choice' of nucleotides during this process is directed by base complementarity, so that the sequence of RNA synthesized is the reverse complement of the DNA template strand. RNA polymerase does not require a primer to initiate transcription. RNA polymerase catalyzes the sequential addition of a ribonucleotide to the $3'$ end of a growing RNA chain, with the sequence of nucleotides specified by the template.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

88. _____ link together the two strands of double helix.

a. Ionic bonds

b. Hydrogen bonds

c. Electrostatic bonds

d. None of the above

Correct Answer: B

One strand of DNA is oriented in the $5'$ to $3'$ direction while the complementary strand runs in the $3'$to $5'$ direction. Because the two strands are oppositely oriented, they are said to be anti-parallel to each other. The two strands bond

through their nitrogen bases (marked $\mathrm{A}, \mathrm{C}, \mathrm{G}$ or T for adenine, cytosine and guanine). Note that adenine only bonds with thymine and cytosine only bonds with guanine. The nitrogen bases are held together by hydrogen bonds adenine and thymine form two hydrogen bonds; cytosine and guanine form three hydrogen bonds.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

89. Energy for the DNA polymerisation is provided by

a. the hydrolysis of ATP.

b. the hydrolysis of GTP,

c. the hydrolysis of incoming nucleoside triphosphates.

d. All of the above

Correct Answer: C

Each incoming nucleotide supplies the energy for its addition in the high-energy bond between the beta and gamma phosphates that are ejected upon addition. It is not the release of the pyrophosphate that drives the reaction, but rather the subsequent hydrolysis that takes place. A much larger amount of energy is released when the two phosphates are separated into individual phosphates through the hydrolysis reaction.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

90. How often does DNA polymerase make an error during DNA replication?

a. One in every 100 nucleotide pairs.

b. One in every $1,00,000$ nucleotide pairs.

c. One in every $10,000,000$ nucleotide pair.

d. One in every $1,000$ nucleotide pair.

Correct Answer: C

DNA polymerase copies the DNA (template), which then needs a primer to get started the other way. The process involves nucleotide base pairs, $\mathrm{A}-\mathrm{G}-\mathrm{C}-\mathrm{T}$. The DNA synthesis happens only in the $5'$ to $3'$ direction. The two DNA strands are antiparallel. Leading strand synthesis is continuous. Lagging strand synthesis is discontinuous. These DNA strand breaks are going on all the time. Oxygen free radicals are floating around making these breaks all the time. Some plants create poisons that can cause these. Chemotherapy involves double strand breaks that kill off cancer cells a little bit faster than normal cells.

This only happens during replication times and the strands must be approximately 95% or more homologous.

Replication is accurate, 1 error in every $10,000,000$ bases.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

91. Holiday Junction can be best described as

a. a section of DNA where base pairing is not exact.

b. a strand of DNA containing genetic material from two different chromosomes.

c. an interaction of two-strands of DNA from homologous chromosomes.

d. a three stranded DNA structure where single stranded DNA has invaded a double helix.

Correct Answer: C

In a Holliday junction, the two homologous DNA helices that have initially paired are held together by the reciprocal exchange of two of the four strands present, one originating from each of the helices.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

92. Identify the correct sequence of events proposed by the double-strand break model of recombination.

I. Strand invasion and D loop formation

II. DNA gap repair synthesis

III. Generation of single stranded DNA segments

IV. Resolution

a. I. II, Ill, IV

b. IV, III, II, I

c. III, I, II, IV

d. I, II, IV, III

Correct Answer: C

According to the original Holliday model, after two homologous double-stranded DNA molecules (i.e., cellular

or viral chromosomes) become aligned, a nick is made in one strand of each of the recombining DNAs (step 1). The two nicked strands then invade each other, a process called strand exchange, at the site of the nicks and the cut $3'$ ends are joined to the $5'$ ends of the homologous strand, producing a crossed-strand. Holliday structure (step 2). The branch point then migrates, creating a heteroduplex region containing one strand from each parental DNA molecule. Two mechanisms have been proposed for separation or resolution of the connected duplexes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

93. Aspartic acid (Asp) is specified by the codon GAU and GAG. After mutation, Asp is changed to alanine represented by GCX, where X may be U, A, C or G. The reversion of the mutation could only be done with reactive oxygen species. The nature of the mutation is considered to be

a. transition

b. transversion

c. depurination

d. None of the above

Correct Answer: B

Transversion is a point mutation in which a purine is replaced by a pyrimidine or a pyrimidine is replaced by a purine. Thus, aspartic acid which is coded by GAU and GAG after mutation is changed to alanine represented by GCU, GCA, GCC, GCG.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

94. RNA primer Is considered essential during DNA synthesis by DNA polymerase III because this enzyme requires

a. a free $3'-PO_4$ group

b. a free $3'-OH$ group

c. a free $5'-PO_4$ group

d. a free $5'-OH$ group

Correct Answer: B

The requirement for a free $3'$ hydroxyl group is fulfilled by the RNA primers that are synthesized at the initiation sites by these enzymes. A free $3'OH$ group is required for replication, but when the two chains separate no group of that nature exists. RNA primers are synthesized and the free $3'OH$ of the primer is used to begin replication.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

95. Transient breaks that are made by _____ enable the strands of DNA to separate in the absence of helix rotation.

a. DNA topoisomerase

b. D-loops

c. DNA helicase

d. Single-strand binding proteins

Correct Answer: A

One type of topoisomerase, called topoisomerase I, produces a transient single-strand break (or nick); this break in the phosphodiester backbone allows the two sections of DNA helix on either side of the nick to rotate freely relative to each other, using the phosphodiester bond in the strand opposite the nick as a swivel point. Any tension in the DNA helix will drive this rotation in the direction that relieves the tension. As a result, DNA replication can occur with the rotation of only a short length of helix the part just ahead of the fork.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

96. What is the histone octamer in DNA tertiary structure?

a. It is a complex consisting of eight positively charged histone proteins (two of each $H2A, H2B, H3$ and $H4$) that aid in the packaging of DNA.

b. It is a complex consisting of eight negatively charged histone proteins (two of each $H2A, H2B, H3$ and $H4$) that aid in the packaging of DNA.

C. It is a complex consisting of nine positively charged histone proteins ($H1$ and two of each $H2A, H2B, H3$ and $H4$) that aid in the packaging of DNA.

d. It is a complex that consist of nine negatively charged historic proteins ($H1$ and two of each $H2A, H2B, H3$ and $H4$) that aid in the packaging of DNA.

Correct Answer: A

A histone octamer isa complex of eight positively charged histone proteins (two of each $H2A, H2B, H3$ and $H4$) that aid in the packaging of DNA. Negatively charged DNA wraps around these historic octamers to form the nucleosome. The DNA is held there by ionic bonds. Linker historic HI binds to each nucleosome where the DNA enters and exits and this draws a string of nucleosome closer together to form the $10\,nm$ fibre.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

97. Which among the following statements regarding the housekeeping genes is correct?

a. They are constitutively expressed.

b. They have highly methylated CpG islands.

c. They encode proteins required only in specific tissues.

d. All of these

Correct Answer: A

Housekeeping genes are constitutively expressed to maintain cellular function. As such, they are presumed to produce the minimally essential transcripts necessary for normal cellular physiology.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

98. What is the difference between Type I and Type II topolsomerases?

a. Type IA/IIA are linked to the free $5'$ end of the polynucleotide, while Type IB/IIB are linked at the $3'$ end.

b. Type I is present only in bacteria but not in eukaryotes.

c. Bacteria universally possess Type IB and IIB.

d. The active site for Type I topoisomerase possesses only tyrosine whereas the amino acids in the active site of Type II topoisomerase can vary.

Correct Answer: A

Type I and II topoisomerases are subdivided according to the precise chemical structure of the polynucleotide tyrosine linkage. With type IA and IIA enzymes the link involves a phosphate group attached to the free $5'$ end of the cut polynucleotide and type lB and II B enzymes the linkage is *via* a $3'$ phosphate group. The A and B topoisomerases probably evolved separately. Both types are present in eukaryotes, but type IB and II B enzymes are very uncommon in bacteria.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

99. What kind of mutation is represented in AGC to AGA change in codon?

a. Frameshift mutation

b. Nonsense mutation

e. Missense mutation

d. Deletion

Correct Answer: C

In genetics, a missense mutation (a type of non-synonymous substitution) is a point mutation in which a single nucleotide change results in a codon that code for a different amino acid.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

100. DNA Polymerase III is oftenly called _____, as it Is actually an aggregate of several different protein subunits.

a. primosome

b. holoenzyme

c. Both A and B

d. None of the above

Correct Answer: B

Holoenzyme consists of ten protein subunits and it is a dimeric enzyme with one half that copies the leading strand and another half that copies the lagging strand. The two halves of the enzyme communicate with one another such that both strands are replicated more or less simultaneously.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

101. Which enzyme proceeds along one of the strands a DNA molecule adding deoxy-nucleotide-triphosphates to hydrogen bond with their appropriate

complementary dNTP on the other single strand and to form a covalent phosphodiester bond with the previous nucleotide of the same strand?

a. DNA polymerase I

b. DNA polymerase II

c. DNA polymerase III

d. All of the above

Correct Answer: C

As DNA helicase moves down the DNA molecule and separates the two strands by breaking the bonds between the nitrogenous bases, DNA Polymerase III adds the appropriate complementary bases to the now exposed bases on the single strands. DNA polymerase III holoenzyme is the enzyme primarily responsible for replicative DNA synthesis in E. *coil.* It carries out primer-initiated $5'$ to $3'$ polymerization of DNA on a single-stranded DNA template, as well as $3'$ to $5'$ exonucleolytic editing of mispaired nucleotides.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

102. Which enzyme replaces the nucleotides of the RNA primer with the appropriate DNA nucleotides?

a. DNA polymerase I

b. DNA polymerase II

c. RNA polymerase

d. All of the above

Correct Answer: A

DNA polymerase I digests away the RNA primer (on the Lagging strand) and replaces the RNA nucleotides of the primer with the proper DNA nucleotides to fill the gap before DNA ligase links the strands together. Hence, the enzyme that replaces the RNA primer with DNA is DNA polymerase I.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

103. What is the point mutation called that involve the changes in the cation that specify an amino acid into a stop codon?

a. Frameshift mutation

b. Deletion mutation

C. Non-sense mutation

d. Missense mutation

Correct Answer: C

In genetics, a nonsensemutation is a point mutation in a sequence of DNA that results in a premature stop codon or a nonsense cotton in the transcribed mRNA and in a truncated, incomplete and usually nonfunctional protein product. It differs from a missense mutation, which is a point mutation where a single nucleotide is changed to cause substitution of a different amino acid.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

104. _____ are not mutagens.

a. UV rays

b. Jumping genes

c. Both A and B

d. None of the above

Correct Answer: D

A mutagen increases the number of mutations that occur during DNA replication above the natural background level. Mutagens can be chemical compounds or radiation. Ultraviolet radiation, retroviruses and transposons are mutagens.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

105. In DNA, mutations at G-C sequences occur quite frequently as $5-$ methyl cytosine easily deaminates to form

a. adenine

b. cytosine

e. thymine

d. uracil

Correct Answer: C

Cytosine can be methylated into $5-$ methylcytosine (by an enzyme called DNA methyltransferase) which can undergo spontaneous deamination to form Thymine.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

106. Which one among the following is the cause of mutation?

a. Cosmic rays

b. Pheromones

c. Crossing over

d. X-rays

Correct Answer: D

Mutations can be artificially induced with the help of mutagenic agents which can be broadly classified into two groups, physical mutagens and chemical mutagens. Physical mutagens are mainly radiations, although change in pH value (acidity) or temperature shocks may also induce mutations. Among ionizing radiations, more commonly X- rays, gamma rays beta rays and neutrons are used for inducing mutations. X- rays are produced in X- ray machine when energy charged particles like cathode rays (electrons) impinge on a suitable target like tungsten.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

107. Radiolabelled _____ can be used to measure the DNA synthesis.

a. thymidine

b. uracil

c. Both A and B

d. None of the above

Correct Answer: A

Autoradiography is the study of labelled precursors like $^{3}\mathrm{H}$ by knowing the movement of radioactivity with the help of photographic films and emulsions at short intervals. Radioactive material like tritiated thymidine which is formed by replacing normal hydrogen of thymidine with $^{3}\mathrm{H}$ (heavy isotope of hydrogen). Thymidine only is used for this purpose because RNA will not be labelled by this.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

108. The base that is considered as hot spot for spontaneous point mutations is

a. $5-$ bromouracil

b. $5-$ methylcytosine

v. guanine

d. adenine

Correct Answer: C

Mutations are rare events in nature and are then described as spontaneous mutations. Some of these mutations originate from mistakes in normal duplication of DNA. Transitions may be produced by tautomeric shift or ionization of bases which leads to mistaken, $\mathrm{A}-\mathrm{C}$ base pairing and more frequently mistaken $\mathrm{G}-\mathrm{T}$ base pairing. Guanine pairs with the rare cool form of thymine and is thus considered as hot spot for spontaneous point mutations.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

109. What is true regarding the two strands of DNA molecules of first generation bacteria, If an *Escherichia coli* that is fully labelled with $^{15}\mathrm{N}$ is allowed to grow in $^{14}\mathrm{N}$ medium?

a. They will have different density and do not resemble parent DNA.

b. They will have different density but resemble parent DNA.

c. They will have same density and resemble parent DNA.

d. They will have same density but do not resemble parent DNA.

Correct Answer: A

E *.coli* fully labelled with $^{15}\mathrm{N}$ is allowed to grow in $^{14}\mathrm{N}$ medium. The two strands of DNA molecule of the first generation bacteria have different density and do not

resemble parent DNA. Meselson and Stahl, 1958 by using $^{14}\mathrm{N}$ and $^{15}\mathrm{N}$ confirmed that the replication of DNA in E. *Coli* is semi-conservative in nature.

Core Concept:

Topic:

Difficulty Level:

Complexity:

110. _____ results from defects in nucleotide excision repair.

a. Lynch syndrome

b. Xeroderma pigmentosum (XP)

c. Both A and B

d. None of the above

Correct Answer: B

Xerodermapigmento sum, or Xp, is an autosomal recessive genetic disorder of DNA repair in which the ability to repair damage caused by ultraviolet (UV) light is deficient. Therefore they are unable to carry out efficient repair on sunlight damage and they are hypersensitive to sunlight. They have to protect their skin from daylight or risk getting skin cancer.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

111. During the mismatch repair system the parental (*i.e.*, correct) DNA strand and the newly synthesised strand containing the mismatched base can be distinguished as

a. thymine in the parental strand of the helix is methylated at GATC.

b. thymine in the new strand of the helix is methylated at GATC.

c. guanine in the parental strand of the helix is methylated at GATC.

d. guanine in the new strand of the helix is methylated at GATC.

