SOLUTIONS

6.1: Structure and replication of DNA

1. **B**
   Cytosine pairs with guanine in DNA, and the diagram in option B correctly shows this base pair with three hydrogen bonds between them.
2. **D**
   The bond labeled X represents the phosphodiester bond, which links the phosphate group of one nucleotide to the sugar of another, forming the sugar-phosphate backbone of DNA, ensuring strand stability.
3. **C**
   Row C is correct as Cytosine is a pyrimidine with a single-ring structure and forms three hydrogen bonds with guanine.
4. **C**
   The template strand of DNA serves as a guide for mRNA synthesis during transcription, ensuring accurate protein production.
5. **D**
   A gene mutation alters the DNA sequence, leading to a change in the codon during transcription, which may result in a non-functional protein. However, mutations do not occur during transcription (statement 1 is incorrect), and tRNA anticodon changes are not part of gene mutations (statement 3 is incorrect).
6. **B**
   Adenine (A) pairs with thymine (T) using 2 hydrogen bonds, while cytosine (C) pairs with guanine (G) using 3 hydrogen bonds.
7. **A**
   XNA (Xeno nucleic acid) is a synthetic nucleic acid where the five-carbon sugar (ribose or deoxyribose) is replaced by a different chemical structure, but the coding bases remain unchanged.
8. **D**
   DNA polymerase catalyzes the formation of phosphodiester bonds between nucleotides, linking the phosphate group of one nucleotide to the sugar of another, forming the backbone of DNA.
9. **C**
   Thymine is diagram 2, and cytosine is diagram 3. Both are pyrimidine bases found in DNA.
10. **A**
    In nucleotides, the nitrogenous base is attached to carbon atom 1 of the pentose (1), the phosphate group is linked to carbon atom 5 (2), and condensation reactions join both the base and the phosphate to the pentose (3). Statement 4 is incorrect because nucleotides are not linked via phosphate-phosphate bonds.
11. **D**
    In a circular DNA molecule with 2700 base pairs, there are 5400 nucleotides, and each nucleotide is linked by a phosphodiester bond, totaling 5400 bonds in the entire molecule.
12. **B**
    Purines (A, G) are larger than pyrimidines (C, T, U) (1). Complementary base pairing happens during translation (2), and uracil pairs with adenine by forming two hydrogen bonds (4).
13. **C**
    During DNA replication, the leading strand (S1) is synthesized continuously in the 5' to 3' direction, while the lagging strand (S2) is synthesized discontinuously in short fragments. Diagram C correctly shows this with S1 proceeding smoothly and S2 with gaps, representing Okazaki fragments.
14. **C**
    Phosphodiester bonds in the DNA backbone are formed between nucleotides by DNA ligase, ensuring the stability of the DNA strand.
15. **B**
    After one generation in ^{14}N, all DNA is hybrid, containing both ^{15}N and ^{14}N. After two generations, 50% of the DNA is hybrid (one strand ^{15}N, one strand ^{14}N), and 50% is purely ^{14}N due to semi-conservative replication.

16. D

In DNA, adenine (A) pairs with thymine (T), and cytosine (C) pairs with guanine (G). Option D correctly shows these base pairings and a deoxyribose-phosphate backbone, unlike the other options which show incorrect bases or pairings.

17. D

The short fragments of DNA (Okazaki fragments) formed during lagging strand replication have sequences complementary to the leading strand and consist of a single polynucleotide strand. DNA also contains more elements than just carbon, hydrogen, oxygen, and nitrogen, like phosphorus.

18. D

Purines (A and G) make up 40%, so pyrimidines (C and T) make up 60%. When transcribed, T is replaced by U, meaning 60% of the bases in the RNA will be cytosine and uracil.

19. B

The correct statement about mRNA (messenger RNA) is:
B: Each nucleotide subunit contains the sugar ribose.
mRNA contains ribose sugar in its nucleotide subunits and uracil as a base, unlike DNA, which contains deoxyribose sugar and thymine as a base.

20. C

The molecules that make up the structure of ATP (adenosine triphosphate) are:
Adenine: Adenine is one of the four nitrogenous bases found in DNA and RNA. In ATP, it's part of the adenine nucleotide.
Deoxyribose: Deoxyribose is a five-carbon sugar that forms the backbone of DNA. In ATP, a similar sugar, ribose, is used, but it's not deoxyribose.
Phosphate: ATP stands for "adenosine triphosphate," which means it contains three phosphate groups.
So, the correct combination of molecules is:
C 1, 4, and 5 (Adenine, Phosphate, Ribose)

21. B

	number of nucleotide bases			
	A	C	G	T
strand 1	5	3	7	4
strand 2	4	7	3	5

Strand 1 has a total of 19 bases
Strand 2 also has a total of 19 bases
In strand 1, it's given that there are 4 T
This means that strand 2 will have 4 A as two stands have compliment pairing of bases.
This also means that stand 1 has 5 A and stand 2 has 5 T
Using the same method it can be said that stand 1 has 7 G as strand 2 has 7 C
For each of the strands adding A + C + G + T = 19
Taking for example strand 1:
5 + 7 + 4 + C = 19
C = 3

22. D

The correct statement about the role of DNA polymerase in the process of semi-conservative replication of DNA is:
D DNA polymerase moves along leading and lagging strands in the 5' to 3' direction.
DNA polymerase is the enzyme responsible for synthesizing new DNA strands during DNA replication. It adds new nucleotides to the growing DNA strand in the 5' to 3' direction. DNA replication is a complex process that involves the leading strand (where replication occurs continuously) and the lagging strand (where replication occurs in short, discontinuous fragments known as Okazaki fragments). DNA polymerase is involved in both strands, moving in the 5' to 3' direction to add nucleotides and build the new DNA strands.

