1. The five nitrogen bases found in nucleotides:

   - Adenine
   - Guanine
   - Cytosine
   - Thymine
   - Uracil

2. A nucleoside is a purine or pyrimidine base linked to a sugar molecule, usually ribose or deoxyribose. A nucleotide is a purine or pyrimidine base linked to a ribose or deoxyribose sugar which in turn is linked to a phosphate group.

3. There are three structural differences between DNA and RNA.
   (a) In RNA the sugar molecule is always ribose. In DNA, the sugar molecule is always deoxyribose, which has H instead of OH at carbon number two.
   (b) Both molecules use a mixture of four nitrogen bases. Both use cytosine, adenine, and guanine. In DNA, the fourth base is thymine. In RNA, the fourth base is uracil.
   (c) DNA exists as a double helix whereas RNA is a single strand of nucleotides.

4. The major function of ATP in the body is to store chemical energy, and to release it when called upon to carry out many of the complex reactions that are essential to most of our life processes. An equilibrium exists with ADP.

   \[
   \text{ATP} + \text{H}_2\text{O} \xrightarrow{\text{energy utilization}} \text{ADP} + \text{P}_i + 35 \text{ kJ}
   \]
5. The structure of DNA as proposed by Watson and Crick is a double-stranded helix. Each strand has a backbone of alternating phosphate and deoxyribose units. Each deoxyribose unit has one of the four nitrogen bases attached, but coming off the backbone, not part of the backbone. These nitrogen bases thus link to their complementary nitrogen base on the other strand of the double helix.

6. Complementary bases are the pairs that “fit” to hydrogen bond to each other between the two helixes of DNA. For DNA the complementary pairs are thymine with adenine, and cytosine with guanine, or T-A and C-G. For RNA it is U-A and C-G.

7. The genetic code is the sequence of nitrogen bases in a strand of DNA. The code determines the sequence of amino acids in protein molecules which will be assembled according to the code. It takes three nucleotides to make a codon, which determines one amino acid in a sequence.

8. Since there are only four different bases to make up the code, one nucleotide could only specify four possible amino acids; two nucleotides could specify 16 amino acids; 3 nucleotides could specify 64 amino acids. Since there are at least 20 amino acids needed, three nucleotides are required.

9. A brief outline of the biosynthesis of proteins:
   (a) A DNA strand produces a complementary mRNA strand which leaves the nucleus and travels to the cytoplasm where it becomes associated with a cluster of ribosomes, binding to five or more ribosomes.
   (b) With the aid of an enzyme, the proper amino acid attaches to a tRNA molecule by an ester linkage.
   (c) The amino acids are brought to the protein synthesis site by tRNA.
   (d) The initiation of a polypeptide chain always uses the mRNA codon AUG or GUG, which ties to the tRNA anticodon UAC. This code brings N-formylmethionine for procaryotic cells. The amino group is blocked by the formyl group, leaving the carboxyl group available to react with the amino group of the next amino acid.
   (e) The next tRNA, bringing an amino acid, comes in to the mRNA and links up, anticodon to codon. The peptide linkage is then made between amino acids.
   (f) The first tRNA is ejected, and a third enters the ribosome.
   (g) The polypeptide chain terminates at a nonsense or termination-codon. The protein molecule breaks free.

10. Initiation of protein synthesis requires a special codon and starts with a single amino acid. In contrast, elongation requires an unfinished protein chain and, depending on the mRNA, may use any of the standard codons.
11. Termination of protein synthesis occurs when a “nonsense” or termination codon appears. Since no tRNA’s recognize these codons, protein synthesis stops. In contrast, elongation requires an unfinished protein chain and, depending on the mRNA, may use any of the standard codons.

12. A codon is a triplet of three nucleotides, and each codon specifies one amino acid. The cloverleaf model of transfer RNA has an anticodon loop consisting of seven unpaired nucleotides. Three of these make up the anticodon, which is complementary to, and hydrogen-bonds to the codon on mRNA.

13. The role of N-formylmethionine in procaryotic protein synthesis is to start the polypeptide chain so it goes in the right direction. It can only build from the carboxyl end. After the synthesis, the N-formylmethionine breaks loose from the protein.