Correct Answer: D

Mismatch repair is a system that repairs mismatches that have slipped evaded proofreading during DNA replication. DNA becomes methylated at the G of GATC sequences after replication; however, this does not occur immediately so the new strand, containing the error, can be distinguished from the methylated parental strand.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

112. Telomeres are found in

a. human mitochondrial DNA

b. human chromosomes

c. Both A and B

d. None of the above

Correct Answer: B

Telomeres arc found at the ends of the linear double-stranded DNA molecules in human chromosomes. They protect chromosome ends from nucleases and they also provide a special mechanism for replication of chromosome ends, using the enzyme telomerase. Circular molecules such as bacterial chromosomes and most mitochondrial geriatrics do not need these specialised DNA ends

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

113. The supercoils which are formed in front of a newly synthesizing DNA chain in the case of DNA replication are positively supercoiled, resulting from overwinding of the helix.

a. True

b. False

C. May be true or false

d. Can't say

Correct Answer: A

Unwinding of the double helix during DNA replication causes overwinding in front of the replication fork and the build-up of positive supercoils. These supercoils are released by the enzyme, topoisomerase I, which nicks the DNA, allows rotation of the helix, and then reseals the DNA duplex.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

114. The reaction catalysed by DNA ligase, in case of DNA replication is

a. formation of a phosphodiester bond between the $3'-\mathrm{OH}$ of one Okazaki fragment and the $5'-$ phosphate of the next on the lagging strand.

b. addition of new nucleotides to the lagging strand.

c. base pairing of the template and the newly formed DNA strand,

d. All of the above

Correct Answer: A

In the case of the leading strand, primase lays down a single RNA primer at the origin of initiation and the DNA polymerase proceeds from there until replication is complete, but the same will not suffice for the lagging strand. The solution is that, as the DNA unwinds, there is repeated initiation of the lagging strand by primase, each primer being extended by the polymerase into a short stretch of DNA synthesis, $1,000-2,000$ bases long in E. *coil* and $100-200$ in eukaryotes. The short stretches

of DNA attached to RNA primers on the lagging stand are called Okazaki fragments. DNA ligase catalyses formation of a phosphodiester bond between the $3'-\mathrm{OH}$ of one Okazaki fragment and the $5'-$ phosphate of the next, a process requiring energy. In some prokaryotes and all eukaryotes, ATP supplies this.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

115. All of the following statements regarding the E *coli* chromosome are correct, except

a. The E *. coil* chromosome is a single replicon.

b. Replication begins at oriC.

c. Replication can start at any point in the chromosome.

d. None of the above

Correct Answer: C

The E *. coil* chromosome is a circular, double-stranded DNA molecule. it replicates as a single replicon, beginning at the origin, oriC, with two replication forks travelling in opposite directions (bidirectional replication) until the entire chromosome has been replicated. Replication takes place at about 1000 base pairs per second and the entire chromosome takes about 40 minutes to be completely replicated.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

116. What is the function of Yeast artificial chromosomes (YAC)?

a. To clone the large segments of DNA.

b. To clone only the yeast genomic sequences.

c. To clone only cDNA sequences.

d. To clone all DNA except plant DNA sequences.

Correct Answer: A

The yeastartificial chromosome (YAC), is an artificially constructed system that can undergo replication. The design of a YAC allows extremely large segments of genetic material to be inserted. Subsequent rounds of replication produce many copies of the inserted sequence, in a genetic procedure known as cloning.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

117. How can we detect the infection of E. *coli* by bacteriophage λ?

a. By resistance of the bacteria to an antibiotic.

b. By the growth of single bacterial colonies on an agar plate.

c. By the appearance of areas of lysed bacteria on an agar plate.

d. By the restriction digest of the bacterial DNA.

Correct Answer: C

Every λ bacteriophage has a characteristic burst size. Different phage also take different amounts of time to go through one growth cycle. We knows that a phage has successfully reproduced when we are able to detect plaques or circular areas with little or no bacterial growth on an agar plate covered with a thin layer of bacteria.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

118. What is the role of $T4$ polynucleotide Masse?

a. Labeling of $3'$ ends of DNA.

b. Labeling of $5'$ ends of DNA.

c. Creating of sharp ends of DNA.

d. Dephosphorylation and phosphorylation of DNA.

Correct Answer: B

Thermo Scientific $T4$ Polynucleotide Kinase ($T4$ PNK) catalyzes the transfer of the gamma-phosphate from ATP to the $5'-OH$ group of single- and double-stranded DNAs and RNAs, oligonucleotides or nucleoside $3'-$ monophosphates (forward reaction). The reaction is reversible. In the presence of ADP $T4$ Polynucleotide Kinase exhibits $5'-$ phosphatase activity and catalyzes the exchange of phosphate groups between $5'-P$-oligo-polynucleotides and ATP (exchange reaction). Hence, used in the labeling of $5'$ ends of DNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

119. The $EcoRl$ digested DNA of E *coli,* after southern transfer, was probed with labeled eDNA probe of a gene which occurs only once In the H. *coil genome. If the gene contains one* $EcoRl$ *cleavage site* near its centre, the number of radioactive bands you are most likely to find on autoradiography would be

a. 3

b. 4

c. 2

d. 3

Correct Answer: C

If a person have isolated and cloned a segment of DNA that is known to be a unique sequence in the genome. It maps near the tip of the X chromosome and is about

$10\,\mathrm{kb}$ in length. Labeling at the $5'$ ends with $^{32}\mathrm{P}$ and cleave the molecule with *Eco*RI. There are two fragments obtained one is $8.5\,\mathrm{kb}$ long; the other is $1.5\,\mathrm{kb}$.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

120. What is the substrate for the restriction enzyme?

a. ss RNA

b. partially ds RNA

c. mRNA

d. ds DNA

Correct Answer: D

The substrates for restriction enzymes are more-or-less specific sequences of double-stranded DNA called recognition sequences. Restriction enzymes hydrolyze the backbone of DNA between deoxyribose and phosphate groups. This leaves a phosphate group on the $5'$ ends and a hydroxyl on the $3'$ ends of both strands. A few restriction enzymes will cleave single stranded DNA, although usually at low efficiency.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

121. Restriction enzymes X and Y have 8 and 4 base pairs as their recognition sites. What will be the ratio of the number of fragments that they *will* generate on restriction digestion of a genomic DNA of $\mathit{Sau}3\mathrm{A}$?

a. $4:8$

b. $8:4$

c. $1:64$

d. $1:256$

Correct Answer: D

The length of the recognition sequence is roughly proportional to the frequency of occurrence of the site in the generate. A simplistic theoretical estimate is that a six base pair recognition sequence will occur once in every $4096\left(4^6\right)$ base pairs while a four base pair recognition sequence will occur once every $256\left(4^4\right)$ base pairs. *Sau*3A recognition sites are 4 bases long and are expected to occur randomly every 4^4 or 256 bases. The human genome contains about 3×10^9 bases; one would expect $3\times10^9/256=1.2\times10^7-12,000,000$ fragments.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

122. What is the role of terminal transferase enzyme?

a. To add base at the $3'$ end of the DNA.

b. To add base at the $5'$ end of the DNA.

c. To carry out translation.

d. To transfer phosphate at the $5'$ end.

Correct Answer: A

Terminal transferase catalyzes the template independent addition of deoxy and dideoxy-nucleoside triphosphates to the $3'-\mathrm{OH}$ ends of double and single-stranded DNA fragments and oligonucleotides. Terminal transferase incorporates digoxigenin, biotin and fluorochrome-labeled deoxy and dideoxynucleoside triphosphates as well as radioactively labeled deoxy and dideoxynucleoside triphosphates.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

123. What can be inferred from the statement that many plasmids have ampicillin marker?

a. The plasmids contain genes for ampicillin biosynthesis.

b. Ampicillin is required for bacterial growth after transformation.

C. Plasmid contains the gene encoding $\beta-$ lactamase.

d. All of the above

Correct Answer: C

The ampR gene on the plasmid codes for an enzyme that is secreted into the periplasmic space of the bacterium, where it catalyzes hydrolysis of the li-lactam ring of ampicillin, with con-comitant detoxification of the drug. The *bla* gene encodes $\beta-$ Inctamase that confers resistance to ampicillin which is commonly known as a broad-spectrum antibiotic.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

124. Which of the following is true about interaction between TBP and TATA sequence?

a. TBP interacts with minor groove and bends DNA by about $80°$.

b. TBP interacts with major groove and bends DNA by about $80°$.

c. TBP interacts with minor groove with no significant bending.

d. TBP interacts with major groove with no significant bending.

Correct Answer: A

The TBP interacts with the DNA by at the TATA box. X-ray crystallography has shown that the highly conserved $C-$ terminal $180-$ aminoacid domain binds with the TATA box promoter DNA with high affinity and a slow dissociation rate. The underside of the 'saddle' binds to the minor groove and bends the DNA at an 80 degree angle. It is quite strange that TB? would bind to the minor groove of the DNA since it offers less selectivity than the major groove. The underside contains a curved, eight-stranded, antiparallel $\beta-$ sheet. This large, concave surface provides excellent contact with the minor groove and the eight base pairs of the TATA box.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

125._____ enzyme does not require a primer.

a. RNA dependent DNA polymerase

b. DNA dependent DNA polymerase

c. DNA dependent RNA polymerase

d. All of the above

Correct Answer: C

To initiate this reaction, DNA polymerases require a primer with a free 3'-hydroxyl group already base-paired to the template. They cannot start from scratch by adding nucleotides to a free single-stranded DNA template. RNA polymerase. in contrast, can initiate RNA synthesis without primer, they donot require primer and are therefore able to initiate RNA chains

Core Concept:

Topic:

Difficulty Level:

Complexity:

126. Transfer RNA specifies amino acid, during proteins synthesis. tRNA is charged with amino acid at $3'$ end and its anticodon pairs with cation of mRNA. Select the Incorrect statement out of the following.

a. Information is transmitted between 3' end of tRNA and anticodon.

b. Codon-anticodon interaction occurs in A site of ribosome.

c. Each tRNA has specific anticodon.

d. Each codon is triplet.

Correct Answer: A

The loop on the bottom of the cloverleaf contains the anticodon, which binds complementarily to the mRNA codon. Because anticodons bind with codons in antiparallel fashion, they are written from the $5'$ end to $3'$; end, the inverse of codons. At the $3'$; end of the tRNA molecule, opposite the anticodon, extends a three nucleotide acceptor site that includes a free $-\mathrm{OH}$ group. A specific tRNA binds to a specific amino acid through its acceptor stem.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

127. Why do the changes In RNA polymerase III promoters result in changes in the sequence of the gene product?

a. RNA polymerase III initiates transcription at various positions within the genomne.

b. The promoter elements are located within the coding region of the gene.

c. Promoters are located far away from the upstream of the gene transcribed.

d. Polymerase is unable to bind to the promoter region.

Correct Answer: B

A promoter is a regulatory region of DNA located upstream (towards the $5'$ region) of a gene, providing a control point for regulated gene transcription. The promoter contains specific DNA sequences that are recognized by proteins known as transcription factors. These factors bind to the promoter sequences, recruiting RNA

polymerase, the enzyme that synthesizes the RNA from the coding region of the gene.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

128. Termination of mRNA genes in eukaryotes occurs at

a. polyadenylation sites.

b, by the formation of a strong hairpin structure in the vicinity of polyadenylation site.

c. termination factor that is bound to the termination site in the vicinity of polyadenylation site.

d. pause sites

Correct Answer: C

Multiple mechanisms can promote transcription termination of Pol II in eukaryotic organisms. For protein-coding genes, the major transcription termination mechanism uses a poly(A) site (PAS) comprising a central AAUAAA sequence in humans and less conserved, degenerate $\mathrm{Py}(\mathrm{A})_{\mathrm{n}}$ sequence in S. cerevisiae.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

129. Choose the correct match from the following.

a. RNA pol I-tRNA; RNA pol II-mRNA

b. RIM Pol II-mRNA; RNA pol III-rRNA

C. RIM pol I-rRNA; RNA pol II- mRNA

d. RNA pol I-tRNA; RIM pol III-rRNA

Correct Answer: C

RNA polymerase I is specifically devoted to transcription of the three largest species of rRNAs, which are designated $28S, 18S$, and $5.8S$ according to their rates of sedimentation during velocity centrifugation. RNA polymerase II is responsible for the synthesis of mRNA from protein-coding genes, it has been the focus of most studies of transcription in eukaryotes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

130. The holoenzyme has the subunit structure _____ in prokaryotic RNA polymerase.

a. $\alpha\alpha\beta\beta'\sigma$

b. $\alpha\beta\sigma$

c. $\alpha\beta$

d. $\alpha\beta\beta$

Correct Answer: A

In prokaryotes single type of RNA polymerase is present which is responsible for synthesis of all types of RNA. Eubacterial RNA pot is named as holoenzyme, is a multisubunit protein which contain five subunits $\alpha\alpha\beta\beta\sigma$ structure of RNA polymerase is given as

$\alpha-$ Assembly of core enzyme.

$\beta\beta-$ Performs all enzymatic and catalytic function.

$\sigma-$ Recognizes promoter sequence.

$\alpha\alpha\beta\beta'$ forms core enzyme.

Holoenzyme $=$ Core enzyme $+$ Sigma factor

Core Concept:

Topic:

Difficulty Level:

Complexity:

131. _____ carry out the first *in vitro* synthesis of RNA and DNA.

a. Kornberg and Nirenberg

b. Ochoa and Nirenberg

c. Nirenberg and Khorana

d. Ochoa and Kornberg

Correct Answer: D

Kornberg's first experiment on DNA synthesis performed in the spring of 1955 involved $^{14}\mathrm{C}-$ labeled thymidine. a known constituent of DNA. An extract of *Escherichia coli* was chosen because of its known rapid rate of DNA replication and DNA synthesis was measured by conversion of the acid-soluble thymidine to the acid-insoluble form when it is part of DNA. Kornberg received the Nobel Prize for his work along with Severo Ochoa, who discovered an enzyme which made RNA. It turns out that both of them found the "wrong" enzyme, in a sense. Ochoa used ribonucleotide diphosphates (rNDPs) instead of rNTPs as his substrate and ended up characterizing an enzyme which normally breaks down RNA to rNDPs, but under the right conditions can go in reverse.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

132. Why do the genes that have been artificially synthesized without non-coding sequences often fall to yield proteins when placed Inside a cell?

a. Because they are not transcribed.

b. As they bound to the DNA.

c. Because their mRNA molecules fail to move through the pores, in the nuclear envelop.

d. None of the above

Correct Answer: C

The sole channels through the nuclear envelope are provided by the nuclear pore complexes, Which allow the regulated exchange of molecules between the nucleus and cytoplasm and also plays a critical role in regulating eukaryotic gene expression. The nuclear pore complex is a complicated structure that is responsible for the selective traffic of proteins and RNAs between the nucleus and the cytoplasm. By controlling the traffic of molecules between the nucleus and cytoplasm, the nuclear pore complex plays a fundamental role in the physiology of all eukaryotic cells. RNAs that are synthesized in the nucleus must be efficiently exported to the cytoplasm, where they function in protein synthesis. Conversely, proteins required for nuclear functions (*e.g*., transcription factors) must be transported into the nucleus from their sites of synthesis in the cytoplasm and wholw this system need coding sequences and if these sequencing are absent, gene will fail to yield protein.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

133. RNA polymerase, in contrast to DNA polymerase

a. synthesizes RNA primer to initiate DNA synthesis.

b. works only in $5' \rightarrow 3'$ direction.

c. fills the gap between okazaki fragments.

d. Both B and C

Correct Answer: A

The initiation of new DNA strands at origins of replication in animal cells requires *de novo* synthesis of RNA primers by primase and subsequent elongation from RNA primers by DNA polymerase alpha. DNA primaseis an enzyme involved in the

replication of DNA. DNA primase is, in fact, a type of RNA polymerase which creates an RNA primer (later this RNA piece is removed by $5'$ to $3'$ exonuclease); next, DNA polymerase uses the RNA primer to replicate ssDNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

134. Who propose the. 'One gene one enzyme hypothesis'?

a. Sutton and Boveri

b. Watson and Crick

c. Jacob and Monod

d. Beadle and Tatum

Correct Answer: D

Beadle and Tatum set out to provide experimental proof of the connection between genes and enzymes. They hypothesized that if there really was a one-to-one relationship between genes and specific enzymes, it should be possible to create genetic mutants that are unable to carry out specific enzymatic reactions.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

135. Which is the most abundant form of RNA in a cell?

a. rRNA

b. mRNA

c. tRNA

d. Primary RNA

Correct Answer: A

Ribosomal RNA, also known as rRNA, is a significant component of the ribosome. rRNA fabricates the polypeptides and provides a mechanism for decoding mRNA into amino acids and interacts with the tRNA during translation. rRNA was once known to be the key component of the structural of ribosomes, but its actually found to be a catalytic clement for protein synthesis. It is the most abundant type of RNA (about 80%) in the cell.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

136. Which among the following statement is true about reverse transcriptase enzyme?

a. It is a RNA dependant RNA polymerase.

b. It is a DNA dependant RNA polymerase.

c. It is a RNA dependant DNA polymerase.

d. It is a DNA dependant DNA polymerase.