23. B

According to Chargaff's rules, in DNA, the amount of guanine (G) is equal to the amount of cytosine (C), and the amount of adenine (A) is equal to the amount of thymine (T). This is because G and C pair together and A and T pair together through hydrogen bonding between the two strands of the DNA double helix. Thus, the percentage of cytosine is the same as that of guanine in the whole molecule and also in each strand, because each C on one strand pairs with a G on the complementary strand. However, the question asks about the whole DNA molecule, not the individual strands.

24. A
DNA replication in eukaryotic cells, Statement 3 is correct; it describes the semi-conservative nature of DNA replication, where each new DNA molecule consists of one strand from the original molecule and one newly synthesized strand. This reflects the work of Meselson and Stahl. DNA replication occurs in the nucleus, not the cytoplasm, and adenine pairs with thymine, not uracil which is in RNA. The guanine content remains constant at 40% in each daughter molecule due to base pairing rules

25. C
Pyrimidines are characterized by a single-ring structure. Thymine and uracil are pyrimidines, while adenine and guanine are purines with a double-ring structure.

26. B
The experiment described is similar to the Meselson-Stahl experiment, which demonstrated the semi-conservative nature of DNA replication. In the second generation after shifting bacteria from a heavy nitrogen (15N) medium to a light nitrogen (14N) medium, each DNA molecule will consist of one old (heavy) strand and one new (light) strand. Therefore, in the second generation, no DNA molecule will be entirely heavy; instead, all DNA molecules will be hybrids.

27. D
A nucleotide in DNA consists of a nitrogenous base and a sugar (deoxyribose). This is fundamental to the structure of DNA molecules.

28. C
Semi-conservative replication of DNA occurs during the S phase of interphase, prior to mitosis and cytokinesis.

29. C
The diagram depicts the relationships between nucleic acid bases in DNA and RNA, illustrating base pairing and the chemical differences between the two nucleic acids.

30. C
Option C is the correct answer as ATP is adenosine triphosphate with a ribose sugar and 2 extra nucleotides as compared to normal nucleotides.

31. C
Option C is the correct answer as the first generation contain all DNA molecules with one heavy strand as that is how semi-conservative replication works where one strand comes from each parent DNA molecule. The second generation has a 50% with the third generation having a 25% as in successive generations the percentage decrease due to possibilities of molecules produced with no heavy DNA strands in them.

32. C
Since 26% of the bases are adenine the adenine thymine pairs will have a total of 52%. This leaves 48% of the bases as cytosine ones which turns out to be 1248072 making option C the correct answer.

33. B
Statements 1, 2 and 3 are correct as the carbohydrate is a pentose sugar, the base does contain nitrogen and adenine pairs with either thymine or uracil. Statement 4 is incorrect as adenine is purine. Hence, option B is the correct answer.

34. C
Option C is the correct answer as DNA synthesis takes places from 5' to 3' and DNA polymerase is the enzymes that add complementary nucleotides to the lagging strands.

35. B
Option B is the correct answer as since there are 23 adenine bases in strand 2 there must be 23 thymine base in strand 1. Subtracting the sum of all bases in strand 1 from 84 the number of guanine bases strand 1 are 18. Since there are 15 cytosine bases in strand 1 there must be 15 guanine bases in strand 2. Adding the guanine bases from the 2 strands gives us 33 guanine bases in total.

36. C
Option C is the correct answer as ATT when transcribed forms the UAA codon which is a STOP codon that stops the polypeptide synthesis prematurely.

37. C
The constant distance between the sugar-phosphate chains in DNA is due to the pairing of a purine (larger) base with a pyrimidine (smaller) base, maintaining uniform width in the double helix. Hence, C is correct.

38. C
Option C is the correct answer as uracil is a pyrimidine and has a single ring structure.

39. B

Option B is the correct answer as before the nucleotide binds with the adjacent nucleotide during replication complementary base pairing should have occurred with the formation of hydrogen bonds between the strands. The formation of phosphodiester bonds joins the nucleotides so it cannot occur before the joining.

40. B

Option B is the correct answer as proteases are enzymes in nature which in turn are proteins. The code for the protease is copied in the form of a mRNA molecule that is used to produce the protein.

41. A

Option A is the correct answer as strand 2 has 7 adenine bases, 5 cytosine bases and 4 guanine bases which makes the total number 16. This leaves behind 2 bases which are thymine.

42. D

Option D is the correct answer as with adenine either thymine or uracil pair which are both single ringed bases and the ratio of carbon to oxygen atoms in the pentose sugar is 5 : 4.

43. B

Option B is the correct answer as thymine is a pyrimidine and base pairing with adenine involves 2 hydrogen bonds. The carbohydrate can only be a deoxyribose sugar.

44. B

Option B is the correct answer as DNA replication results in the formation of 2 molecules of DNA, each containing a sequence of paired nucleotides.

45. C

Since adenine and thymine pairs form 2 hydrogen bonds and cytosine and guanine form 3 hydrogen bonds. Counting the bonds by looking at the number of pairs the number of bonds comes out to 38 making option C the correct answer.

46. A

Statements 1, 2 and 3 are correct as the carbohydrate could be a ribose sugar and the organic base contains nitrogen and cytosine bonds with guanine. Statement 4 is incorrect as cytosine is a pyrimidine. Hence, option A is the correct answer.

47. C

Guanine does not have a single ring structure. It is a purine and joins with cytosine through 3 hydrogen bonds. Hence, option C is the correct answer.

48. A

In the first strand there are 29 adenine bases meaning on the second strand there must be 29 thymine bases. Similarly on the second strand there are 21 adenine bases to on the first strand there must be 21 thymine bases. On the first strand there are 14 guanine bases so on the second strand there must be 14 cytosine bases. Adding up the bases pairs till yet the number comes to 64 meaning that there are 9 base pairs left which are of the cytosine in strand 1 and guanine in strand 2. Hence, option A is the correct answer.