14. From time to time a new trait appears in an individual that is not present in either parents or ancestors. These traits which are generally the result of genetic or chromosomal changes are called mutations.

15. A “DNA fingerprint” is a pattern of tagged DNA fragments on an electrophoretic gel which can be used to identify possible suspects.

16. With the knowledge of gene structure genetic therapists can observe DNA that has genetic defects and work towards deleting the error and replace the defect with a corrected gene. Geneticists will be able to tell in advance who is prone to getting certain diseases. They will be able to more accurately detect and predict birth defects, and in general have a better understanding of inherited diseases.

17. An oncogene is present in cancerous or malignant cells and codes for a protein that controls cell growth.

18. Apoptosis is an internal mechanism that kills cells when they are no longer needed or are malfunctioning. Many cancers occur because the cells’ apoptosis malfunctions. Scientists hope to be able to “restart” apoptosis and cause the cancers to self-destruct.

19. The tumor-suppressor gene codes for cells that allow for cell growth only if the cells are functioning correctly. When the tumor-suppressor gene is active and detects a cellular problem (cancer, for example), it triggers a command that leads to cell destruction.
CHAPTER 31

SOLUTIONS TO EXERCISES

1. The letters are associated with compound names as follows:
   (a) A, adenosine
   (b) AMP, adenosine-5’-monophosphate
   (c) dADP, deoxyadenosine-5’-diphosphate
   (d) UTP, uridine-5’-triphosphate

2. The letters are associated with compound names as follows:
   (a) G, guanosine
   (b) GMP, guanosine-5’-monophosphate
   (c) dGDP, deoxyguanosine-5’-diphosphate
   (d) CTP, cytidine-5’-triphosphate

3. Structural formulas
   (a) A
   (b) AMP
   (c) CDP
   (d) dGMP
4. Structural formulas
(a) U
(b) UMP
(c) CTP
(d) dTMP

5. (a)
(b)
6. 
(a) 
(b) 

7. 

8. 

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9. There are several sequences possible for the three-nucleotide, single-stranded DNA. One possible structure follows:
10. There are several possible sequences for the three-nucleotide, single-stranded RNA. One possible structure follows:

11. The hydrogen bonding between adenine and uracil:

(dotted lines—hydrogen bonds)

adenine  uracil
12. The hydrogen bonding between guanine and cytosine:

\[
\begin{array}{c}
\text{H} \\
\text{O}\cdots\text{N} \\
\text{N}\cdots\text{N} \\
\text{N}\cdots\text{N} \\
\text{H}\cdots\text{O} \\
\text{N} \\
\text{H} \\
\end{array}
\]

(dotted lines—hydrogen bonds)

13. RNA is responsible for moving genetic information to where it can be used for protein synthesis. There are three kinds of RNA:

(a) Ribosomal RNA (rRNA) is found in the ribosomes where it is associated with protein roughly in the proportion 60–65% protein, 30–35% rRNA.

(b) Messenger RNA (mRNA) carries genetic information from DNA to the ribosomes. It is a template made from DNA and carries the codons that direct the synthesis of proteins.

(c) Transfer RNA (tRNA) is used to bring amino acids to the ribosomes for incorporation into protein molecules.

14. DNA is considered to be the genetic substance of life, because it contains the sequence of bases that carries the code for genetic characteristics.

15. Replication is the biological process of making DNA using a DNA template while the transcription process refers to the making of RNA using a DNA template.

16. Transcription is the process of making RNA using a DNA template while translation is a process for making protein using a mRNA template.

17. tRNA binds specific amino acids and brings them to the ribosome for protein synthesis. mRNA carries genetic information from DNA to the ribosome and serves as a template for protein synthesis.

18. Both mRNA and rRNA can be found in the ribosomes. rRNA serves as part of the ribosome structure while mRNA serves as a template for protein synthesis.