Correct Answer: C

A reverse transcriptase, also known as RNA-dependent DNA polymerase, is a DNA polymerase enzyme that transcribes single-stranded RNA into double-stranded DNA. It also helps in the formation of a double helix DNA once the RNA has been reverse transcribed into a single strand cDNA. Normal transcription involves the synthesis of RNA from DNA; hence, reverse transcription is the reverse of this.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

137. All the following statements regarding the HIV genome replication are. correct, except

a. HIV is an enveloped RNA virus.

b. the virion contains an RNA dependant DNA polymerase.

c. a DNA copy of the HIV genome integrates into host cell DNA.

d. virion contains an RNA dependent RNA polymerase.

Correct Answer: D

Retroviruses are the cause of various cancers, lcukemias and immunodeficiencies in a wide variety of animals. The most widespread retrovirus in humans is HIV. Retroviruses differ from other RNA genome viruses in several important ways. One oddity is that the +ss RNA genome is present in two copies in the virion. Also, retrovirus virions contain a novel polymerase, commonly called reverse transcriptase that uses the viral RNA as a template to synthesize DNA (so, it is an 'RNA-dependent DNA polymerase").

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

138. Which of the following statement is incorrect?

a. Viral envelope that attaches the HIV to host cell is gp120 .

b. Genome of retro viruses contain two copies of plus ssRNA.

e. Both a and b

d. HIV contains a single copy of ssRNA.

Correct Answer: D

HIV is a lentivirus having two copies of single strand RNA (ssRNA) as its genetic material. The virus mainly infects the cells of immune system *e.g* T-helper, macrophage, dendritic cells. Since these cells are important for proper working of

body's defense system, reults into development of Acquired immuno Defeciency Syndrome (AIDS).

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

139. What will happen when a growing replication fork encounters an RNA polymerase complex engaged in transcription?

a. Both DNA replication and transcription will stop.

b. Replication will stop but transcription will continue as such.

c. Both the replication and transcription will continue but slowly.

d. Transcription will get paused to allow replication fork to progress.

Correct Answer: D

A replication fork moves 10% faster than RNA polymerase. If they proceeding in the same direction, either the replication fork must displace the RNA polymerase or it must slow, down as it waits for the RNA polymerase to reach its terminator. It appears that a DNA polymerase moving in the same direction as an RNA polymerase can bypass it without disrupting transcription. When a replication fork meets an RNA polymerase traveling in the opposite direction, toward it both the replication and transcription process become stalled and that replication is able to resume after the RNA polymerase is displaced by elements of a transcription coupled repair system (TCR).

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

140. Spilicing of CU-AG lntron

a. involves trans-esterification reaction.

b. occurs in prokaryotic mRNA.

c. form $\gamma -$ shaped branch structure.

d. require maturase activity.

Correct Answer: A

Essential splicing signals are the GU/AG dinucleotides at the exon/ introit and intron/exon junctions ($5'$ and $3'$ splice sites), respectively, the polypyrimidine tract (Py) and the A nucleotide of the branch site. Splicing takes place .in two esterification steps. In the first step the $2'-$ hydroxyl group of the A residue at the branch site attacks the phosphate at the GU $5'$ splice site. This leads to cleavage of the $5'$ exon from the intron and the formation of lariat intermediate. In the following step the two exons are ligated by a second transesterification reaction that involves the phosphate at the $3'$ end of the intron and the $3'$ hydroxyl of the detached exon. This releases the intron, still in the form of a lariat.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

141. If the E . coil cells are infected with the $\mathrm{T4}$ bacteriophage, it generally hacks host machinery for transcription *of* Its own genes. How is it done?

a. By degrading host RNA polymerase.

b. By modifying host RNA polymerase.

c. Via the synthesis of host RNA polymerase.

d. None of the above

Correct Answer: B

The $\mathrm{T4}$ transcriptional pattern reflects its dependence on the host RNA polymerase and the use of phage-encoded proteins that sequentially modify RNA polymerase; transcriptional activator proteins, a phage sigma factor, anti-sigma and sigma decoy proteins also act to specify early, middle and late promoter recognition. Post-

transcriptional controls by T4 provide excellent systems for the study of RNA-dependent processes, particularly at the structural level.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

142. Enhancer elements are known to increase the rate of transcription when present at the upstream side of the promoter sequences. What will happen if the same enhancer element is placed in reverse orientation?

a. The rate of transcription will increase as compared to upstream side.

b. The rate of transcription will decrease as compared to upstream side.

c. The rate of transcription will remain same as compared to upstream side.

d. No transcription will be observed.

Correct Answer: C

An enhancer is a nucleotide sequence to which transcription factor(s) bind and which increases the transcription of a gene. It is not part of a promoter, the basic difference being that an enhancer can be moved around anywhere in the general vicinity of the gene (within several thousand nucleotides on either side or even within an intron) and it will still function. It can even be clipped out and spliced back in backwards and will still operate. A promoter, on the other hand, is position and orientation-dependent. Some enhancers are "conditional" in other words, they enhance transcription only under certain conditions, for example in the presence of a hormone.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

143. The set of genes, that codes for proteins required for sporulation, from *Bacillus sublilis,* have a conserved DNA sequence -35 and -10 nucleotides before the site of transcript initiation, although the sequence at -35 is different from that seen in most other genes from that species. Which of the following best explains this difference?

a. A novel sigma factor is required for transcription initiation at these genes.

b. The -35 sequence is the binding site for a repressor of transcription.

c. The replication of these genes requires a specifically modified DNA polymerase.

d. Translation of the mRNAs transcribed from these genes require specific ribosomes that recognize a modified Shine-Dalgarno Sequence.

Correct Answer: A

Sigma factors provide promoter recognition specificity to RNA polymerase holoenzyme, contribute to DNA strand separation, and then dissociate from the core enzyme following transcription initiation. As the regulon of a single sigma factor can be composed of hundreds of genes, sigma factors can provide effective mechanisms for simultaneously regulating expression of large numbers of prokaryotic genes.

Core Concept:

Topic:

Difficulty Level:

Complexity:

144. Match the terms in group I with group II

	Group I		Group II
P.	Rnase-P.	1.	lac operon
Q.	Leucine zipper	2.	rRNA gene transcription
R.	RNA pot-I	3.	tRNA gene transcription
S.	Attenuation	4.	transcription factors
		5.	ribozymes
		6.	trp operon
		7.	mRNA splicing

a. $\mathrm{P}-7,\ \mathrm{Q}-5,\ \mathrm{R}-3,\ \mathrm{S}-1$

b. $P-4, Q-5, R-2, S-1$

c. $P-5,\ Q-4,\ R-2,\ S-6$

d. $P-4,\ Q-5,\ R-3,\ S-6$

Correct Answer: C

Ribonuclease P (RNase P) is one of only two known universal ribozymes and was one of the first ribozymes to be discovered. It is involved in RNA processing, in particular the $5'$ maturation of tRNA. Basic leucine-zipper (bZIP) proteins are transcription factors that consist of three modular functional regions mediating dimerization, DNA binding and transcriptional regulation. RNA Polymerase (Pol) I produces ribosomal (r)RNA, an essential component of the cellular protein synthetic machinery that drives cell growth, underlying many fundamental cellular processes. *In vivo,* termination of transcription at the attenuator site of die tryptophan (trp) operon off. *coli* is influenced by the protein termination factor rho.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

145. The promoter of the gene is

a. always located upstream of transcription start site.

b. always located downstream of translation start site.

c. different that is recognized by different RNA polymerase.

d. recognized due to their different secondary structures.

Correct Answer: C

In genetics, a promoter is a region of DNA that initiates transcription of a particular gene. Promoters are located near the transcription start sites of genes, on the same strand and upstream on the DNA (towards the 5' region of the sense strand). They can be about 100-1000 base pairs long. Initiation of transcription is a complicated process involving several different phases promoter location by RNA polymerase, formation of a competent initiation complex, synthesis of the initial phospbodiester bonds and movement of RNA polymerase from the promoter as it enters the elongation phase.

And hence, there are different promoter sequences that are recognized by different polymerases.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

146. Which of the following is characteristic of eukaryotic transcription but not prokaryotic transcription?

a. Transcription and translation are coupled.

b. There is one form of RNA polymerase.

c. RNA polymerase ii is responsible for synthesis of mRNA.

d. RNAs can be polycistronic.

Correct Answer: C

Eukaryotes have three nuclear DNA-dependent RNA polymerases (RNAPs) RNAP I, RNAP II and RNAP HI. RNAP 11, responsible for the synthesis of all mRNA as well as many noncoding RNAs (ncRNAs), consists of 12 polypeptides, of which Rpbl, which possesses the enzyme's catalytic activity, is the largest.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

147. What is the site of wobble between a codon and an anticodon?

a. First nucleotide of the codon and the first nucleotide of the anticodon.

b. First nucleotide of the codon and the third nucleotide of the anticodon.

c. Third nucleotide of the codon and the first nucleotide of the anticodon.

d. Third nucleotide of the codon and the third nucleotide of the anticodon.

Correct Answer: C

The original wobble rules suggested that the first nucleoside of the anticodon can pair with more than one nucleoside at the third position of the codon. Thus, anticodons with a U at the first position could interact with codons having either A or G at the third position. Those presenting a G at position 34 could interact with codons terminating with U or C. More interestingly, tRNA presenting an inosine (deaminated adenosine) at position 34 could recognize codons terminating with either C, U or A.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

148. How do CREB activate transcription?

a. By acting as a heterodimer

b. By phosphorylation

c. By binding to cAMP

d. By binding to RNA polymerase

Correct Answer: B

In order for CREB to activate transcription, CREB and be phosphorylated, resulting in the active form phosphor-CREB (pCREB), which then binds to the cyclic AMP responsive element (CRE) of target genes as well as to an adaptor protein (or mediator) known as CREB-binding protein (CBP) that, in turn, contacts and activates the basal transcriptional apparatus.

Core Concept:

Topic:

Difficulty Level:

Complexity:

149. Formation of pre-initiation complex, in eukaryotic transcription by RNA polymerase II

a. begins with the binding of TB? to the TATA box of the promoter.

b. require the ordered addition of several transcription factors and the RNA polymerase.

c. Both A and B

d. None of the above

Correct Answer: C

The most common type of core promoter in eukaryotes is a short DNA sequence known as a TATA box, found $25-30$ base pairs upstream from the start site of transcription. The TATA bod, as a core promoter, is the binding site for a transcription factor known as TATA-binding protein (TBP), which is itself a subunit of another transcription factor, called Transcription factor II D (TFIID). After TFIID binds to the TATA box via the TBP, five more transcription factors and RNA polymerase combine around the TATA box in a series of stages to form a preinitiation complex. The archaeal preinitiation complex assembles at a TATA-box binding site; however, in archaea, this complex is composed of only RNA polymerase II, TBP and TFB (the archaeal homologue of eukaryotic transcription factor II B(TFIIB).

150. Which one of the following statements is false regarding the Klenow fragment that are isolated from E *. coli?*

a. Klenow fragment is constituent of DNA polymerase I and II.

b. Klenow fragment has DNA polymerase activity.

C. Klenow fragment has $3'$ to $5'$ exonuclease activity but it is devoid of the $5'$ to $3'$ exonuclease activity.

d. While Klenow fragment is primarily associated with DNA repair functions, DNA polymerase I is essential for DNA replication.

Correct Answer: D

The klenow fragment incorporates individual deoxyribonucleotides at a relatively modest rate of 50 nucleotides and is moderately processive (on average, it

synthesizes 50 nucleotides after binding and before dissociation). The klenow fragment also acts as a reverse transcriptase by copying RNA templates, albeit distributively (*i.e.*, incorporating one to two nucleotides per binding event), but the biological relevance of this activity is not known. The smaller $35-\mathrm{kDA}$ domain that has $5'-3'$ exonuclease activities functions in pol I to degrade DNA and RNA to monomers and small oligomers. The polymerase and $5'-3'$ exonuclease domains act in concert during nick translation to remove Okazaki Fragments by using the $5'-3'$ exonuclease activity and to fill in the resulting gap.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

151. The transcription factor that is involved in promoter recognition in eukaryotes is

a. TFIIF

b. TFIIB

c. TFIID

d. TFIIE

Correct Answer: C

The first step in formation of a transcription complex is the binding of a general transcription factor call TFIID to the TATA box (TFindicates transcription factor; II indicates polymerase II). TFIID is itself composed of multiple subunits, including the TATA-binding protein (TBP), which binds specifically to the TATA consensus sequence and $10-12$ other polypeptides, called TBP-associated factors (TAFs). TFIID bind to the large promoter DNA.

Core Concept:

Topic:

Difficulty Level:

Complexity:

152. As shown below one of the Intron is mutated in a eukaryotic gene

Normal: $5'$ TTTCCCACCCTTAG $3'$

Mutant: $5'$ TTTCCCACCCTTCG $3'$

The process that is most likely to be affected by the mutation is

a. capping

b. hybridization

C. polyadenylation

d. splicing

Correct Answer: D

Following transcription, genes are expressed as precursor mRNAs (pre-mRNAs) which are spliced co-transcriptionally and the flanking exons are joined together to form a continuous mRNA. Mis-regulation of splicing and alternative splicing can result from mutations in *cis* regulatory elements within the affected gene or from mutations that affect the activities of trans-acting factors that are components of the splicing machinery.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

153. Which among the following statement is correct?

P. Group I intron show homing.

Q. Group II intron show retrohoming.

R. Many Group I introns have open reading frame.

S. Group I Intron acts as riboswitch.

a. P and Q

b. Only S

c. P, Q and R

d. P and S

Correct Answer: A

Group I introns are found in the nuclear small subunit ribosomal RNA gene (SSU rDNA) of some species of the genus *Porphyra* (Bangiales, Rhodophyta). Size polymorphisms in group I introns has been interpreted as the result of the regeneration of homing endonuclease genes (HEG) inserted in peripheral loops of intron paired elements. Mobile group II introns retrohome by an RNP-based mechanism in which the excised intron lariat RNBA fully reverse splices into a DNA site *via* 2 sequential transesterification reactions and is reverse transcribed by the associated intron-encoded protein.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

154. Which codons are recognized by the release factor $\mathrm{RF1}$, in E *.coli?*

a. UAG and UGA

b. UAA and UGG

c. UAG and UAA

d. UAG and UUA

Correct Answer: C

Non-sense codons known as amber (UAG), ochre (UAA) and opal (UGA), signal termination of protein synthesis on the ribosome. Unlike sense-codon recognition, no tRNAs are involved in nonsense (stop) codon recognition. Instead, termination of protein synthesis in bacteria depends on the class I release factors $\mathrm{RF1}$ and $\mathrm{RF2}$. Peptidyl-tRNA hydrolysis is promoted by $\mathrm{RF1}$ in response to a UAG or UAA stop codon, and by $\mathrm{RF2}$ in response to a UGA or UAA codon.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

155. Reverse transcriptase has both ribonuclease and polymerase activities. Ribonuclease activity is required for

a. the synthesis of new RNA strand

b. the degradation RNA strand

c. the synthesis of new DNA strand

d. the degradation of DNA strand

Correct Answer: B

A Reverse transcriptase (RT) is an enzyme used to generate Complementary DNA (cDNA) from an RNA template, a process termed reverse transcription. It has two activities DNA polymerase activity and RNase H activity. RNase H is a ribonuclease that degrades the RNA from RNA-DNA hybrids, such as is formed during reverse transcription of an RNA template. This enzyme functions as both an endonuclease and exonuclease in hydrolysing its target.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

156. In vertebrate genes, transcription regulatory regions that contain CpG Islands are Inactivated by _____ of CpG modification.

a. methylation

b. myristylation

C. phosphorylation

d. acetylation

Correct Answer: A

Vertebrate CpG islands (CGIs) are short interspersed DNA sequences that deviate significantly from the average genomic pattern by being GC-rich, CpG-rich and predominantly nonmethylated. Most, perhaps all, CGIs are sites of transcription initiation, including thousands that are remote from currently annotated promoters. Silencing of CGI promoters is achieved through dense CpG methylation or polycomb recruitment, again using their distinctive DNA sequence composition.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

157. The component of RNA polymerase that facilitates the recognition of promoter sequence is

a. α subunit

b. ϕ subunit

c. χ subunit

d. σ subunit

Correct Answer: D

The σ subunit of bacterial RNA polymerase (RNAP) has been implicated in all steps of transcription initiation, including promoter recognition and opening, priming of RNA synthesis, abortive initiation and promoter escape. The post-promoter-recognition σ functions were proposed to depend on its conserved region $\sigma 3.2$ that directly contacts promoter DNA immediately upstream of the RNAP active centre and occupies the RNA exit path.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

158. Transcription of each set of rRNA genes by RNA polymerasel produces

a. a single $45S$ rRNA precursor molecule,

b. a single $65S$ rRNA precursor molecule.

c. a single $28S$ rRNA precursor molecule.

d. a single $30S$ rRNA precursor molecule.