49. C

Option C is the correct answer as replicating 3 times results in a greater percentage of ^{14}N in the DNA of the bacteria.

50. C

Statements 1 and 3 are correct as for semi conservative replication each strand of double stranded DNA is used as a template and hydrogen bonds within bases of the DNA may be present due to folding. Statement 2 is incorrect as cytosine and guanine will occur in equal amount but the percentage of adenine or thymine cannot be calculated unless one of the percentages of the bases is known. Hence, option C is the correct answer.

51. B

Only statements 1 and 3 are correct as replication takes place in the nucleus and each new DNA strand contain one strand form the original molecule. Statements 2 and 4 are incorrect as adenine pairs with thymine and the percentage of guanine in the new molecule can be determined by the percentage of cytosine in the original. Hence, option B is the correct answer.

52. C

Thymine has a single ring structure, is a purine and pairs with adenine using 2 hydrogen bonds. Hence, option C is the correct answer.

53. A

Adding 6, 3 and 4 gives us 13 base pairs meaning that there are 2 remaining base pairs of guanine in the 1st strand and cytosine in the 2nd strand. This makes option A the correct answer.

54. D
Statements 3 and 4 are correct as HNA nucleotides are larger than normal nucleotides and as a result cannot fit into the active site of DNA polymerase. Hence, option D is the correct answer.

55. C
Statements 1 and 3 are correct as during DNA replication each strand of DNA acts as a template for the other strand and the hydrogen bonds between the bases are broken. Statement 2 is incorrect as DNA polymerase link the sugars together with the phosphate groups not the bases. Hence, option C is the correct answer.

56. A
Cytosine has a single ring structure, is a pyrimidine and joins with guanine using 3 hydrogen bonds. Hence, option A is the correct answer.

57. D
Option D is the correct answer as in the second generation there is a greater percentage of molecules with light nitrogen about 75% and DNA molecules with both light and heavy nitrogen would be about 50%. Hence, option D is the correct answer.

58. B
Statements 1 and 2 are correct as adenine and guanine have a double ring structure and any one of them can be found in rRNA and these double ring bases are called purine meaning any one of them can be present. Hence, option B is the correct answer.

59. B
Statements 1 and 3 are correct as in prokaryotic cells there is no nucleus present meaning that replication will take place in the cytoplasm and each new molecule contains one strand from the original molecule. Hence, option B is the correct answer.

60. C
In the first generation there will be 100% of hybrid DNA since the initial strands used contain both heavy nitrogen and there would be 50% of light strands. Hence, option C is the correct answer.

61. A
All 3 statements are correct as the sugar can be ribose or deoxyribose. Guanine bonds with cytosine using 3 hydrogen bonds and it is a purine. Hence, option A is the correct answer.

62. C
Option C is the correct answer as adenine and guanine are purines.

63. A
Option A is the correct answer as adenine and guanine are purines and thymine and cytosine are pyrimidines. Adenine binds with thymine.

64. C
DNA polymerase is responsible for the formation of the sugar phosphate backbone of the complementary strand of the DNA. Hence, option C is the correct answer.

65. C
According to the semi-conservative model of DNA replication each strand is used as a template. Hence, option C is the correct answer.

66. B
In the second generation there will be 50 percent hybrid molecules and 25 percent of heavy DNA strands. Hence, option B is the correct answer.

67. B
Since 24% are adenine bases there must be 24% thymine bases as well. This means that 52% are guanine and cytosine pairs. Halving this gives 26% as the percentage of either guanine or cytosine making option B the correct answer.

68. D
The greatest number of hydrogen bonds in bases are in guanine and cytosine bases that are 3. Assuming all the base pairs are these base pairs 2100 is the maximum number of hydrogen bonds. Hence, option D is the correct answer.

69. C
Option A is incorrect as adenosine is present in ATP. Option B is incorrect as hydrogen bonds are not present in ATP. Option D is incorrect as ribose is present in RNA but not in DNA. Hence, option C is the correct answer as RNA, DNA and ATP all contain phosphate groups.

70. B
Option B is the correct answer as adenine and guanine are purines.

71. D

Semi-conservative DNA replication refers to the fact that the template strand used is one strand of the original molecule. Hence, option D is the correct answer.

72. B

Statements 1 and 2 are correct as there are 3 cytosine and thymine molecules which are pyrimidines. Adenine and thymine form 2 hydrogen bonds and guanine and cytosine form 3 hydrogen bonds so the double stranded molecule will have 26 bonds. Statement 3 is incorrect as each strand has 9 phosphodiester bonds meaning 18 bonds in both strands. Hence, option B is the correct answer.

73. A

Options B, C and D are incorrect as the bases play a role in coding and the phosphate groups do as well since they hold together the molecules through phosphodiester bonds. Hence, option A is the correct answer as the 5 carbon sugar can be replaced since it does not play a part in coding.

74. C

In the first generation there will be 100% of hybrid DNA since the initial strands used contain both heavy nitrogen and there would be 50% of light strands. Hence, option C is the correct answer.

75. A

Guanine is a purine meaning it has a 2 ringed structure. They form 3 hydrogen bonds with cytosine. Hence, option A is the correct answer.

76. A

Option A is the correct answer as the first nucleotide has 2 bonds meaning that it has to be an adenine thymine base pair. Since the first nucleotide has 2 ringed structure that means it is adenine and that makes nucleotide 2 thymine.

77. D

Option A is incorrect as Q is not deoxyribose. Option B is incorrect as there are 3 phosphate molecules do it cannot be a phosphate group. Option C is incorrect as R is not phosphorus. Hence, option D is the correct answer as P is a purine due to the 2 ringed structure, Q is a pentose sugar and R are phosphates.

78. C

After the first division all the molecules will be hybrids meaning they will be at L. The second generation will contain molecules that are hybrids and molecules containing the light nitrogen so half will be at K and half will be at L. Hence, option C is the correct answer.