19. Three nucleotides are required to specify one amino acid. If there are 146 amino acid residues in the beta chain of hemoglobin, then the number of required nucleotides in mRNA is \(3 \times 146 = 438\).
20. Three nucleotides are required to specify one amino acid. For the 573 amino acid residues in the phosphoglycerate kinase enzyme, the number of required nucleotides in mRNA is
\[ 3 \times 573 = 1719. \]

21. For a DNA sequence, TCAATACCCGCG,
(a) the complementary mRNA will be: AGUUAUGGGCGC.
(b) the anticodon order in tRNA will be: UCAAUACCCGCG.
(c) the sequence of amino acids coded by the DNA will be: Ser-Tyr-Gly-Arg

22. A segment of DNA strand consists of GCTTAGACCTGA.
(a) The order in the complementary mRNA will be: CGAAUCUGGACU.
(b) The anticodon order in tRNA will be: GCUUAGACCUGA.
(c) The sequence of amino acids coded by the DNA is Arg-Ile-Trp-Thr.

23. Transcription makes a polymer of nucleotides by forming phosphate ester bonds to connect the nucleotides to each other. The phosphate ester combines a phosphoric acid with an alcohol.

24. Translation makes a polymer of amino acids by forming amide bonds to connect the amino acids to each other. The amide bond combines an amine with a carboxylic acid.

25. Translation termination occurs when the ribosome reaches a “nonsense” or termination codon along the mRNA. No tRNA (in normal cells) has the anticodon to match the termination codon and so no more amino acids are added to the newly synthesized protein chain. The peptidyl-tRNA connection is broken and the protein chain is released from the ribosome.

26. Translation initiation occurs when the ribosome reaches a special AUG or GUG codon along the mRNA. Since there is commonly more than one AUG or GUG codon, the ribosome must use other information to choose the special AUG or GUG. This codon is the starting point for protein synthesis and is bound by either a special tRNA carrying N-formylmethionine (in procaryotes) or a tRNA carrying methionine (in eucaryotes).

27. mRNA codons and corresponding tRNA anticodons follow:
(a) GUC: anticodon is CAG
(b) AGG: anticodon is UCC
(c) UUU: anticodon is AAA
(d) CCA: anticodon is GGU

28. mRNA codons and corresponding tRNA anticodons follow:
(a) CGC: anticodon is GCG
(b) ACA: anticodon is UGU
(c) GAU: anticodon is CUA
(d) UUC: anticodon is AAG
29. The original mRNA sequence codes for amino acids, …Leu-Pro-Thr… The mutation changes the first amino acid to Phe, so the sequence becomes …Phe-Pro-Thr… This mutation can change the function of the protein.

30. The original mRNA sequence codes for the amino acids …Val-Gln-Lys… The mutation changes the second codon to a termination or nonsense codon UAA. The protein will end at this point and may cause a major disruption of the protein function.

31. “Recombinant” means the DNA has genes that have been rearranged to contain new or different hereditary information.

32. “Nonsense” means the codon does not code for an amino acid. Instead, this codon causes translation to stop. (It is also known as a termination code.)
37. Thymine and adenine are complementary bases in DNA; therefore each time one appears, its complement appears. There is no fixed relationship between the amount of thymine and the amount of guanine, since they are not complementary. Table 31.2 shows that the one set of bases is often far different from the other set, varying by as much as a 3:2 ratio. The complementary bases “fit” with each other with respect to H-bonding between them; also with respect to the size of the molecules.

38. This thymine isomer now has the appropriate H-bonding groups to connect with guanine instead of adenine.

39. A substitution mutation will change one codon. An insertion mutation will shift the sequence position of all bases following the insertion by one. Each base will take the position of its neighbor. For example, if base $\underline{C}$ is inserted into the sequence $\ldots$ UUC ACG GCC $\ldots$, every codon will change, $\ldots$ U$\underline{C}$ U CAC GGC C $\ldots$

In general, every codon following an insertion is changed.

40. For the mRNA segment, UUUCAUAAG,
   (a) the coded amino acids are: Phe-His-Lys.
   (b) the sequence of DNA for this mRNA is: AAAGTATTC.

41. In DNA fingerprinting, DNA polymerase is used to copy very small samples of DNA so that enough will be available to separate and visualize on gel electrophoresis.

42. The Human Genome Project is a cooperative effort by leading scientific laboratories to sequence the entire human genome (approximately 3 billion base pairs).

43. No, RNA would not be predicted to have a 1:1 ratio of guanine to cytosine. In DNA, these bases have a 1:1 ratio because they are complementary and, thus, are found in equal amounts in the double stranded nucleic acid. Since RNA is most often found as a single stranded molecule, there is no requirement that the ratio of guanine to cytosine be set.