Correct Answer: A

The $28S$ and $5.8S$ rRNAs associated with the large $(60S)$ ribosomal subunit and the $18S$ rRNA associated with the small $(40S)$ ribosomal subunit in higher eukaryotes are encoded by a single type of pre-rRNA transcription unit. Transcription by RNA polymerase I yields a $45S$ $(13.7-\mathrm{kb})$ primary transcript (pre-rRNA), which is processed into the mature $28S, 18S$ and $5.8S$ rRNAs found in cytoplasmic ribosomes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

159. In eukaryotic genes

a. exons are not transcribed.

b. exons and introns both are transcribed.

c. exons are transcribed, but the RNA transcribed from introns does not leave the nucleus.

d. introns are transcribed, but the RNA transcribed from introns does not leave the nucleus.

Correct Answer: C

Eukaryotic genes are split up into parts that are expressed as RNA products and parts that are not. Exons are the parts of a eukaryotic gene that are expressed through transcription and translation and are scattered throughout the gene. All introns in a pre-mRNA must be completely and precisely removed before protein synthesis. The

process of removing introns and reconnecting exons is called splicing. Introns are removed and degraded while the pre-mRNA is still in the nucleus. Splicing occurs by a sequence-specific mechanism that ensures introns will be removed and exons rejoined with the accuracy and precision of a single nucleotide.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

160. A geneticist isolates a. gene for a specific trait under study and its corresponding mRNA. Upon comparison, the mRNA is found to contain $1,000$ fewer bases than the DNA sequence. What can be concluded from the above situation?

a. mRNA is made from a DNA template and should be the same length as the gene sequence.

b. mRNA should contain more bases than the DNA sequence because bases flanking the gene are also transcribed.

C. The final mRNA contains only exons, the introns were removed.

d. mRNA was partially degraded after it was transcribed.

Correct Answer: C

Eukaryotic genes are often interrupted by sequences that do not appear in the final RNA. The intervening sequences that are removed are called introns. The process by which introns are removed is referred to as splicing. The sequences remaining after the splicing are called exons. All of the different major types of RNA in a eukaryotic cell can have introns. Although higher eukaryotic genes have introns, some do not.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

161. _____ regulate which genes or subset of genesare transcribed in a particular cell type.

a. Transcription factors

b. Chaperone proteins

c. RNA polymerases

d. Transcription is not regulated

Correct Answer: A

Each individual segment, usually involving about $6-12$ base pairs of DNA, serves as a binding target for a DNA binding protein which functions as a transcription factor. One gene regulatory segment may contain binding sites for a large set of different transcription factors, five-len or more. These different transcription factors often have their binding targets dispersed over a wide area within the gene regulatory element which may involve DNA segments several thousand base pairs upstream and/or downstream of the promoter and which may be located within the transcribed gene, *e.g*. in an intron.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

162. What will happen immediately after the transcription?

a. A methylated guanine cap will be added to the $3'$ end of the transcript.

b. A methylated guanine cap will be added to the $5'$ end of the transcript.

c. A methylated adnine cap will be added to the $5'$ end of the transcript.

d. A poly adenylation signal is added at the $5'$ end.

Correct Answer: B

While the pre-mRNA is still being synthesized, a 7- methylguanosine cap is added to the $5'$ end of the growing transcript by a $5'$- to -$5'$ phosphate linkage. This moiety protects the nascent mRNA from degradation. In addition, initiation factors involved in protein synthesis recognize the cap to help initiate translation by ribosomes. The

guanosine that is added is always methylated at the 7 position of the guanine base $(7\mathrm{mG})$. This is called cap 0. In addition a methyl group is added to $2'\text{-}\mathrm{OH}$ of the original base in the mRNA. This is catalyzed by $2'\text{-}\mathrm{O}\text{-}$ methyl-transferase and this methyl group is referred to as cap 1. A methylated guanine cap is added to the $5'$ end of the transcript immediately after the transcription.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

163. $\alpha-$ amanitin Inhibits

a. Only RNA polymerase I

b. only RNA polymerase II

c. only RNA polymerase Ill

d. all RNA polymerases

Correct Answer: B

alpha-Amanitin or α- *amanitin* is a cyclic peptide of eight amino acids. It is an inhibitor of RNA polymerase II and III. α- *Amanitin* can also be used to determine which types of RNA polymerase are present. This is done by testing the sensitivity of the polymerase in the presence of α- *amanitin*. RNA polymerase I is insensitive, RNA polymerase II is highly sensitive (inhibited at $1\mu\mathrm{g}/\mathrm{ml}$), RNA polymerase III is moderately sensitive (inhibited at $10\mu\mathrm{g}/\mathrm{ml}$), and RNA polymerase IV is slightly sensitive (inhibited at $50\mu\mathrm{g}/\mathrm{ml}$).

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

164. The ribosome stall on region 1 during attenuation because

a. translation of this region requires tRNA trp.

b. high levels of tryptophan interfere with ribosome function.

c. low levels of tryptophan lead to intrinsic termination.

d. binding of the repressor protein prevents further translation.

Correct Answer: A

The availability of tryptophan-charged tRNA *Trp* is also sensed as a regulatory signal in controlling *trp* operon transcription – by a transcription attenuation mechanism. The relevant features of the □160 nucleotide (nt) *trp* operon leader transcript responsible for charged tRNA Trp sensing and for regulation by transcription attenuation. When most of the cellular tRNATrp is uncharged, difficulty in translating the two Trp codons of *trpL*mRNA results in ribosome stalling at one of these Trp codons.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

165. Nuclear receptors belong to _____ class of transcription factor.

a. helix-loop-helix protein

b. helix-turn-helix protein

C. leucine zipper protein

d. zinc finger proteins

Correct Answer: D

Steroid receptors are membrane of the nuclear receptor family of zinc finger transcription factors, which also includes receptors for thyroid hormone, vitamin D and retinoic acid. (Retinoic acid is important in embryonic development). Nuclear receptors contain two zinc fingers, one of which is actually involved in protein-protein rather than protein-DNA interactions.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

166. What is the sequence of bases called that Is located prior to the gene (along the DNA strand), to which a complex of RNA polymerase and sigma factors attache itself to initiate transcription?

a. Terminator

b. Promoter

C. Operator

d. None of the above

Correct Answer: B

A promoter may be described as a sequence of bases at which RNA polymerase begins transcription. Once the RNA polymerase-sigma factor complex recognizes the promoter sequence, the sigma factor dissociates from RNA polymerase which unwinds the DNA helix thus exposing a template for transcription. They are located near the transcription start sites of genes, on the same strand and upstream on the DNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

167. _____ act as an inhibitor of prokaryotic transcription.

a. Erythromycin

b. Chloramphanicol

C. Rifampicin

d. All of the above

Correct Answer: C

Rifampicin is a bactericidal antibiotic drug of the rifamycin group. Rifampicin inhibits bacterial DNA-dependent RNA synthesis by inhibiting bacterial DNA-dependent RNA polymerase. It is an inhibitor of prokaryotic transcription initiation. It binds only to bacterial RNA polymerase but not to eukaryotic RNA polymerase. Therefore, rifampicin is a powerful drug for treatment of bacterial infections.

Core Concept:

Topic:

Difficulty Level:

Complexity:

168. A segment of DNA that include regions that precede and follow the coding DNA (introns as well as exons) is called

a. Cistron

b. retrotransposon

c. operon

d. None of the above

Correct Answer: A

The terms cistron and gene are approximately the same. A gene could have several cistrons but this is unusual. Cistron is a section of DNA that contains the genetic code for a single polypeptide and functions as a hereditary unit. A cistron can include regions that precede and follow the coding region, introns and exons.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

169. A base sequence that is the part of DNA of an organism and appears to have coded a gene product, such as a protein or transcription factor, but no longer does so Is called

a. psuedogene

b. jumping gene

c. oncogene

d. selfish gene

Correct Answer: A

Pseudogenes are inactive sequences of genomic DNA which have a similar sequence to known functional genes and are considered to be evolutionary relatives to normally functioning genes. Pseduogenes are relatives of functional genes that have lost their functions.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

170. GC- rich stretch of nucleotides, that is followed by an ATrich stretch of nucleotides is the signal for

a. Rho dependent termination

b. Rho independent termination

c. Initiation

d. polyadenylation

Correct Answer: A

For rho-independent termination, there is a GC- rich stretch of nucleotides, followed by an AT rich stretch of nucleotides. When this stretch is transcribed into RNA, the sequence of the nucleotides is such that the RNA molecule forms a short double-stranded region called a hairpin which significantly slows down RNA polymerase causing it to pause in the AT-rich region. Because the AT rich region is relatively unstable, the transcription complex falls apart, ending transcription.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

171. CpG island methylation

a. enhances binding of regulatory transcription factors.

b. interferes directly with the binding site of RNA polymerase.

c. leads to gene silencing.

d. All of the above

Correct Answer: C

Methylation of CpG sites within the promoters of genes can lead to their silencing. Methylation of CpG islands prevents activation of promoter within it. Repression is caused by proteins that binds to methylated CpG doublets.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

172. What are intrinsic terminators?

a. They are the DNA sequences that assist in the termination of transcription.

b. They are the RNA sequences that assist in the termination of transcription.

c. They are the protein sequences that assist in the termination of transcription.

d. None of the above

Correct Answer: B

In genetics, a transcription terminator is a section of nucleic acid sequence that marks the end of a gene or operon in genomic DNA during transcription. Intrinsic

termination (also called Rho-independent termination) is a mechanism in prokaryotes that causes RNA transcription to be stopped.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

173. Which of the systems (below) would typically necessitate the use of a viral vector and packaging cell line system for shRNA delivery?

a. To silence a gene of interest that is known to be expressed at low abundance in a cell line with a fast division rate.

b. To silence a gene of interest that is known to be expressed at high abundance in primary cells.

c. To silence a gene of interest that is known to be expressed at high abundance in a cell line with a slow division rate.

d. To silence a gene of interest that is known to be expressed at low abundance in a cell line with a slow division rate.

Correct Answer: B

Generation of stable cell lines with the use of a recombinant plasmid containing the shRNA sequence alleviate limitations of siRNA with respect to low expression transcripts and/or high cell division rates. However, plasmid-based shRNAs are typically incapable of transfeeting primary cells. In such cases a viral-based vector (containing Long Terminal Repeats which flank the expression shRNA cassette) will be used to generate virions with the use of a packaging cell line. The virions can then be used to infect the primary cells.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

174. Which of the below hypothetical endpoint RT- PCR results for transient validation of shRNA demonstrate that It is unsuitable for use downstream in stable cell line generation?

a. Target mRNA-shRNA' cell line shows no amplicon. Wild type' cell line shows no amplicon. 'Vector only-shRNA' cell line shows no amplicon. 'Transfection

reagent only' cell line shows an amplicon.

b. Target mRNA-shRNA' cell line shows no amplicon 'Wild type' cell line shows an amplicon. 'Vector only-shRNA' cell line shows no amplicon. 'Transfection reagent only' cell line shows an amplicon.

C. Target mRNA-shRNA' cell line shows no amplicon. 'Wild type' cell line shows an amplicon. Vector only-shRNA' cell line shows an amplicon. 'Transfection reagent only' cell line shows an amplicon.

d. None of the above

Correct Answer: B

'Vector only-shRNA' cell line shows no amplicon. 'Transfection reagent only' cell line shows an amplicon. To ensure that any silencing effect elicited by an shRNA is specific, it must be compared to a series of negative controls. If the 'transfection reagent only' cell line or the 'vector only-shRNA' cell line show the target mRNA is silenced this would demonstrate that an off-target (and most probably a global) imbalance in gene expression has occurred. Any validation which depicts the silencing of the target transcript in the 'target mRNA-shRNA' cell line can therefore not be confirmed to be specific.

This does not indicate that the 'target mRNA-shRNA' cell line has failed (even though it may have) but rather that either preparation of the RT-PCR assay in this instance has failed or 'if results are reproducible', a general error in the assay design such as incorrect primers has occurred. Once either of these issues is rectified and a successful amplicon for the target mRNA is demonstrated in the wild type cell line, the 'target mRNA-shRNA' cell line can be reassessed for silenced transcript.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

175. It is beneficial to drive expression of the shRNA sequence from an expression vector containing an RNA pal Ill promoter because

a. if an RNA pol III terminator sequence (TTTT) was incorporated downstream of the antisense strand, the RNA pol III promoter in the expression vector generates an shRNA with a "UU" 3' overhang characteristic of pre-miRNAs; thus negating the need for any pri-shRNA to pre-shRNA processing by Drosha.

b. if an RNA pal III terminator sequence (AAAAA) was incorporated downstream of the antisense strand, the RNA pol III promoter in the expression vector generates an shRNA with a "AA" 3' overhang characteristic of pre-miRNAs; thus negating the need for any pri-shRNA pre-shRNA processing by Drosha.

c. the use of an RNA pot ill promoter does not require the incorporation of a stem loop into the shRNA design since the RNA pol Ill terminator sequence (TTTTT) generates fully-processed mature shRNA duplexes.

d. None of the above

Correct Answer: A

If an RNA pol III terminator sequence (TTTT) has been incorporated downstream of the antisense sequence during the shRNA sequence design, then ligation of this shRNA sequence into an expression vector containing an RNA pol III promoter such as "U6" results in transcribed shRNAs, once self-annealed, to contain a two-nucleotide "UU" 3' overhang, characteristic of the endogenous pre-miRNA sequences. This negates the requirement for Drosha to process pri-shRNAs to pre-shRNAs. The absence of this additional processing step reduces the possibility that the shRNA will be aberrantly processed and hence increases the likelihood of successful silencing.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

176. The 'cap' modification of eukaryotic mRNA includes

a. a modified guanine nucleotide that is added to the 3' end of the transcript.

b. a modified guanine nucleotide that is added to the 5' end of the transcript.

c. a string of adenine nucleotides that are added to the $3'$ end of the transcript.

d. a string of cytosine nucleotides that are added to the $3'$ end of the transcript.