79. D

The first generation will contain all hybrids meaning that the band will be between the 2 control bands. Hence, option D is the correct answer.

80. C

In DNA, Adenine (A) pairs with Thymine (T) using 2 hydrogen bonds, and Guanine (G) pairs with Cytosine (C) using 3 hydrogen bonds. On average, the maximum number of hydrogen bonds would be approximately 1.5 bonds per base pair, resulting in 1050 hydrogen bonds for 700 nucleotides. Hence, C is correct.

81. C

Adenine is a purine meaning it has a 2 ringed structure. It pairs with thymine using 2 hydrogen bonds. Hence, option C is the correct answer.

82. C

Options A, B and D are incorrect as all of these are correct comparisons. Hence, option C is the correct answer as DNA is found also in multiple areas throughout the cell such as in organelles.

83. D

P and R are both histones and Q is the associated DNA that forms strands that fold around and twist to condense and form chromatids. Hence, option D is the correct answer.

84. C

The minimum number of hydrogen bonds in a length of DNA would occur if all base pairs were adenine (A) paired with thymine (T), which forms 2 hydrogen bonds per pair. For 700 base pairs, this would result in 1400 hydrogen bonds. Hence, C is correct.

85. C

Adenine is a purine meaning it has a 2 ringed structure. It bonds with thymine using 2 hydrogen bonds. Hence, option C is the correct answer.

86. D

A nucleotide is the smallest unit that can be altered by a mutation. Hence, option D is the correct answer.

87. D
Option D is the correct answer as helicase makes the strands of DNA available as templates, topoisomerase release tension caused by unwinding, single strand binding protein prevents original strands from forming complementary base pairs and DNA polymerase adds nucleotides to the growing 3' chain.

88. D
Deoxyribose is the sugar found in DNA and it is a reducing sugar. Hydrogen bonds are found in a DNA molecule.

89. B
Option A is incorrect as adenine and guanine are purines. Option C is incorrect as purines have a double ringed structure. Option D is incorrect as uracil replaces thymine in RNA. Hence, option B is the correct answer as ATP is a phosphorylated nucleotide.

90. D
Statements 3 and 4 are correct as HNA nucleotides are larger than normal nucleotides and as a result cannot fit into the active site of DNA polymerase. Hence, option D is the correct answer.

91. A
The medium DNA molecules are hybrid meaning one strand contains ^{15}N and the other contains ^{14}N. The light DNA molecules 50 percent contain only ^{14}N and 50 percent contain only ^{15}N. Hence, option A is the correct answer.

92. D
Options A and B are incorrect as adenine is a purine and cytosine is a pyrimidine. Option C is incorrect as guanine has a double ringed structure. Hence, option D is the correct answer as uracil is a pyrimidine having a single ring structure.

93. B
In the first generation all the molecules will be hybrid whereas in the third generation one quarter will be hybrids and three quarters will be light. Hence, option B is the correct answer.

94. B
Option B is the correct answer as cytosine is a pyrimidine meaning it has a single ringed structure and it pairs with guanine using 3 hydrogen bonds.

95. A
Since 29% is adenine 29% must be thymine. This accounts for 58% so the remaining 42% must be cytosine guanine pairs. Halving this gives 21% of either cytosine or guanine making option A the correct answer.

96. C
Option C is the correct answer as thymine is pyrimidine meaning it has a single ring structure.

97. A
Statements 1, 2 and 3 are correct as cytosine pairs with guanine using 3 hydrogen bonds. Purines and pyrimidines are of different sizes and complementary base paring allows transcription to occur as mRNA is produced from template strands. Statement 4 is incorrect as the pairs have the same length. Hence, option A is the correct answer.

98. B
Option B is the correct answer as in the second generation 50% will be hybrid DNA and 50% will be light DNA.

99. B
Purines are larger than pyrimidines meaning that 2 and 4 are purines. Hence, option B is the correct answer.

100. C
DNA contains the pyrimidine base thymine which is joined to adenine with 2 hydrogen bonds. Hence, option C is the correct answer.

101. D
Statement 1 is incorrect as adenine and guanine are purines. Statements 2 and 3 are correct as RNA contains nucleotides with the ribose sugar and purines only pair with pyrimidines. Hence, option D is the correct answer.

102. C
Option C is the correct answer as DNA polymerase synthesizes a new strand of DNA using an existing strand as a template.

103. B
42.2 % are cytosine guanine pairs. This means that the remaining 57.6% are adenine thymine pairs and halving this gives 28.8% for either base making option B the correct answer.

104. B
Option B is the correct answer as AT pairs have 2 hydrogen bonds while CG pairs have 3 hydrogen bonds.

105. C
Option C is the correct answer as AT pairs have 2 hydrogen bonds while CG pairs have 3 hydrogen bonds.

106. B
The scientist would find large amounts of p53 mRNA in X and Y groups since ionizing radiation and ultraviolet light cause significant damage to DNA upon prolonged exposure. Hence, option B is the correct answer as nicotine does not damage DNA.

107. A
AT pairs are joined by 2 hydrogen bonds and CG bonds are joined via 3 hydrogen bonds. Adding up we get a total of 11 hydrogen bonds making option A the correct answer.

108. A
Option A is the correct answer as the complementary base of adenine is thymine and it is attached to the deoxyribose sugar and has a double ringed structure.

109. C
DNA contains reducing sugar and has hydrogen bonds between bases and covalent bonds which are phosphodiester bonds. Hence, option C is the correct answer.

110. C
Options A, B and D are incorrect as sugar phosphate arrangement, double helical arrangement and paring of purines with pyrimidines are all constant. Hence, option C is the correct answer as the number of hydrogen bonds varies between the AT and CG pairs.

111. C
Option C is the correct answer as regions 3 and 4 contain little circles which are phosphate groups attached to the sugar.