Correct Answer: A

The RNA of the eukaryotic gene primary transcript immediately undergoes a modification at its $5'$ end, called capping. At the $5'$ end of the primary RNA transcript there is a triphosphate group because the first nucleotide triphosphate simply accepts a nucleotide on its $3'\text{-OH}$. The terminal phosphate of this is removed and a GMP residue is added from GTP. The $5'-5'$ triphosphate linkage is unusual. The G is then methylated in the N-7 position as is also the $2'\text{-OH}$ of the second nucleotide. The cap protects the end of the mRNA from exonuclease attack and it is involved in initiation of translation. Termination of transcription in eukaryotic cells is less understood than the prokaryotic mechanism. Most, though not all, eukaryotic mRNAs end in a string of up to 250 adenine residues known as a $3'$ polyA tail. The polyA tail is not directly encoded by the gene, but its position is directed by a polyadenylation signal (AAUAAA) that is encoded by the gene and transcribed in the primary transcript.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

177. What was the observation that was least expected during the release of human genome draft sequence?

a. Large amount of repetitive DNA.

b. Total genome size.

c. Individual chromosome size.

d. The small number of protein- coding genes.

Correct Answer: D

There appear to be about $30,000-40,000$ protein-coding genes in the human genome-only about twice as many as in worm or fly. However, the genes are more complex, with more alternative splicing generating a larger number of protein

products. The full set of proteins (the 'proteome') encoded by the human genome is more complex that those of invertebrates. This is due in part to the presence of vertebrate-specific protein domains and motifs (an estimated 7% of the total), but more to the fact that vertebrates appear to have arranged pre-existing components into a richer collection of domain architectures.

Core Concept:

Topic:

Difficulty Level:

Complexity:

178. For continuation of protein synthesis in bacteria, ribosomes need to be released from the mRNA as well as to dissociate into subunits. These processes do not occur spontaneously. They need the following possible conditions:

A.RRF and EF-G aid in this process

B. An intrinsic activity of ribosomes and all uncharged tRNA are required

C. IF -1 promotes dissociation of ribosome

U. IF -3 and IF -1 promote dissociation of ribosome

Which of the following sets is correct?

a. A and D

b. A and B

c. A and C

d. B and D

Correct Answer: A

Initiation of protein synthesis in E. *coli* requires initiation factors $\text{IF-1}, \text{IF-2}$ and IF-3. A ribosomal recycling factor (RRF) is required, with EF-G-GTP and IF-3, for release of uncharged tRNA from the P site, and dissociation of the ribosome from mRNA with separation of the two ribosomal subunits. IF-3 binds to the 30S ribosomal subunit, freeing it from its complex with 50S subunit. IF-1 assists binding of IF-3 to the 30S ribosomal subunit. Binding of IF-1 also occludes the A site domain of the small ribosomal subunit, helping to insure that the initiation aminoacyl-tRNA, fMet-

tRNAfMet, can bind only in the P site and that no other aminoacyl-tRNA can bind in the A site during initiation.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

179. What would be the most likely effect if a single nucleotide pair is Inserted near the $5'$ end of a protein-coding DNA sequence?

a. A protein with a single altered amino acid will be formed.

b. A protein with an almost completely altered sequence will be formed.

c. Protein formed will be terminated in between.

d. No protein will be formed at all.

Correct Answer: B

Due to the triplet nature of gene expression by codons, the insertion or deletion can change the reading a completely different translation from the original. Hence, in case there is a single nucleotide pair inserted near the $5'$ end of a protein-coding DNA sequence, protein with almost completely altered sequence will be formed.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

180. What could be inferred from the statement that at one time the genetic code was believed to be universal, but today we know that there are some variations in the code?

a. The word 'code' is inappropriate.

b. Different codons can code for the same amino acid.

c. Different amino acids can be encoded by the same codon.

d. All of the above

Correct Answer: C

The genetic code is the relation between the sequence of bases in DNA (or its RNA transcripts) and the sequence of amino acids in proteins. Proteins are built from a basic set of 20 amino acids, but there are only four bases. Simple calculations show that a minimum of three bases are required to encode at least 20 amino acids. Genetic experiments showed that an amino acid is in fact encoded by a group of three bases or codon. Some amino acids are encoded by more than one codon, in as much as there are 64 possible base triplets and only 20 amino acids. In fact, 61 of the 64 possible triplets specify particular amino acids and 3 triplets (called stop codons) designate the termination of translation. Thus, for most amino acids, there is more than one code word.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

181. _____ are involved in the majority of the ATP-dependent cytosolic degradation of proteins in eukaryotes.

a. Cathepsins

b. Calpains

C. Lysosomes

d. $26S$ proteasomes

Correct Answer: D

In eukaryotic cells, proteasome is an essential component of the ATP-dependent proteolytic pathway which is responsible for the degradation of most cellular proteins. A chain of four or more moieties is, in general, the minimal requirement for substrate recognition by the $26S$ proteasome complex the major ATP-dependent degradation pathway-although for some proteins monoubiquitination or multiple monoubiquitinations can efficiently target substrates for proteasomal degradation.

Nearly all proteins in the cytosol and nucleus are degraded via the ubiquitin-proteasome pathway, in eukaryotic cells. The $26S$ proteasome is built from approximately 31 different subunits, which catalyzes protein degradation.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

182. Wobble base pairs function during protein synthesis by allowing a non- Watson Crick base pair to be formed between

a. G at the $5'$ end of the anticodon and U at the $3'$ end of the codon.

b. G at the $3'$ end of the anticodon and U at the $5'$ end of the codon.

c. A at the $5'$ end of the anticodon and G at the $3'$ end of the codon.

d. A at the $3'$ end of the anticodon and G at the $5'$ end of the codon.

Correct Answer: A

The G-U wobble base pair is fundamental unit of RNA secondary structure that is present in nearly every class of RNA from organisms of all three phylogenetic domains. It has comparable thermodynamic stability to Watson-Crick base paris and is nearly isomorphic to them. Therefore, it often substitutes for G-C or A-U base pairs. The G-U wobble base pair also has unique chemical, structural, dynamic and ligand-binding properties, which can only be partially mimicked by Watson-Crick base pairs or other mispairs. G-U pairs have now been found in virtually every class of functional RNA and have been shown to play many essential roles that are based upon the unique chemical and structural properties of the wobble pair. Structural features of G-U wobble pairs and other non-Watson-Crick pairs have recently been reviewed elsewhere.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

183. What will be the order of bases in mRNA lithe DNA chain acting as template for RNA synthesis has the following order of bases, AGCTTCGA?

a. TCOAAGCT

b. UOGAAGCU

C. UCCAAGCU

d. LJGCUACCT

Correct Answer: C

The formation of stable hydrogen bonds depends on the distance between two strands, the size of the bases and geometry of each base. Stable pairings occur between guanine and cytosine and between adenine and thymine (or adenine and uracil in RNA). Three hydrogen bonds form between guanine and cytosine. Two hydrogen bonds form between adenine and thymine or adenine and uracil.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

184. _____ site of tRNA molecule bind with hydrogen bonds too mRNA molecule.

a. Anticodon

b. Codon

c. 5' end of the tRNA molecule

d. 3' end of the tRNA molecule

Correct Answer: A

The structure of the anticodon of tRNA helps to explain the degeneracy of the genetic code. Each tRNA has a three-base sequence called the anticodon which binds to a complementary triplet on the mRNA according to the base-pairing rules having hydrogen bonds.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

185. Amino acid selenocysteine (See) is incorporated into polypeptide chain during translation by

a, charging of Sec into tRNAser followed by incorporation through serine codon

b. charging of serine into tRNAser followed by modification of serine into selenocysteine and then

c. charging of Sec into tRNAsec and then incorporation through selenocysteine codon

d. charging of serine into tRNAser followed by modification of serine into selenocysteine and then incorporation through a specially placed stop codon

Correct Answer: D

Selenocysteine (Sec) is the major biological form of the element selenium, which in trace amounts is essential for human health. See is incorporated into polypeptides to form selenoproteins during translation. The 21^{st} amino acid is typically found in catalytic centers of selenoproteins where it plays a functionally essential role. Unlike most amino acids, Sec is universally synthesized on its cognate tRNA. During translation, selenocysteinyl-$tRNA^{sec}$ (sec-$tRNA^{sec}$) is delivered to the ribosome by a specific translation factor that requires a characteristic stem-loop structure in the mRNA to actively recode an inframe UGA from stop codon to Sec sense codon.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

186. Which among the following can be correct for wobble hypothesis?

a. An anticodon of rRNA can recognize more than one codon of mRNA.

b. An anticodon of tRNA can recognize more than one codon of mRNA.

e. An anticodon of mRNA can recognize more than one codon of tRNA.

d. An codon of tRNA can recognize more than one codon of mRNA.

Correct Answer: B

Accurate incorporation of amino acids during translation depends on correct "reading" of the genetic code specified by three-base codons. Because there are only 20 amino acids, it is obvious there is excess coding capacity among the 64 possible permutations of the triplet code. Naively, one might expect to find only a subset of the possible codon combinations in use by a particular organism to simplify the cellular machinery needed to translate all possible proteins. Thus, most amino acids are coded for more than one synonymous codon triplet. If one tRNA were required for each possible codon, this would require the cell to maintain over 60 different tRNA species to be able to translate all possible codons. In fact, many tRNAs specifically recognize more than one codon through non-Watson-Crick base pairings, commonly known as the 'wobble hypothesis'.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

187. What is the first event in the translation?

a. Binding of mRNA leader to the larger ribosomal unit.

b. Binding of mRNA leader to the smaller ribosomal unit.

c. Binding of mRNA leader to the polysomal core.

d. Binding of mRNA leader to the tRNA.

Correct Answer: B

The bacterial $70\mathrm{S}$ ribosome is composed of a large $50\mathrm{S}$ and a small $30\mathrm{S}$ subunit. It has three tRNA binding sites designated the aminoacyl (A), peptidyl (P) and exit (E) sites. Binding of $\mathrm{IF3}$ to the $30\mathrm{S}$ ribosomal subunit promotes dissociation of the ribosome into subunits and thus couples ribosome recycling and translation initiation. Initiation factor $\mathrm{IF1}$ binds specifically to the base of the A- site of the

30S ribosomal subunit and is thought to direct the initiator tRNA to the ribosomal P-site by blocking the A-site.

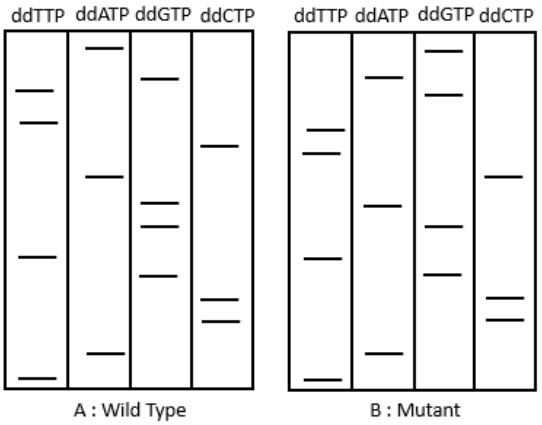
Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

188. Figures A and B respectively represent the dideoxy sequencing gels obtained for partial sequences from 5′ ends of a bacterial gene and its mutant (with a point mutation).



What type of mutation has occurred in the gene?

a. Nonsense

b. Missense

c. Frameshift

d. transversion

Correct Answer: C

A frameshift mutation (also called a framing error or a reading frame shift) is a genetic mutation caused by indels (insertions or deletions) of a number of nucleotides in a DNA sequence that is not divisible by three. Due to the triplet nature of gene expression by codons, the insertion or deletion can change the reading frame (the grouping of the codons), resulting in a completely different translation from the original. The earlier in the sequence the deletion or insertion occurs, the

more altered the protein. A frameshift mutation is not the same as a single-nucleotide polymorphism in which a nucleotide is replaced, rather than inserted or deleted. A frameshift mutation will in general cause the reading of the codons after the mutation to code for different amino acids. The frameshift mutation will also alter the first stop codon ("UAA", "UGA" or "UAG") encountered in the sequence. The polypeptide being created could be abnormally short or abnormally long, and will most likely not be functional.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

189. The ribosomes of polysome are same. How?

a. They all are involved in translating the same genetic code.

b. They all carry the genetic code within the core.

c. They all contain the nitrogen for synthesizing amino acids.

d. They all contain the essential amino acids.

Correct Answer: A

Ribosomes are sites for the meeting and binding of mRNA and transfer RNA (tRNA), they are the structures where amino acids transported by tRNA are united by peptide bonds forming polypeptide chains (proteins). Each mRNA molecule is simultaneously translated by many ribosomes, all reading the mRNA $5'$ to $3'$ and synthesizing the polypeptide from the N terminus to the C terminus. The complete mRNA/poly-ribosome structure is called a polysome.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

190. weaker bonds play major role in maintaining structural Integrity. Tertiary structure of protein is well balanced by H-bonds and sometimes by Ionic interactions. Covalent bonds on the other hand are difficult to break and hence stronger. It also needs higher energy to break. Then why would the proteins, amino acids in specific, not bond by weak Interactions, even though covalent bond formation is much difficult?

a. Weak bonds acts only in small distance.

b. Covalent bonds are rigid, do not allow for movement.

c. Weak bonds impose no restrictions on relative orientations.

d. Covalent bonds are much stronger, impose no restrictions for movement.

Correct Answer: C

Hydrogen bonding occurs when an atom of hydrogen is attracted by rather strong forces to two atoms instead of only one, so that it may be considered to be acting as a bond between them. Hydrogen bond strength is given by the weaker of the two interactions of the flanking atoms with the central hydrogen atom and is strongest when these interactions are equal. Hydrogen bond strength may be estimated theoretically from the quantum theory of atoms in molecules. Hydrogen bonding is characterized by its preferred dimensions, molecular orientation, approximate linearity and changes in infrared frequency and intensity.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

191. Which of the statement(s) is/are correct about spliceosomes?

P. They are composed of RNA sequences that signal for removal of Introns

Q. They recognize RNA sequences that signal for removal of introns.

R. They can produce different mRNA molecules by splicing at alternate site.

a. P and Q

b. P and R

c. Q and R

d. All of the above

Correct Answer: D

The spliceosome is a dynamic machine; it is assembled on pre-mRNA from separate components and parts enter and leave it as the splicing reaction proceeds. During the splicing reaction, recognition of the $5'$ splice junction, the branch point site and the $3'$ splice junction is performed largely through base-pairing between the snRNAs and the consensus RNA sequences in the pre-mRNA substrate. The removal of introns in mRNA is carried out by the splicing machinery spliceosome, a large assembly containing various small nuclear RNAs (snRNAs) that from complexes with proteins (snRNPs). Alternative splicing allows more than one protein to be produced from a gene and is an important regulatory step in determining which functional proteins are produced from gene expression.

Core Concept:

Topic:

Difficulty Level:

Complexity:

192. Khorana *et al* synthesised RNA with copolymer of UGUGUGUGUG...., it produced a peptide with alternative cysteine and valine. Which among the following are the codons for cysteine and valine?

a. UGU and GUG

b, UUG and GGU

c. GUG and UGU

d. UGG and GUU

Correct Answer: A

a) One letter Code – C

Three letter code – Cyc

Amino acid – Cysteine

Possible codons – UGC, UGU

b) One letter code – V

Three letter code – Val

Amino acid – Valine

Possible codons – GUA, GUC, GUG, GUU.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

193. What are the regions on the tRNA that are required for the specificity of the enzyme, aminoacyl-tRNA synthetase which carries the same amino acid as a specific aminoacyl-tRNA?

a. Anticodon and acceptor region

b. D loop, and acceptor region

c. Anticodon alone

d. The $\mathrm{T\psi C}$ loop and anticodon

Correct Answer: A

tRNA synthetases, better known as aminoacyl tRNA synthetases, play a major role in translation during protein synthesis. The translation of genetic information is mediated by adaptor molecules, tRNAs, which recognize a triplet on the mRNA through a complementarity region called an anticodon and carry a covalently attached amino acid corresponding to that triplet in the genetic code. The anticodon triplet in the loop at the bottom is complementary to the mRNA codon and will make base pairs with it. The acceptor stem at the top of the cloverleaf is the site where the amino acid will be attached at the $3'$ terminus of the tRNA. This stem always has the sequence $5'\ldots\mathrm{CCA\text{-}OH}\ldots3'$.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

194. The start sites of the proteins, in eukaryotes are identified by

a. Shine-Dalgarno sequences.

b. scanning from the $5'$ end of the mRNA for the first AUG.

c. the 'cap' structure of eukaryotic mRNA that overlaps with the first AUG.

d. the transcription start site.