112. C
Option C is the correct answer has the correct order is from S to P to T to Q to R.

6.2: Protein synthesis

1. B
The mRNA codons are GGG, CUU, AAA, GUU (complementary to DNA). The corresponding tRNA anticodons are CCC, GAA, UUU, CAA, which match option B.

2. D
P is the primary transcript made during transcription, Q is the template strand used by RNA polymerase, and R is the non-transcribed strand.

3. C
The mRNA codons transcribed from the DNA sequence are CGC (Arg), GCC (Ala), GGC (Pro), and CGC (Arg), based on the provided codon table. Therefore, C is correct.

4. D
RNA polymerase binds to the template strand to synthesize a complementary mRNA strand during transcription.

5. B
During mRNA formation, condensation reactions join nucleotides, polymerisation links them into a chain, and transcription copies the DNA sequence into mRNA. Replication does not occur in mRNA synthesis.

6. D
The phosphodiester bond links the phosphate group of one nucleotide to the sugar of another, forming the sugar-phosphate backbone of nucleic acids.

7. D
The anticodon for tryptophan (ACC) pairs with the mRNA codon (UGG). The corresponding DNA template strand must be complementary to mRNA, meaning it should have the triplet CCT for tryptophan. Thus, the correct sequence is CCT ACC CAT.

8. **B**
Anticodons 1 (UCA) and 2 (ACC) pair with mRNA codons specifying serine and threonine, respectively. Only these anticodons specify an amino acid other than threonine.

9. **B**
Exons are the coding sequences in RNA that are spliced together to form mRNA, while non-coding introns are removed during RNA processing in eukaryotic cells.

10. **A**
The production of an extracellular enzyme starts in the nucleus (where mRNA is transcribed), moves to the ribosome (for translation), then to the rough ER for folding, and finally to the Golgi body for modification and packaging before secretion.

11. **B**
The mRNA codons for the sequence "CGG GCC CCG CGG" translate to Arg (CGG), Gly (GGC), Ala (GCC), and Ala (GCG). Therefore, the correct sequence of amino acids is Ala-Arg-Gly-Ala.

12. **D**
DNA polymerase adds nucleotides to the 3' end, making the leading strand continuous and the lagging strand discontinuous. In option D, the strands are correctly oriented, and the lagging strand is replicated in fragments.

13. **D**
Translation requires mRNA, ribosomes, amino acids, and tRNA to synthesize proteins by decoding the mRNA.

14. **D**
The deletion of one nucleotide causes a frameshift mutation, changing the entire reading frame from the deletion onwards, altering all subsequent codons and the amino acid sequence.

15. **C**
Statement 1 is correct as mRNA is used to produce a specific amino acid chain in translation. Statements 2 and 3 describe transcription and the tRNA-codon interaction inaccurately, hence option C is the correct choice.

16. **C**
The non-transcribed DNA strand is identical to the mRNA sequence, replacing uracil (U) with thymine (T), giving GAT CTG TAA CGG.

17. **A**
Amylase is a protein, and the synthesis of proteins is directly controlled by DNA through the processes of transcription and translation. Other molecules like cholesterol and phospholipids are not directly synthesized by DNA.

18. **A**
The sickle cell mutation changes the codon from CTC to CAC, which alters the amino acid sequence. A tRNA with the anticodon GUG will pair with CAC, leading to the incorporation of valine instead of glutamic acid. This causes the abnormal Hb^{S} protein.

19. **C**
The DNA sequence in the template strand codes for a complementary mRNA codon. Using the RNA codon wheel, the mRNA codon UGG translates to the amino acid tryptophan (Trp).

20. **B**
In transcription, RNA polymerase converts a section of DNA into RNA (statement 2 correct). Statements 1 and 3 describe translation, not transcription. Hence, option D is correct.

21. **B**
The DNA sequence ATT is transcribed into the mRNA codon UAA. The anticodon on the tRNA must be complementary to this mRNA codon, which is AUC.

22. **A**
A universal genetic code means that all living organisms, regardless of their species or complexity, use the same triplet code for amino acids. This universal genetic code ensures that the information stored in DNA is consistent and can be accurately translated into proteins by the cellular machinery, such as ribosomes, in all organisms. So, the correct option is A: All living organisms use the same triplet code for amino acids.

23. **B**
mRNA (messenger RNA) carries genetic information from DNA to ribosomes for protein synthesis, while tRNA (transfer RNA) helps translate the genetic code into amino acids during protein synthesis. tRNA has anticodons that base-pair with mRNA codons to ensure correct amino acid incorporation.

24. C

A substitution mutation in the DNA triplet can result in:

- cysteine being translated instead of tyrosine (if the mutation changes the codon)
- Tyrosine still being translated (f the mutation is redundant or a conservative substitution)
- Translation stopping prematurely at the triplet (if the mutation introduces a stop codon)

Note that statement 2 is incorrect because it would require two substitutions for tyrosine to be translated as tryptophan, but the question only considers a single substitution.

25. B

Transcription is the process by which the information in a strand of DNA is copied into a new molecule of messenger RNA (mRNA) by the enzyme RNA polymerase. The DNA template strand is the strand of DNA that is read by RNA polymerase to synthesize the RNA strand. Anticodons are part of tRNA molecules and are not involved in the transcription process but rather in translation during protein synthesis. Therefore, the DNA template strand and RNA polymerase are involved in transcription (indicated by ticks), while anticodons are not involved (indicated by an 'x').

26. C

Messenger RNA (mRNA) structure, including its ribose sugar-phosphate backbone, is key in understanding RNA's role in protein synthesis. The structure of mRNA contrasts with DNA in terms of sugar components and the bases present.

27. D

In accordance with the central dogma of molecular biology, a gene is a segment of DNA that contains the instructions for making a particular protein. The process begins with transcription, where the gene is copied into messenger RNA (mRNA), and then translation, where the mRNA is used to assemble a chain of amino acids into a polypeptide. Each gene thus corresponds to one polypeptide, which may function as a protein or part of a protein.

28. C

The fifth DNA triplet 'CAA' transcribes to the mRNA codon 'GUU,' which codes for glutamine. If the first base C is replaced by A, the triplet becomes 'AAA,' which would transcribe to 'UUU.' The mRNA codon 'UUU' codes for phenylalanine, not cysteine as indicated in the answer. There appears to be a discrepancy in the question or the provided answer key, as the change should result in glutamine to phenylalanine.

29. C

Thymine (T) is one of the four nitrogenous bases found in DNA (deoxyribonucleic acid) but is not part of the process of translation in protein synthesis. Protein synthesis involves two main processes: transcription and translation.

Transcription: During transcription, a DNA template is used to create a complementary RNA molecule. In this step, thymine (T) is replaced by uracil (U) in the RNA strand. This is because RNA contains uracil instead of thymine. The RNA molecule produced in transcription is called messenger RNA (mRNA) and carries the genetic code from the DNA to the ribosome for protein synthesis.

Translation: In translation, the information in the mRNA is used to build a protein. This process takes place at the ribosome, where transfer RNA (tRNA) molecules bring amino acids to the ribosome based on the codons in the mRNA. Thymine (T) is not involved in the translation process; it is specific to DNA.

tRNA brings a complementary anticodon based on the condons in the mRNA. This is represented by Option C

30. D

The difficulty in sequencing the PDX1 gene in sand rats may stem from the strength of hydrogen bonding between DNA strands, which is proposed in statement 3. Stronger hydrogen bonds could impede strand separation, a necessary step in many sequencing techniques. Statements 1 and 2 relate to gene prevalence and expression but do not directly hinder the sequencing process itself.

31. C

To identify tissues actively synthesizing mRNA, substances that are incorporated into mRNA during transcription must be labeled. mRNA is composed of ribonucleic acids, which include the bases adenine, cytosine, guanine, and uracil (not thymine as in DNA), a ribose sugar, and a phosphate group. Adenine is found in both DNA and RNA, while uracil is specific to RNA. Inorganic phosphate is part of the RNA backbone, and ribose is the sugar component of the ribonucleotide. Thus, all the listed substances except adenine (which is also part of DNA) would be suitable for this experiment, as they are specific to RNA or essential to its structure.

32. D

In sickle cell anemia, the mutated DNA sequence leads to the substitution of valine for glutamic acid in the hemoglobin beta chain. The DNA triplet code for valine can be inferred from the anticodon information provided.

33. B
During transcription, temporary hydrogen bonds form between the DNA template strand and the complementary RNA nucleotides. This process ensures accurate transcription of the genetic code from DNA to mRNA.

34. D
A mutation in the DNA sequence can lead to an altered amino acid sequence in the protein, potentially resulting in a non-functional protein. However, the formation of mRNA stop codons or the inhibition of ribosome translation would require specific changes not necessarily implied by the given mutation.

35. B
Translating the mRNA sequence based on the genetic code and the frequency of amino acids provided results in a specific sequence of amino acids that aligns with the number of each amino acid present in the polypeptide.

36. B
Rifampicin, which binds to RNA polymerase, would stop transcription immediately, while streptomycin causes errors in translation, resulting in the production of faulty proteins.

37. C
After culturing E. coli in a heavy nitrogen medium and then in a light nitrogen medium, the DNA bands indicate semi-conservative replication, with hybrid DNA containing both heavy and light nitrogen.

38. D
The mRNA for α-globin contains three nucleotides per amino acid. With 141 amino acids and an initial methionine that is removed, the mRNA must have 426 nucleotides.

39. D
Option D is the correct answer as inhibiting RNA polymerase means that enzyme synthesis cannot occur since enzymes are made using ribosomes which are made of ribosomal RNA which is produced using RNA polymerase.

40. B
Option A is incorrect as hydrogen bonds join the DNA strands. Option C is incorrect as three hydrogen bonds form between only adenine and thymine base pairs. Option D is incorrect as the number of cytosine bases equals the number of guanine bases. Hence, option B is the correct answer as the antiparallel strands help in the formation of the double helix.

41. C
Option C is the correct answer as a shorter polypeptide means that there is a premature STOP codon in the triplet code. This is shown in option C where the T in TTC is replaced by ATC resulting a premature STOP codon.

42. D
Option D is the correct answer as the tRNA anticodon is the exactly same as the DNA codon with the exception that thymine is replaced with uracil.

43. A
Option A is the correct answer as since the direction of transcription is upwards the part represented by option A is the portion of the strand that has not been transcribed.

44. D
Option D is the correct answer as cytosine is a pyrimidine as there are 3 hydrogen bonds between cytosine and guanine. 2 is ribose as the strand is being replicated in the 5' to 3' direction.

45. B
Option B is the correct answer as first mRNA binds to the ribosome and then tRNA enters carrying a specific amino acid. This is followed by the formation of hydrogen bonds between codons and anticodons and finally the peptide bonds between adjacent amino acids form.

46. C
1 is incorrect as this mRNA produces 248 amino acids as the stop codon does not code for any amnio acids. 3 is incorrect as during translation an RNA adenine will pair with a RNA uracil. 4 is incorrect as DNA and RNA has pentose sugars not hexose. Hence only statement 2 is correct as the 2 codons have a combined total of 14 hydrogen bonds.

47. D
Option D is the correct answer as before leaving the nucleus during transcription complementary base bonds are broken and formed twice when DNA is unzipped and when mRNA molecule is produced.

48. C
Option C is the correct answer as the fourth codon is changed which codes for glycine now instead of arginine and all the rest of the codons are the same.

49. B
Option B is the correct answer as 1 gene codes for the alpha globin chain while the other codes for the beta globin chain.