Correct Answer: B

Recognition of the translation start site by the small ribosomal subunit in the eukaryotic preinitiation complex requires different types of factors than in prokaryotic cells. The mRNA-bound ribosome subunit travels along the $5'$-untranslated end of the mRNA until it reaches the first AUG codon that will serve as the start codon for the translation process. This process, known as scanning, requires energy (ATP) and additional initiation factors.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

195. All of the following statements about the $3'$ poly(A) tall of mRNA are true, except

a. it is transcribed from DNA sequence.

b. it is added to the primary transcript in the nucleus.

c. it is essential for protein synthesis.

d. None of the above

Correct Answer: A

While RNA Polymerase II is still transcribing downstream of the proper end of a gene, the pre-mRNA is cleaved by an endonuclease-containing protein complex between an AAUAAA consensus sequence and a GU-rich sequence. This releases the

functional pre-mRNA from the rest of the transcript, which is still attached to the RNA Polymerase. An enzyme called poly (A) polymerase (PAP) is part of the same protein complex that cleaves the pre-mRNA and it immediately adds a string of approximately 200 A nucleotides, called the poly (A) tail, to the $3'$ end of the just cleaved pre-mRNA. The poly (A) tail protects the mRNA from degradation, aids in the export of the mature mRNA to the cytoplasm and is involved in binding proteins involved in initiating translation.

Core Concept:

Topic:

Difficulty Level:

Complexity:

196. Aminoacyl -tRNA synthetase should be capable of recognizing which of the following?

a. A specific tRNA and a specific amino acid.

b. A specific rRNA and a specific amino acid.

c. A specific tRNA and the $40S$ ribosomal subunit.

d. A specific amino acid and the $40S$ ribosomal subunit.

Correct Answer: A

The activation reaction is catalysed by specific aminoacyl-tRNA synthetases, which are also called activating enzymes. The first step is the formation of an aminoacyl adenylate from an amino acid and ATP. This activated species is a mixed anhydride in which the carboxyl group of the amino acid is linked to the phosphoryl group of AMP; hence, it is also known as aminoacyl-AMP. The next step is the transfer of the aminoacyl group of aminoacyl-AMP to a particular tRNA molecule to form aminoacyl-tRNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

197. How do the suppressor tRNAs differ from normal tRNAs?

a. They are smaller in size.

b. They do not carry an amino acid.

c. They do not obey regular genetic code.

d. Both B and C

Correct Answer: C

tRNA suppressors can arise by mutations in a gene encoding a tRNA. For example, the wild-type *tyr T* gene encodes a tRNA that recognizes a $5'$ UAC $3'$ codon in the mRNA and inserts tyrosine into the growing polypeptide chain. A mutation in the gene changes the anticodon so that it recognizes the stop codon $5'$ UAG $3'$ in the mRNA and instead of terminating, inserts a tryrosine at that position in the polypeptide chain.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

198. Choose the correct order of the steps in protein synthesis.

1. A peptide bond is formed.

2. The small ribosomal subunit is loaded with initiation factors, mRNA and initiation aminoacyl-tRNA.

3. The intact ribosome slides forward three bases to read a new codon.

4. The primed small ribosomal subunit binds with the large ribosomal subunit.

5. Elongation factors deliver aminoacyl-tRNA to bind to the A site.

a. 1, 2, 5, 4, 3

b. 2, 3, 4, 5, 1

c. 4, 5, 1, 2, 3

d. 2, 4, 1, 3, 5

Correct Answer: D

In most cases, the first AUG codon in a eukaryotic mRNA is used as the initiation codon, thus the small subunit locates the correct initiation codon simply by scanning along the mRNA starting at the $5'$ end until it reaches the first AUG codon.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

199. Which of the following characteristic of eukaryotic gene is also commonly true for most prokaryotic genes?

a. Genes are packaged into nucleosomes in chromatin

b. Many genes contain introns

c. Both A and B

d. The initiation codon for protein synthesis is usually AUG

Correct Answer: D

The protein synthetic machinery must select the appropriate starting points for mRNA reading and peptide bond formation. AUG is usually used as the starting codon and essentially all proteins begin with a methionine. AUG is also the codon for methionine that occurs in the interior of a protein as well. Both prokaryotes and eukryotes have a standred AUG codon as an initiation codon.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

200. siRNa(s) interfere at what site?

a. At the transcriptional level.

b. At the post-transcriptional level

c. At the DNA replication level

d. At the translational level

Correct Answer: B

Small interfering RNAs (siRNAs) act through RNA interference (RNAi) pathways to silence gene expression either at the transcriptional or post-transcriptional level. Small interfering RNA (siRNA), sometimes known as short interfering RNA or silencing RNA, is a class of double-stranded RNA molecules, $20-25$ base pairs in length. They interfere with the expression of specific genes with complementary nucleotide sequence and also act in RNAi-related pathways, *e.g.*, as an antiviral mechanism or in shaping the chromatin structure of genome.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

201. The factors that are needed for the translation terminiation at an amber codon (UAG) and release of the finished polypeptide chain are

a. $\mathrm{RF2, RF3, EF-5}$ and RRF

b. $\mathrm{RF1, RF3, EF\text{-}Tu}$ and RRF

c. $\mathrm{RF1, RF3, EF\text{-}G}$ and RRF

d. $\mathrm{RF2, RF3, EF\text{-}P}$ and RRF

Correct Answer: C

Chain termination requires participation of release factors $\mathrm{RF\text{-}1, RF\text{-}2}$ and $\mathrm{RF\text{-}3, RF\text{-}3}$ is small GTP-binding protein. $\mathrm{RF\text{-}1}$ and $\mathrm{RF\text{-}2}$ recognize and bind to STOP codons. One or the other binds when a stop codon is reached. $\mathrm{RF\text{-}3}$- GTP facilitates binding of $\mathrm{RF\text{-}1}$ or $\mathrm{RF\text{-}2}$ to the ribosome. Once the release factors occupy the A site on the ribosome, the ribosomal Peptidyl Transferase catalyzes

transfer of the peptidyl group to water (hydrolysis). Hydrolysis of GTP on $\mathrm{RF\text{-}3}$, to $\mathrm{GDP} + \mathrm{P_i}$, causes a conformational change that results in dissociation of release factors. A ribosomal recycling factor (RRF) is required, with EF-G-GTP and $\mathrm{IF\text{-}3}$, for release of uncharged tRNA from the P site and dissociation of the ribosome from mRNA with separation of the two ribosomal subunits.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

202. The pair that is correctly matched with regard to codon and Its corresponding amino acid is

a. AAA- Lysine

b. UUA- Valine

c. CCC- Alanine

d. None of the above

Correct Answer: A

Lysine is an α- amino acid with the chemical formula $\mathrm{HO_2CCH(NH_2)(CH_2)_4NH_2}$. It is an essential amino acid for humans. Lysine's codons are AAA and AAG.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

203. Which among the following sequence is correct regarding the 'central dogma'?

a. DNA>RNA>Translation>Transcription

b. Transcription>Translation>Protein sorting>DNA

C. DNA>Transcription>RNA>Translation

d. DNA>Translation>-RNA>Transcription

Correct Answer: C

The central dogma of molecular biology describes the flow of genetic information in cells from DNA to messenger RNA (mRNA) to protein. It states that genes specify the sequence of mRNA molecules, which in turn specify the sequence of proteins. Because the information stored in DNA is so central to cellular function, the cell keeps the DNA protected and copies it in the form of RNA. An enzyme adds one nucleotide to the mRNA strand for every nucleotide it reads in the DNA strand. The translation of this information to a protein is more complex because three mRNA nucleotides correspond to one amino acid in the polypeptide sequence.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

204. The reaction,

Amino acid + ATP $\rightarrow$ Aminoacyl-AMP + P-P is a part of

a. Amino acid translocation

b. Amino acid activation

c. Amino acid assimilation

d. None of the above

Correct Answer: B

During amino acid activation the amino acids (aa) are attached to their corresponding tRNA. The coupling reactions are catalysed by a group of enzymes called aminoacyl-tRNA synthetases (named after the reaction product aminoacyl-tRNA or aa-tRNA). The coupling reaction proceeds in two steps;

i. aa + ATP aa-AMP + PP, (pyrophosphate)

ii. aa-AMP + tRNA aa-tRNA + AMP

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

205. What is the mode of action of Gentamycin?

a. It bind to the $50S$ subunit of ribosome.

b. It bind to the $70S$ subunit of ribosome.

c. It bind to the $80S$ subunit of ribosome.

d. It bind to the $30S$ subunit of ribosome.

Correct Answer: D

Gentamicin is a broad spectrum aminoglycoside antibiotic. Aminoglycosides work by binding to the bacterial $30S$ ribosomal subunit, causing misreading of t-RNA, leaving the bacterium unable to synthesize proteins vital to its growth.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

206. What is the mode of action of Linezolid?

a. It interfere at the initiation stage.

b. It interfere at the elongation stage.

c. It interfere at the termination stage.

d. All of the above

Correct Answer: A

Linezolid acts at the initiation stage, probably by preventing the formation of the initiation complex, although the mechanism is not fully understood.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

207. Inhibition of translation leads to

a. neutrilization of siRNA effect.

b. synthesis of mRNA during stress conditions.

c. Both A and B

d. None of the above

Correct Answer: B

Post-transcriptional control mechanisms play an important role in regulating gene expression during cellular responses to stress. For example, many stresses inhibit translation and at least some stresses inhibit mRNA turnover in yeast and mammalian cells.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

208. Amino acids lysine, proline, glycine and phenylalanine, are specified by the codons AAA, CCC, CGG and UUU respectively. The DNA sequences that would specify the peptide pro-gly-lys-phe if present in the template strand would be

a. 3′-CCCGGGAAATTT-5′

b. 3′-CCCGGGAAAUUU-5′

c. 3′-GGGCCCTTTAAA-5′

d. 5′-GGGCCCUUUAAA-3′

Correct Answer: C

Every amino acid has a particular code that is not shared by any other amino acid. The amino acid proline, glycine, lysine and phenylalanine codes with GGG, CCC, TTT and AAA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

209. What is the translational regulatory protein?

a. It binds to DNA and prevents translation.

b. It binds to mRNA and prevents translation.

c. It binds to rRNA and prevents translation.

d. It binds to tRNA and prevents translation.

Correct Answer: B

Mechanism of translational regulation in eukaryotic cells, resulting in global effects on overall translational activity rather than on the translation of specific mRNAs, involves modulation of the activity of initiation factors, particularly eIF-2. eIF-2 (complexed with GTP) binds to the initiator methionyl tRNA, bringing it to the ribosome. The subsequent release of eIF-2 is accompanied by GTP hydrolysis, leaving eIF-2 as an inactive GDP complex.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

210. The mismatch repair activity of E. *coli* repairs misincorporated bases which are not removed by the proofreading activity of DNA polymerase. However, while doing

so, it has to decide which strand of the DNA is newly synthesized and which one is parental. Mismatch repair system does It by which one of the. following ways?

a. It recognizes nearby GATC sequence.

b. It recognizes any nearby palindromic sequence.

c. It recognizes a specific repetitive sequence.

d. It recognizes the hemi-methylated CIATC sequence nearby.

Correct Answer: D

DNA mismatch repair is a method for recognizing and repairing erroneous insertion, deletion and mis-incorporation of bases that can arise during DNA replication and recombination and repair. In E . *coli*, DNA is methylated at the $\mathrm{N6}$ position of adenine residues in GATC sequences, but the newly replicated daughter strand is transiently unmethylated in these sequences. It is these hemimethylated GATC sequences that allow repair to be targeted at the newly synthesized daughter strand, where the incorrect base is located.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

211. In prokaryotic mRNA, a particular base sequence (AGGACGU) exists near the AUG start codon. What is this sequence called, which is also referred to as the ribosome binding site?

a. Promoter sequence

b. Shine Dalgarno sequence

c. Kozak's Consesus sequence

d. None of the above

Correct Answer: B

The Shine Dalgarno sequence is a section of nucleotides on a prokaryotic mRNA molecule upstream of the translational start site, that serves to bind to ribosomal

RNA and thereby bring the ribosome to the start codon on the mRNA. It is complementary to the $3'$ end of $16S$ rRNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

212. What is the difference in the products translated from a tricistronic mRNA molecule by the ribosomes of prokaryotes and eukaryotes?

a. The prokaryotic ribosome translates only one cistron while the eukaryotic ribosome translates all cistrons.

b. The eukaryotic ribosome translates only one cistron while the prokaryotic ribosome translates all cistrons.

c. The eukaryotic ribosome will produce one polyprotein instead of three smaller proteins.

d. None of the above

Correct Answer: B

In eukaryotes, reinitiation of polypeptide synthesis following an encounter of a ribosome with a stop codon does not occur. Eukaryotic mRNA is always polycistronic. The prokaryotic ribosome translates all of the cistrons, but the eukaryotic ribosome translates only one cistron the one nearest to the $5'$ terminus of the mRNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

213. Which statement is true regarding Type 1 proteins (plasma membrane)?

a. They have a cleavage N-terminal signal sequence and a hydrophobic stop transfer sequence.

b. They have cleavage N-terminal signal sequence that doubles and the membrane anchoring sequence.

c. They have a multiple signal sequence and a hydrophobic stop transfer sequence.

d. They have a multiple signal sequence that doubles as the membrane anchoring sequence.

Correct Answer: A

Plasma membrane proteins are also synthesized on the RER but become inserted into the RER membrane (and hence ultimately the plasma membrane) rather than being released into the RER leumen. The plasma membrane proteins may pass once through the plasma membrane (Type I and Type II integral membrane proteins) or may loop back and forth, passing through many times. The orientation of the protein in the membrane is determined by topogenic sequences within the polypeptide chain. Type I proteins have a cleaved N terminal signal sequence and a hydrophobic stop transfer sequence.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

214. What will happen if the σ- factor of a strain of bacteria is non-functional?

a. These bacteria will be unable to assemble RNA polymerase onto the DNA strand.

b. These bacteria will be unable to identify and tightly bind promoter elements.

c. These bacteria will be unable to convert a closed complex to an open complex.

d. These bacteria will be unable to synthesize RNA once an open complex is formed.

Correct Answer: B

A sigma-factor (σ- factor) is a protein needed only for initiation of RNA synthesis. It is bacterial transcription initiation factor that enables specific binding of RNA polymeraseto gene promoters. The specific sigma factor used to initiate transcription of a given gene will vary, depending on the gene and on the environmental signals needed to initiate transcription of that gene. Hence, if the

bacterial sigma factor is non-functional then the bacteria will be unable to identify and tightly bind promoter elements.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

215. The addition of a new amino acid residue into a partially completed peptide chain on the ribosome involves

a. the peptide transfer to link *via* its N- terminal end to the $-\mathrm{COOH}$ of the amino acid.

b. the amino acid transfer to link *via* its $-\mathrm{NH_2}$, group to the C- terminal end of the peptide.

c. the peptide transfer to link *via* its C- terminal end to the $-\mathrm{NH_2}$ of the amino acid.

d. the amino acid transfer to link *via* its $-\mathrm{COOH}$ group to the N- terminal end of the peptide.