50. B
Option B is the correct answer as using the complementary base paring and replacing thymine with uracil we find this to be the correct mRNA codon sequence.

51. C
Option C is the correct answer as since the DNA is double stranded that means one single strand has 6×10^3 nucleotides. Since each amino acid is coded for by 3 codons dividing this by 3 gives 2×10^3 as the maximum number of amino acids.

52. D
Option D is the correct answer as purines and pyrimidines have different sizes due to their ring structure. Adenine forms 2 hydrogen bonds with both thymine and uracil. The base pairs in DNA are all of an equal length and width. Cytosine forms 3 hydrogen bonds with guanine.

53. B
Option B is the correct answer as a eukaryotic gene is a sequence of nucleotides that forms part of a DNA molecule and codes for a polypeptide.

54. D
Statement 1 is incorrect as deletion of C from the leu codon will not result in any stop codon forming. Statements 2 and 3 are correct as deletion of C from the tyr codon causes a premature STOP codon to form and when the ribosome reaches the UAA codon the polypeptide synthesis stops. Hence, option D is the correct answer.

55. C
The 8th nucleotide in the sequence is changed as changing it from G to C results in the stop codon UGA coming after 2 amino acids. Hence, option C is the correct answer.

56. C
Option C is the correct answer as the codon sequence would be AUG and the DNA sequence complementary to this would be TAC.

57. B
In the first generation all the molecules will be hybrid whereas in the third generation one quarter will be hybrids and three quarters will be light. Hence, option B is the correct answer.

58. B
Antibiotics binding to RNA polymerase means that they will stop the condensation reactions that cause the RNA nucleotides to join to each other and as a result mRNA won't be formed. Hence, option B is the correct answer.

59. D
The tRNA anticodons for asparagine, threonine, proline, and glutamic acid are UUA, UGA, GGA, and CUU respectively. The corresponding mRNA codons would be AAU, ACU, CCU, and GAA. The DNA sequence complementary to these mRNA condons is TTATGGGACTT, making option D the correct answer.

60. C
In haemoglobin C, a mutation changes GAG (which codes for glutamic acid) to AAG (which codes for lysine). This amino acid substitution results in a change from glutamic acid to lysine. Hence, C is correct.

61. B
Option B is the correct answer as it this point if a thymine base is inserted the mRNA codon UAG occurs which stops the translation.

62. A
The maximum number of codon-anticodon interactions in a ribosome are 2 making option A the correct answer.

63. B
Statements 1 and 2 are correct as tRNA contain a site for the attachment of an amino acid and a site for attachment to the ribosome. tRNA contain a ribose-phosphate backbone and areas within the folded polynucleotide that allows for base pairing to occur. Statement 3 is incorrect as the DNA triplet would contain thymine instead of uracil so the sequence cannot be the same. Hence, option B is the correct answer.

64. B

Statements 1 and 3 are correct as complementary base pairing occurs during translation between codons and anticodons and all the base pairs are of the same length. Statements 2 and 4 are incorrect as purines are larger than pyrimidines and adenine forms 2 hydrogen bonds with uracil.

65. B

Since the DNA is double stranded that means one strand would contain 3000 nucleotides. Since a codon consists of 3 nucleotides dividing 3000 by 3 gives 1000 amino acids. Hence, option B is the correct answer.

66. C

Statements 1 and 3 are correct as hydrogen bonds hold tRNA against mRNA during translation and tRNA translates the mRNA sequence into amino acids that form a polypeptide chain. Statement 2 is incorrect as the base sequence between tRNA and mRNA is complementary. Hence, option C is the correct answer.

67. C

Option C is the correct answer as the subunits of ribosomes consist of rRNA and protein.

68. A

Since the DNA is double stranded that means one strand would contain 60 nucleotides. Since a codon consists of 3 nucleotides dividing 60 by 3 gives 20 amino acids. Hence, option A is the correct answer.

69. C

Option C is the correct answer as the codon would be CAU which means that the DNA sequence would be GTA.

70. C

Option C is the correct answer as the person with the disease is missing the AAA sequence which translates to UUU codon.

71. B

Option B is the correct answer as the serine codon is AGU which corresponds to TCA in the DNA.

72. A

All the 3 statements are correct as in DNA replication, transcription and translation ATP provides energy, complementary base pairing occurs and condensation reactions occur. Hence, option A is the correct answer.

73. C

Option C is the correct answer as by finding the complementary RNA sequence of the nucleotide sequence gives we can find the correct amino acid sequence.

74. B

Option B is the correct answer as first the mRNA enters the ribosome. Then the tRNA carrying the specific amino acid hydrogen bonds with the codon and a peptide bonds forms between the adjacent amino acids.

75. C

There are 2 possibilities. The first one is that there is a premature STOP codon and the second one is that the codon for tryptophan emerges which does not contain any sulfur atom so no disulfide linkage can form. The DNA sequences for the STOP codon and tryptophan are ACT and ACC respectively making option C the correct answer.

76. C

Option C is the correct answer as inhibiting RNA polymerase would cause the inability of the bacteria to carry out transcription and then translation as no mRNA is produced.

77. D

Multiple ribosomes forming chains means that the polypeptides are produced more rapidly and different chains can be joined together to form the end product. Hence, option D is the correct answer.

78. B

Option B is the correct answer as the A nucleotide replaced the T from the normal sequence and this results in valine being incorporated into the polypeptide.

79. A

All the 3 statements are correct since tRNA molecules fold in on themselves and form hydrogen bonds with the complementary bases. They are also single stranded molecules. Hence, option A is the correct answer.

80. D

Options A, B and C are incorrect as mRNA does not have the same sequence as the DNA strand form which it is made and in transcription tRNA is not synthesized and in translation mRNA is not made. Hence, option D is the correct answer as in translation ribosomes produced mRNA which has a sequence complementary to the DNA nucleotides.

81. C
Rifampicin inhibits RNA polymerase, directly blocking transcription (the synthesis of RNA from DNA). It does not affect ATP synthesis or transaltion directly. Hence, C is correct.

82. A
All the 3 statements are correct as assuming a mutation occurs at the nucleotide level that sequence changes which results in the sequence of mRNA changing and this ultimately causes a different protein to be produced. Hence, option A is the correct answer.

83. A
Option A is the correct answer as leu is coded by 2 different codons. Option B is incorrect as the code can be read in the opposite direction as well but the result will be different. Option C is incorrect as this does not show in any way that the triplet code in universal. Option D is incorrect as the stop codons are not shown in the sequence.

84. D
Statements 1 and 2 are correct only since before leaving the nucleus bonds between complementary bases are broken twice once when the DNA molecule is acted upon by helicase and second when the mRNA detaches form the DNA strand. Similarly, the bonds between complementary bases also form twice once when the DNA zips back together and second when mRNA is being produced. Hence, option D is the correct answer.

85. A
All the 3 statements are correct since tRNA molecules fold in on themselves and form hydrogen bonds with the complementary bases. They are also single stranded molecules and contain uracil in place of thymine. Hence, option A is the correct answer.

86. B
Option B shows the correct sequence after checking the complementary mRNA sequence of the nucleotide sequence given.

87. A
Adding 4,5 and 9 gives 16 base pairs meaning the remaining 2 must be adenine thymine pairs. Hence, option A is the correct answer.

88. A
Option A is the correct answer as the Ala-Ala-Cys-Ala is the correct sequence that forms as a result of the complementary mRNA.

89. B
If the formation of peptide bonds in inhibited this means that the amino acids cannot be condensed. Hence, option B is the correct answer.

90. D
Transcription refers to the production of mRNA which is accomplished via RNA polymerase. Hence, option D is the correct answer.

91. D
Option D is the correct answer as in an amino acid the peptide bonds hold together adjacent amino acids.

92. C
Option C is the correct answer the ribosomes subunits are made of rRNA and protein.

93. B
Option B is the correct answer as AU pairs are held together by 2 hydrogen bonds and CG pairs are held together by 3 hydrogen bonds.

94. C
Option C is the correct answer as AU pairs are held together by 2 hydrogen bonds and GC pairs are held together by 3 hydrogen bonds.

6.3: Multiple topics

1. A
At a replication rate of 50 base pairs per second, replicating 150 million base pairs in 1 hour requires about 835 replication forks to ensure the DNA is copied in time.

2. **A**
Mutations in both *BRAC1* and *p53* genes lead to uncontrolled cell division, increasing the likelihood of breast cancer development. A normal gene for *p53* (tumor suppressor) or *BRAC1* (growth inhibitor) would reduce this risk.
3. **C**
Option C is the correct answer as an error during replication could result in the sequence of nucleotides being altered which results in a different protein being produced.
4. **B**
Statements 1 and 2 are correct as uracil is a pyrimidine and since it is found in RNA only it contains the ribose sugar. Statement 3 is incorrect as uracil forms 2 hydrogen bonds with adenine. Hence, option B is the correct answer.
5. **B**
Option B is the correct answer as uracil is a pyrimidine meaning it has a single ring structure. It pairs with adenine using 2 hydrogen bonds.
6. **B**
Option B is the correct answer as even with the nucleotide mutations the codons still code for the same amino acid meaning that the polypeptide produced is the same.
7. **A**
Option A is the correct answer as inhibiting protein synthesis in mitochondria means the rate of ATP production decreases and transcription of nuclear DNA also decrease since it does not inhibit processes in the cytoplasm but transcription occurs in the nucleus.
8. **D**
Option D is the correct answer as inhibiting RNA polymerase means that transcription can no longer take place.
9. **B**
Option B is the correct answer as thymine is a pyrimidine meaning it has a single ring structure. It pairs with adenine using 2 hydrogen bonds.
10. **C**
Option C is the correct answer as hydrolysis, transcription and translation occur in both eukaryotes and prokaryotes but mitosis only occurs in eukaryotes as prokaryotes divide via binary fission.
11. **C**
Option C is the correct answer as statements 1, 3 and 4 are correct. Statement 2 is incorrect as nucleotides form RNA contain the sugar ribose while those from DNA contain deoxyribose so they are not the same.
12. **A**
As the cells divide the telomeres keep on shortening. Hence the cell with the least number of total bases has undergone the most mitotic divisions. This makes option A the correct answer.
13. **B**
Since there are alpha and beta globin and then they are repeated only 2 genes are requires for the synthesis of each polypeptide. Hence, option B is the correct answer.
14. **B**
Option B is the correct answer as tRNA carry the specific amino acids to the ribosome and they hold them in place during the process of translation.
15. **A**
Option A is the correct answer as in DNA replication, transcription and translation ATP always provides the energy, condensation reactions occur and purines pair with pyrimidines.
16. **C**
Option A is incorrect as ribosomes do not join amino acids to tRNA. Option B is incorrect as codons are on mRNA and anticodons are on tRNA. Option D is incorrect as rRNA is not produced by ribosomes. Hence, option C is the correct answer as peptide bonds will not be able to be formed between adjacent amino acids.
17. **D**
Option D is the correct answer as mRNA carries genetic code from the nucleus to the ribosomes.
18. **D**
Option D is the correct answer as only statement 2 is correct as a codon changed in the mRNA can cause a non-functional protein to be produced.

19. C

Option C shows the correct sequence where form the ribosome the protein goes to the rough ER and from there it is packaged into a vesicle and sent to the Golgi body for modifications.

20. A

Option A is the correct answer as both DNA and RNA contain purines and pyrimidines. They both also contain a pentose sugar and folding in RNA molecules can cause complementary base pairing to occur.

21. A

Option A is the correct answer as DNA and mRNA are involved in transcription and mRNA and tRNA are involved in translation.