Correct Answer: C

Peptides are synthesized from N- terminal to C- terminal, so an incoming amino acid is added via its $-\mathrm{NH_2}$ group to form a peptide bond with the free $-\mathrm{COOH}$ at the C- terminal end of the peptide. Both the amino acid and the peptide are linked to t-RNAs *via* their $-\mathrm{COOH}$ groups and have free $-\mathrm{NH_2}$ groups. They are bound at adjacent sites on the ribosome and perhaps counter-intuitively, it is the peptide which is transferred to link to the amino acid. It is released from its t-RNA freeing its $-\mathrm{COOH}$ group. This can now link to the free $-\mathrm{NH_2}$ group of the amino acid, which remains bound to its t-RNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

216. It takes 40 minutes for a typical E. *coli* cell to completely replicate its chromosome. Simultaneous to the ongoing replication, 20 minutes of a fresh round of replication is completed before the cell divides. What would be the generation time of E. *coil* growing at $37^{o}\mathrm{C}$ in complex medium?

a. 20 minutes

b. 40 minutes

c. 60 minutes

d. 30 minutes

Correct Answer: A

In a rich supplemented medium the doubling time or generation time for most E .coli, at $37°\mathrm{C}$ is between 20 to 40 minutes. Now, it is given that the fresh round of replication took 20 minutes. That means the generation time of the bacteria is 20 minutes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

217. Which among the following is the correct constitution of a eukaryotic ribosome?

a. $70\mathrm{S}$ overall with a $50\mathrm{S}$ and a $30\mathrm{S}$ subunit

b. $80\mathrm{S}$ overall with a $60\mathrm{S}$ and a $20\mathrm{S}$ subunit

c. $80\mathrm{S}$ overall with a $60\mathrm{S}$ and a $40\mathrm{S}$ subunit

d. None of the above

Correct Answer: C

With very large structures such as a ribosome, their sizes are measured in terms of the rate at which they sediment in an ultracentrifuge – expressed as Svedberg units or S values. (An ultracentrifuge spins so fast and therefore generates such a high G

force that large molecules in solution move towards the bottom of the tube.) A ribosome consists of two subunits. An E. *Coli* ribosome is $70\mathrm{S}$, the subunits being $50\mathrm{S}$ and $30\mathrm{S}$ (the S values are not simply additive, since S depends both on mass and shape). Eukaryotic ribosomes are somewhat larger, $80\mathrm{S}$ overall, with a $60\mathrm{S}$ and a $40\mathrm{S}$ subunit.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

218. Which of the following is a common feature of Nuclear Localization Signals?

a. They are rich in acidic amino acid residues and are located at the C-terminus of the protein.

b. They are rich in basic amino acid residues and are located at the C-terminus of the protein.

c. They are rich in basic amino acid residues and may be located anywhere in the protein sequence.

d. They are rich in acidic amino acid residues and may be located anywhere in the protein sequence.

Correct Answer: C

Large ($> 40,000$ Daltons), nuclear-localized proteins need a nuclear localization signal (NLS). Many nuclear proteins contain NLSs that are rich in basic arginine and lysine residues, which may be located anywhere in the polypeptide chain. The 'prototype' of this class of NLS is that found in a protein known as the 'T antigen' of the $\mathrm{SV40}$ virus, which is transported into the nucleus as part of the infective process. The T antigen NLS is PKKKRKV (using single-letter abbreviations of amino acids). Other members of this class of basic NLS are bipartite; an example is found on nucleoplasmin, a chromatin assembly protein. The sequence of this is KR, followed by a 10 amino acid spacer, then by KKKK. Mutation of an NLS results in a normally nuclear-located protein remaining in the cytosol, whereas artificial addition of such a signal to a normally cytosolic protein results in it being transported into the nucleus.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

219. Which of the following names is appropriate for the sequence $5'$-G/ANNAUG-$3'$ in a mammalian mRNA?

a. Shine-Dalgamo sequence

b. Kozak sequence

C. Internal ribosome entry sites

d. Translation termination site

Correct Answer: B

The signals that identify initiation codons are different in prokaryotic and eukaryotic cells. Initiation codons in bacterial mRNA are preceded by a specific non-translated leader sequence called the Shine-Dalgarno sequence. This leader sequence seen in the mRNA aligns with a complementary sequence of the $16S$ ribosomal RNA. However, eukaryotic mRNAs have no leader sequence equivalent to Shine-Dalgarno sequence. Instead the ribosomes recognize the initiation codons by scanning from the $5'$ terminus downstream until they encounter an AUG initiation codon. The AUG initiation codon in eukaryotes is embedded in a short sequence called the Kozak sequence. This is called the scanning model for initiation. The sequences surrounding the AUG initiation codon for cellular mRNAs is important in determining the efficiency of translation. The consensus sequence, G/ANNAUG was identified by Marilyn Kozak, where N is any nucleotide. The mRNAs bearing sequences closest to this are most readily recognized by ribosomes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

220. $\mathrm{Hsp60}$ (GroEL/ GroES) In protein folding helps in

a. providing a sequestered chamber where protein folding can occur without interference from surrounding molecules.

b. directing the three dimensional folding of a protein.

c. Both A and B

d. None of the above

Correct Answer: A

Proteins fold spontaneously into their tertiary structures. This folding is not directed, but it can be assisted by chaperones and chaperonins. The simplest way this can happen is that Hsp70 chaperone proteins bind to hydrophobic areas on the peptide emerging from the ribosome, holding it in extended form until its synthesis is complete. It is then released and can fold spontancously. If Hsp70 did not do this the protein would fold as it emerged from the ribosome and incorrect structures could result. Some proteins require rather more assistance than this to fold properly and chaperonins, like Hsp60 in eukaryotes and GroEL/GroES in prokaryotes and mitochondria, provide a chamber which can accommodate the unfolded protein, giving it a space where it can fold, out of contact with the surroundings.

Hsp60 cannot unfold denatured proteins and give them the opportunity to refold but another type of chaperonin, called Hsp100 in eukaryotes and ClpB in prokaryotes, may be able to do this.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

221. Proteins enter peroxisomes

a. in a folded manner, using an N- terminal or internal. signal sequence.

b. in folded manner, using a C- terminal or internal signal sequence.

c. in an unfolded manner, using a, C- terminal or internal signal sequence.

d. in an unfolded manner, using a N- terminal or internal signal sequence

Correct Answer: B

Peroxisomal proteins are fully folded in the cytoplasm and enter the organelle in folded form. The most common signal sequence which directs proteins to peroxisomes is a C- terminal Ser-Lys-Leu tripeptide but less commonly a nonapeptide (nine amino acid residues), located internally near the N- terminus can also be used as an 'address' directing proteins to peroxisomes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

222. Which among the following statement is true regarding the transposons?

a. They could be inserted into DNA by homologous recombination.

b. They cannot be transferred by phage mediated transduction.

c. They contain the equivalent of insertion (IS) elements.

d. They could be easily inserted into plasmids but not into the bacterial chromosomes

Correct Answer: C

Transposable elements play a role in the biology of organisms. They cause mutations by insertion into genes and affect the regulation of genes by inserting near promoters. Insertion of IS elements near the promoter region of the bgl operon, which encodes proteins participating in β- glucosidase metabolism, activates transcription in this normally "cryptic" operon. There are numerous other examples of insertions that turn on gene expression. Insertion elements provide portable regions of homology that can serve as substrates for recombination enzymes, creating deletions, duplications and inversions.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

123. The lac operon in E. Coli, is controlled by both "the lac repressor and the catabolite activation protein CAP. In an in vivo experiment with lac operon, the following observations are made

A. cAMP levels are high

B. Repressor is bound with allolactose

C. CAP is Interacting with RNA polymerase

Which one of the following conclusions is most appropriate based on the above observations?

a. Glucose and lactose are present.

b. Glucose is present and lactose is absent

c. Both are absent.

d. Glucose is absent and lactose is present.

Correct Answer: A

The lac operon (lactose operon) is an operon required for the transport and metabolism of lactose in E *.coli* and some other enteric bacteria. It has three adjacent structural genes, lacZ, lacy and lacA. The genes encode β- galactosidase lactose permease and galactoside O-acetyl transferase respectively. In its natural environment, the lac operon allows for the effective digestion of lactose. Lactose permease, which is embedded in the cytoplasmic membrane, transports lactose into the cell. β- galactosidase, a cytoplasmic enzyme, subsequently cleaves lactose into glucose and galactose. However, it would be wasteful to produce the enzymes when there is no lactose available or if there is a more preferable energy source available, such as glucose. Gene regulation of the lac operon was the first genetic regulatory mechanism to be understood clearly, so it has become a foremost example of prokaryotic gene regulation. It is often discussed in introductory molecular and cellular biology classes at universities for this reason.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

224. In the strain that have a genotype _____ synthesis of β- galactosidase will be constitutive.

a. $I^{+}Z^{*}Y^{-}$

b. $I^{-}Z^{+}Y^{*}$

c. $I^{*}Z^{-}Y^{+}$

d, $I^{*}Z^{+}Y^{-}$

Correct Answer: B

If there is no lacI gene (that code for the repressor) then there is no formation or the availability of repressor gene that could repress the operator. Hence, the other genes *i.e*. Lac Z, Lac Y and Lac A will be active and there will be the consecutive production of beta-galactosidase, permease and transacetylase.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

225. The partial diploids that will express β- galactosidase constitutively is

a. $F' lacO^{c} lacZ^{+} / lacO^{+} lacZ^{*}$

b. $F' lacI^{-} lacZ^{+} / lacI^{+} lacZ^{+}$

c. Both A and B

d. None of the above

Correct Answer: A

A mutant of E. *Coli* cannot be induced to synthesize large amount of β-galactosidase or β- galactoside permease when lactose is added to the medium. However, a partial diploid formed from this mutant and an episome bearing the genes $lacI P^{+} Oc Z^{-} Y^{+}$ synthesizes large amounts of lactose permease in the presence or absence of lactose. The partial diploid synthesizes large amounts of β-galactosidase only in the presence of lactose.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

226. What will be the result of mutation in *LacI,* repressor encoded by *LacI* gene that regulate the lac operon negatively?

a. Constitutive phenotype that will be recessive.

b. Uninducible phenotype that will be dominant.

C. Constitutive phenotype that will be dominant.

d. Uninducible phenotype that will be recessive.

Correct Answer: B

Lac repressor is the negative control where the repressor blocks open complex formation. *LacI* is a non-functional repressor mutation that has catastrophic effects on the protein's function. I^-/I^- merodiploid is an inducible phenotype: I^- is recessive to wild type.

Core Concept:

Topic:

Difficulty Level:

Complexity:

227. How do the lactose enter the cells to induce lac operon, in cells that have not been previously exposed to lactose?

a. IPTG would induce the expression of lac operon instead of lactose.

b. Lactose would enter by diffusion without the need for permease.

c. Other transport protein facilitate the entry of lactose.

d. Basal level expression of lac operon, leading to the low level synthesis of permease.

Correct Answer: D

The lac operon consists of three linked structural genes that encode enzymes of lactose utilization, plus adjacent regulatory sites. The three structural genes $-z, y,$ and $a-$ encode β- galactosidase, β- galactoside permease – also called permease – (a transport protein) and thiogalactoside transacetylase (an enzyme with a relatively obscure function), respectively. The concentration of β- galactosidase is very low in cells normally (basal level); but when lactose is the sole carbon source, the concentration of the enzyme is elevated markedly (a process called induction). After all the lactose is metabolized, β- galactosidase returns to a very low level in the cell.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

228. What is the possible cause that a lysogen of *E. coli* becomes resistant to further infection by bacteriophage lambda?

a. *E. coli* no longer contains receptors on cell surface.

b. One copy of phage is already present in the cell.

c. The presence of repressor in the cell.

d. *E. coli* is dead.

Correct Answer: C

Bacteriophages, the viruses that parasitize and kill bacteria, can be used in several different types of genetic analysis. A lysogenic bacterium or lysogen, is resistant to subsequent infection, because an "immunity" is conferred by the presence of the prophage. The lysogenic state can be transmitted genetically through many bacterial generations. The model of a phage-directed cytoplasmic repressor nicely explains the immunity of the lysogenic bacteria, because any superinfecting phage would immediately encounter a repressor and be inactivated.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

229. _____ genesare defective in patients suffering from severe combined immunodeficiency syndrome (SCID).

a. CFTR

b. Adenosine deaminase

c. Ribonucleotide reductase

d. All of the above

Correct Answer: B

SCID is caused by mutations in a gene that encodes an enzyme called adenosine deaminase (ADA). ADA is essential for the metabolic function of a variety of body cells but especially T-cells. ADA deficiency is the second most common cause of SCID, accounting for 15% of cases. Babies with this type of SCID have the lowest total lymphocyte counts of all and T, B and NK-lymphocyte counts are all very low. This form of SCID is inherited as an autosomal recessive trait.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

230. Which of the following statements are correct for the transposable elements?

P. Barbara McClintock discovered the autonomous and non-autonomous, transposable elements in Maize.

Q. Variations in flower pigmentation in *Antirhinum* are due to the presence of transposable elements Ac and Ds.

R. The Ac transposable element is 4563 bp long and has an 11 bp Inverted repeats.

S. Ds produces the transposase and mobilize the Ac elements.

a. Q, S

b. P, Q

c. P, R

d. P, Q, R and S

Correct Answer: C

For much of the 20^{th} century, genes were considered to be stable entities arranged in an orderly linear pattern on chromosomes. But Barbara McClintock, in the late 1940s, challenged the existing concepts of what genes were capable by discovering that some genes could be mobile. She studied the chromosome breakage in maize which led her to discover a chromosome-breaking locus that could change is position within a chromosome. She went on to discover other such mobile elements, now known as transposons. Each group of TEs contains autonomous and non-autonomous elements. Autonomous elements have ORFs that encode the products required for transposition. In contrast, non-autonomous elements do not encode transposition proteins but are able to transpose because they retain the *cis* sequences necessary for transposition.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

231. Why lysogenic cycle is more beneficial to a virus than lytic cycle under certain circumstances?

a. The Lysogenic cycle prevent local extinction of host while still retaining infectious potential.

b. By integrating with the bacterial chromosomes, the genetic instructions for the virus become refreshed after one or more replication events during binary fission.

c. Lysogenic infection cycles do not harm their host cells, so they can produce virus particles indefinitely.

d. Lysogeny causes more mutations to occur in the virus, creating more variants upon which natural selection can operate.

Correct Answer: A

Lysogeny, or the lysogenic cycle, is one of two cycles of viral reproduction (the lytic cycle is the other) but lysogenic cycle is more beneficial to a virus than lytic cycle. The lysogenic cycle prevent local extinction of host while still retaining infectious potential. In contrast the lysogenic cycle does not result in immediate lysing of the host cell. Their viral genome will integrate with host DNA and replicate along with it fairly harmlessly, or may even become established as a plasmid. The virus remains dormant until host conditions deteriorate, perhaps due to depletion of nutrients; then, the endogenous phages (known as prophages) become active. At this point they initiate the reproductive cycle, resulting in lysis of the host cell. As the lysogenic cycle allows the host cell to continue to survive and reproduce, the virus is reproduced in all of the cell's offspring. An example of a bacteriophage known to follow the lysogenic cycle and the lytic cycle is the phage lambda of E. *Coli*.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

232. The negatively controlled lactose operon in E. *coli* can be best described, by which among the following statement?

a. An inducer (lactose) binds to the operator, thus enhancing transcription and translation of β-galactosidase, permease and transacetylase genes.

b. An inducer (lactose) alters the repressor protein and uncovers the operator and promoter, allowing simultaneous transcription and translation of β-galactosidase, permease and transacetylase.

c. The repressor (lactose) alters the operator protein and uncovers the promoter, allowing simultaneous transcription and translation of β- galactosidase, permease and transacetylase.

d. The repressor (lactose) alters the catabolic repression protein and uncovers the operator and promoter, allowing simultaneous transcription and translation of β-galactosidase, permease and transacetylase.

Correct Answer: B

Lactose can be used as the sole source of carbon by E . Coli. Three genes are required for lactose utilization, β- galactosidase (lac Z, cleaves lactose to Gal and Glc), galactoside permease (lac Y, transports Lac into the cell) and thiogalactoside transacetylase (lac A, function unknown). These genes follow one another on the DNA and have 1 promoter region. On transcription and translation, one long poly-protein is made, which is cleaved post-translationally to form the individual proteins. A gene cluster, including promoter and any regulatory DNA sequences is called an operon, for example, the Lac operon. In this case, transcription from the operon is induced in response to a molecular signal – *i.e*. the presence of lactose or allolactose. Lactose binds to an allosteric site on the repressor protein causing a conformational change due to which the repressor can no longer bind to the operator region and falls off. Hence, the RNA polymerase can then binds to the promoter and transcribe the lac genes.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

233. E . *coil* make a protein called Methionine. The met (methionine) operon in E . coli responds to a repressor protein which in itself is

a. encoded by the other genes.

b. turned off when bound to methionine.

c. turned on when bound to methionine.

d. None of the above

Correct Answer: C

Each of the MetJ (methionine repressor) dimer contains two binding sites for the cofactor S-adenosyl methionine (SAM), a product of biosynthesis of methionine. If SAM is present, it getsbind to MetJ protein which further increases its affinity for its cognate operator site that halts transcription of genes involved in methionine synthesis. And if SAM concentration is low, there pressor dissociates from the operator site, allowing more methionine to be produced.

Core Concept:

Topic:

Difficulty Level:

Complexity:

234. Jacob and Mound conducted many experiments on the lac operon. In one, they had a strain that expressed the lac operon in the absence of lactose. Would this strain express the lac operon in the presence of glucose?

a. Yes, because the strain lacks functional lacI.

b. Yes, as the strain lacks functional lacZ.

c. Yes, because the operator is functional.

d. No, as the cAMP levels would be quite low.

Correct Answer: D

The glucose catabolite modulates the level of an important cellular constituent cyclic adenosine monophosphate (cAMP). When glucose is present in high concentrations, the cell's cAMP concentration is low; as the glucose concentration decreases, the cellular concentration of cAMP increases correspondingly. The high concentration of cAMP is necessary for activation of the *lac* operon.

Core Concept:

Topic:

Difficulty Level:

Complexity:

235. Attenuation is a mechanism involved in the regulation off tryptophan operon in E. *coli* When tryptophan levels are high in the cell, region 2 of the trpL is blocked from pairing with region 3. This allows the pairing of region 3 and 4 leading to the formation a rho-independent terminator. What would be the structure of trpL region in E. *coli* cells. Where protein synthesis has been Inhibited?

a. Region 2 pairs with region 3 allowing transcription of structural genes.

b. Region 1 and 2 will pair, allowing 3 and 4 to pair leading to attenuation.

C. There is no pairing in the trpL region and transcription of structural gene occurs.

d. Regions 2 and 3 will pair leading to attenuation.

Correct Answer: B

Attenuation (in genetics) is a proposed mechanism of control in some bacterial operons which results in premature termination of transcription and which are based on the fact that, in bacteria, transcription and translation proceed simultaneously. When there is a high level of tryptophan in the region, it is inefficient for the bacterium to synthesize more. When the RNA polymerase binds and transcribes the trp gene, the ribosome will start translating. (This differs from eukaryotic cells, where RNA must exit the nucleus before translation starts.) The attenuator sequence, which is located between the mRNA leader sequence ($5'$ UTR) and trp operon gene sequence, contains four domains, where domain 3 can pair with domain 2 or domain 4. The attenuator sequence at domain 1 contains instruction for peptide synthesis that requires tryptophans. A high level of tryptophan will permit ribosomes to translate the attenuator sequence domains 1 and 2 allowing domains 3 and 4 to form a hairpin structure, which results in termination of transcription of the trp operon. Since the protein coding genes are not transcribed due to rho independent termination, no tryptophan is synthesised. In contrast, a low level of tryptophan means that the ribosome will stall at domain 1, causing the domains 2 and 3 to form a different hairpin structure that does not signal termination of transcription. Therefore the rest of the operon will be transcribed and translated, so that tryptophan can be produced. Thus, domain 4 is an attenuator. Without domain 4, translation can continue regardless of the level of tryptophan. The attenuator sequence has its codons translated into a leader peptide, but is not part of the trp operon gene sequence. The attenuator allows more time for the attenuator sequence domains to form loop structures, but does not produce a protein that is used in later tryptophan synthesis.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

236. _____ is found in an inducible system.

a. A repressor protein, which is bound to DNA in the absence of any other factor

b. A repressor protein, which is bound to DNA in the presence of a co repressor

c. An activator protein, which is bound to DNA in the absence of any other factor

d. An activator protein, which is bound to DNA only in the absence of an inhibitor

Correct Answer: A

Positive control of gene expression is illustrated by the transcriptional activator, catabolite gene activator protein (CAP). CAP activates transcription of the lac operon, in addition to many other inducibleoperons. The lac repressor and CAP are examples of regulators of initiation of transcription. Although most regulators act at this level, some act at the level of elongation of the mRNA, after transcription has started.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

237. A certain gene contains the double-stranded sequence

5′- ATGTTTAGCGCC -3′

3′- TACAAATCGCGG -5′

If the top strand is the sense strand and codes for an mRNA whose sequence begins 'ATG', which of the following would be the sequence of the corresponding segment of antisense RNA?

a. 5′- AUGUUUAGCGCC -3′

b. 5′- CCGCGAUUUGUA -3′

c. 5′- GGCGCUAAACAU -3′

d. 5′- UACAAAUCGCGG -3′

Correct Answer: C

An antisense RNA has the complementary sequence to mRNA. In the example, the coding sequence in the DNA is the top strand starting ATG (which is the start codon) so the complementary sequence would be the RNA equivalent of the bottom DNA

strand. U takes the place of T in RNA and all single-stranded molecules are written $5'$-$3'$ so the sequence of the complementary RNA would be $5'$- GGCGCUAAACAU -$3'$.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

238. Why is it beneficial to incorporate A-T residues towards the $5'$ region of the antisense sequence of the target mRNA, while G-C residues towards the $5'$ region of the sense sequence of the target mRNA, during shRNA sequence designing?

a. A-T residues confer more thermodynamic instability than G-C residues.

b. A-T residues confer more thermodynamic instability than G-C residues.

c. G-C residues confer more thermodynamic instability than A-T residues.

d. G-C residues confer more thermodynamic instability than A-T residues.

Correct Answer: B

Thermodynamic instability dictates which $5'$ strand of the processed shRNA duplex becomes incorporated into the RISC complex as the guide strand. We require the antisense sequence to the mRNA to become the guide strand in the RISC. Therefore, the use of less-stable A-T residues at the end of the shRNA duplex containing the $5'$ region of the antisense strand, and the use of more-stable G-C residues at the end of the shRNA duplex containing the $5'$ region of the sense strand, helps to promote loading of the antisense strand into the RISC.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

239. The two RNAI pathways within the eukaryotic cell can be best described as

a. siRNA-mediated gene silencing that represents a cell defence mechanism against exogenous dsRNA; miRNA-mediated gene silencing which is an integral gene expression regulation process.

b. miRNA-mediated gene silencing that represents a backup pathway for siRNA-mediated gene silencing be unsuccessful at silencing the target dsRNA.

c. miRNA and siRNA-mediated gene silencing represent evolutionary-independent pathways which confer identical silencing mechanisms on the target dsRNA.

d. siRNA and miRNA-mediated gene silencing pathways must both be active to successfully silence the target dsRNA.

Correct Answer: A

Whilst experimental rationale is the major determinant for whether siRNA or shRNA technology is utilised; recognition of the respective siRNA and miRNA pathways these technologies exploit is crucial to conceptualising and assessing their efficacy within the laboratory. siRNA-ediated gene silencing pathways principally represent a defence mechanism to protect the cell from foreign bodies whereas miRNA-gene silencing is an integral gene expression regulation process.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

240. If the wild type E *.coli* cells that are growing in normal medium with glucose are transferred to a medium containing only lactose as sugar, what changes will take place?

a. The lac operon is induced.

b. E *. coli* cells stop dividing.

c. The lac operon is repressed.

d. All operons will get induced.

Correct Answer: A

When E *.coli* bacteria are transferred to medium containing lactose, then the lac opeon is induced. The lac operon consists of 3 structural gene (lacZ, lacY and lacA). It involves the synthesis of β- galactosidase enzyme in E *.coli*, which hydrolyses lactose into glucose and galactose.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

241. Which among the following statement is false about the mRNA stability?

a. Prokaryotic mRNAs have a half-life of only a few minutes.

b. Regulation of mRNA stability is a way of regulating gene expression.

c. Histone mRNAs have especially long polyA tails and are especially stable.

d. None of the above

Correct Answer: C

Most prokaryotic mRNAs have half-lives of 2-3 minutes. Eukaryotic mRNAs have half-lives of a few minutes to many hours or even days. PolyA tails are thought to stabilise eukaryotic mRNAs and polyA binding protein protects that mRNA from exonuclease activity. Histone mRNAs do not have polyA tails and their stability is determined by a stem-loop structure at the $3'$ end of the mRNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

242. Which among the following is the most efficient feature of siRNA duplexes?

a. They are $21-23$ nucleotides in length.

b. They possess a $2-$nucleotide overhang at the $3'$ termini end and AA bases at the $5'$ end.

c. Both A and B

d. None of the above

Correct Answer: C

There are two keys goals when utilising siRNA-mediated gene silencing. Firstly, to achieve efficient knockdown of the target gene and secondly to ensure that the knockdown is specific. Hence, when designing siRNA duplexes there a number of key criteria that should be applied in order to maximise both efficiency and specificity. SiRNA is 21-23 nucleotide in length.

Core Concept:

Topic:

Difficulty Level:

Complexity:

243. Which among the following concerning regulation of *trp* operon expression by attenuation is correct?

a. Rapid translation of the leader peptide allows completion of the mRNA transcript.

b. The leader peptide sequence encode enzymes required for tryptophan synthesis.

c. The leader peptide sequence contains no tryptophan residues.

d. Rapid translation of the leader peptide prevents completion of the mRNA transcript.

Correct Answer: D

Translation of the *trp* operon encoded mRNA begins with the synthesis, not of one of the enzymes, but of a short 'leader' peptide encoded by the $5'$ end of the message. The leader peptide contains codons encoding tryptophan. If there is tryptophan in the cell, then tRNA charged with tryptophan will be available and ribosomes will move rapidly along the sequence encoding the leader peptide. The effect of this is to leave part of the mRNA sequence free to base pair with itself, forming a stem-loop transcription termination signal so the mRNA is never completed and the enzymes

needed for tryptophan synthesis are not made. The leader peptide has no other function but to play this regulatory role by its translation and is rapidly degraded.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

244. The main distinction between the origin of the two classes of small regulatory RNAs; sIRNA and miRNA, can be best described as

a. siRNAs originate within the cell cytoplasm; miRNAs originate from the cell genome.

b. siRNAs originate from predominantly exogenous dsRNA; miRNAs originate from the cell genome.

c. Both A and B

d. None of the above

Correct Answer: B

siRNAs are derived almost exclusively from exogenous dsRNA precursors introduced into the cytoplasm through, for example, viral infection or transfection during siRNA technology procedure. In contrast, miRNA genes are found within the genome and are transcribed within the nucleus by RNA polymerase II to generate a single-strand RNA transcript which is then further processes to form miRNA.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

245. In the regulation of transferrin-receptor protein synthesis,

a. when iron is scarce the IRE-binding protein binds to and stabilizes the mRNA that encodes transferrin-receptor protein.

b. the iron-responsive element is in the $5'$ untranslated region of the mRNA that encodes transferrin-receptor protein.

c. when iron is abundant the IRE-binding protein binds to and stabilizes the mRNA that encodes transferrin-receptor protein.

d. None of the above

Correct Answer: A

The synthesis of the transferrin-receptor protein is a case where mRNA stability regulates synthesis of the protein and is itself regulated. The receptor is responsible for the transport of iron into cells by endocytosis and more receptor protein is therefore required when iron is scarce, to increase the efficiency of iron import. In the $3'$ untranslated region of the mRNA is a group of five stem loops called an iron-responsive element (IRE). In the absence of iron, an IRE-binding protein (IRP) attaches to the IRE and stabilizes the mRNA, thus increasing receptor synthesis with a consequent increase in the import of iron into the cell. In iron abundance, iron complexes with the IRP, which then no longer binds to the IRE. The IRE is thus exposed to attack by a specific endonuclease which cleaves the message, leading to its degradation. The result is a reduced import of iron into the cell.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

246. What is the role of CpG Islands and codon bias in eukaryotic genomics?

a. To identify open reading frames.

b. To find regulatory sequences.

c. Both A and B

d. None of the above.

Correct Answer: A

Cytosine and guanine doublets are found in the concentrated near gene-rich region of the genome. Codon bias is the phenomenon often observed in coding regions of DNA for certain codons to be used over others coding for the same amino acid.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

247. The role of methylation of DNA is now viewed as

a. interfering with DNA transcription by blocking base pairing between cytosine and guanine.

b. complexing with enhancers to prevent transcription.

C. prevention of mutation.

d. insuring that genes that are turned off.

Correct Answer: D

In vertebrates DNA methylation is found primarily on transcriptionally silent regions of the genome, such as the inactive X chromosome or genes that are inactivated in certain tissues, suggesting that it plays a role in gene silencing. Vertebrate cells contain a family of proteins that bind methylated DNA. These DNA-binding proteins, in turn, interact with chromatin remodelling complexes and histone deacetylases that condense chromatin so it becomes transcriptionally inactive.

Core Concept:

Topic:

Difficulty Level: Medium

Complexity:

248. A sequence that can be several thousand base pairs upstream or downstream of a eukaryotic promoter and can Increase gene expression as much as $200-$ fold is called

a. Enhancer

b. TATA box

C. Modulator

d. None of the above

Correct Answer: A

Eukaryotic genes often have control elements, called enhancers, which increase gene expression and which can be thousands of base pairs away from the promoter. These can be tissue-specific, enhancing transcription in only certain tissues. The enhancer is brought into proximity with the promoter by looping of the DNA that lies between them.

Core Concept:

Topic:

Difficulty Level:

Complexity:

249. Which among the following statement is true about Operons?

a. They are of approximately uniform in size.

b. They do not bind proteins.

c. They are found in some eukaryotic genes.

d. They are shorter and smaller in lower eukaryotes than higher eukaryotes.

Correct Answer: C

It was thought that polycistronic transcription is a characteristic of bacteria and archaea, where many of the genes are clustered in operons composed of two to more than then genes. By contrast, the genes of eukaryotes are generally considered to be monocistronic, each with its own promoter at the 59 end and a transcription terminator at the 39 end; however, it has recently become clear that not all eukaryotic genes are transcribed mono-cistronically. Numerous instances of polycistronic transcription in eukaryotes, from protists to chordates, have been reported. Polycistronic transcription in eukaryotes was first found in 1988 in trypanosomes, although these polycistronically- transcribed genes do not represent operons in the sense of co-regulation. Widespread operons in an animal were first discovered in the nematode, *Caenorhabditiselegans*, in 1993. Nematode operons are transcribed to produce polycistronic initial transcripts that are co transcriptionally processed to make monocistronic mRNAs.

Core Concept:

Topic:

Difficulty Level:

Complexity: