C1. It is the actual substance that contains genetic information. It is usually DNA, but in some viruses it can be RNA.

C2. The transformation process is described in Chapter 6.

1. A fragment of DNA binds to the cell surface.
2. It penetrates the cell wall/cell membrane.
3. It enters the cytoplasm.
4. It recombines with the chromosome.
5. The genes within the DNA are expressed (i.e., transcription and translation).
6. The gene products create a capsule. That is, they are enzymes that synthesize a capsule using cellular molecules as building blocks.

C3. Transformation means changing from one form to another. In bacterial genetics, transformation involves the uptake of DNA into another bacterium. This may change the form (i.e., phenotype) of the bacterium. For example, transformation may change a rough bacterial strain into a smooth strain. The form or phenotype of the strain has been changed.

C4. The building blocks of a nucleotide are a sugar (ribose or deoxyribose), a nitrogenous base, and phosphate. In a nucleotide, the phosphate is already linked to the 5′ position on the sugar. When two nucleotides are hooked together, a phosphate on one nucleotide forms a covalent bond with a hydroxyl group at the 3′ position on another nucleotide.

C5. The structures can be deduced from Figures 9.8 and 9.9. Guanine is the base by itself. Guanosine is the base attached to a ribose sugar. Deoxyguanosine triphosphate is a base attached to a deoxyribose sugar with three phosphates.

C6. It is a phosphate group connecting two sugars at the 3′ and 5′ positions as shown in Figure 9.11.

C7. The bases conform to the AT/GC rule of complementarity. There are two hydrogen bonds between A and T and three hydrogen bonds between G and C. The planar rings of the bases stack on top of each other within the helical structure to provide even more stability.

C8. 3′–CCGTAATGTGATCCGGA–5′

C9. The sequence of nucleotide bases.

C10. A drawing with 10 bp per turn is like Figure 9.17 in the textbook. To make 15 bp per turn, you would have to add 5 more base pairs, but the helix should still make only one complete turn.

C11. A and B DNA are right-handed helices and the backbones are relatively helical, whereas Z DNA is left-handed and the backbone is rather zigzagged. A DNA and Z DNA have the bases tilted relative to the central axis, whereas they are perpendicular in B DNA. There are also minor differences in the number of bases per turn.

C12. The nucleotide bases occupy the major and minor grooves. Phosphate and sugar are found in the backbone. If a DNA-binding protein did not recognize a nucleotide sequence, it is probably not binding in the grooves, although it could in a nonspecific way. As an alternative, it is probably binding to the DNA backbone (i.e., sugar-phosphate sequence).

C13. DNA has deoxyribose as its sugar while RNA has ribose. DNA has the base thymine while RNA has uracil. DNA is a double helical structure. RNA is single stranded although parts of it may form double-stranded regions.

C14. The structure is shown in Figure 9.8. You begin at the carbon that is to the right of the ring oxygen and number them in a clockwise direction. Antiparallel means that the backbones are running in the opposite direction. In one strand, the sugar carbons are oriented in a 3′ to 5′ direction while in the other strand they are oriented in a 5′ to 3′ direction.

C15. Here is an example of an RNA molecule that could form a hairpin that contains 24 nucleotides in the stem and 16 nucleotides in the loop.

5′–GAUCCCUAAACGGAUCCCAGGACUCCCACGUUUAGGGAUC–3′

The complementary stem regions are underlined.

C16. Double-stranded RNA is more like A DNA than B DNA. See the text for a discussion of A-DNA structure.

C17. The sequence in part A would be more difficult to separate because it has a higher percentage of GC base pairs compared to the one in part B. GC base pairs have three hydrogen bonds compared with AT base pairs, which only have two.

C18. Its nucleotide base sequence.

C19. Complementarity is important in several ways. First, it is needed to copy genetic information. This occurs during replication, when new DNA strands are made, and during transcription, when RNA strands are made. Complementarity is also important during translation for codon/anticodon recognition. It also allows RNA molecules to form secondary structures and to recognize each other.

C20. G = 32%, C = 32%, A = 18%, T = 18%

C21. The key issue in the answer is that there are base pairing rules. Otherwise, it would not be possible to replicate the genetic material. One answer would be that the DNA is composed of double helix obeying the AT/GC rule and the third strand binds to the major groove so that X binds next to AT pairs and Y binds next to GC pairs. This would explain why the amounts of X, A, and T are approximately equal, as are the amounts of Y, G, and C. You could propose other correct scenarios.

C22. One possibility is a sequential mechanism. First, the double helix could unwind and copy itself via a semiconservative mechanism described in Chapter 11. This would produce two double helices. Next, the third strand (bound in the major groove) could copy itself via a semiconservative mechanism. This new strand could be copied to make a copy that is identical to the strand that lies in the major groove. At this point, you would have two double helices and two strands that could lie in the major groove. These could assemble to make two triple helices.

C23. The number of bases per turn is different between an RNA double helix and a DNA double helix. Also, protein binding may be affected by the structure of the sugar, which is ribose in RNA but deoxyribose in DNA.

C24. Lysines and arginines, and also polar amino acids.

C25. Both structures are helical and both are stabilized by hydrogen bonds. An *a* helix in proteins is a single-stranded structure; it is formed from a single polypeptide chain. A DNA double helix is formed from the interaction of two separate strands. With regard to the chemistry of the interactions that stabilize an *a* helix and a DNA double helix, there are some interesting similarities and differences. As already mentioned, hydrogen bonding stabilizes the *a* helix, but it is hydrogen bonding along the backbone; carbonyl oxygens and amide hydrogens in the polypeptide backbone interact with each other. The amino acid side chains, which project from the polypeptide backbone, may also interact favorably, but that is not a consistent feature of an *a* helix. In a DNA double helix, the hydrogen bonds are between bases (that project from the backbone) that are in separate strands. Base stacking also is a consistent feature that stabilizes the DNA double helix. Stacking of amino acid side chains does not occur within a single α helix.

C26. This DNA molecule contains 280 bp. There are 10 base pairs per turn, so there are 28 complete turns.

C27. They always run parallel.

C28. A hydroxyl group is at the 3′ end and a phosphate group is at the 5′ end.

C29. You would conclude that it is probably double-stranded RNA because the amount of A equals U and the amount of G equals C. Therefore, this molecule could be double stranded and obey the AU/GC rule. However, it is also possible that it is merely a coincidence that A happens to equal U and G happens to equal C and the genetic material is really single stranded.

C30. Not necessarily. The AT/GC rule is required only of double-stranded DNA molecules.

C31. There are 10^8 base pairs in this chromosome. In a double helix, a single base pair traverses about 0.34 nm, which equals 0.34×10^{-9} meters. If we multiply the two values together:

$$10^8 (0.34 \times 10^{-9}) = 0.34 \times 10^{-1} \text{ m, or } 0.034 \text{ m, or } 3.4 \text{ cm.}$$

The answer is 3.4 cm, which equals 1.3 inches! That is enormously long considering that a typical human cell is only 10 to 100 μm in diameter. As described in Chapter 10, the DNA has to be greatly compacted to fit into a living cell.

C32. The first thing we need to do is to determine how many base pairs are in this DNA molecule. The linear length of 1 base pair is 0.34 nm, which equals 0.34×10^{-9} m. One centimeter equals 10^{-2} meters.

$$\frac{10^{-2}}{0.34 \times 10^{-9}} = 2.9 \times 10^7 \text{ bp}$$

There are approximately 2.9×10^7 bp in this DNA molecule, which equals 5.8×10^7 nucleotides. If 15% are adenine, then 15% must also be thymine. This leaves 70% for cytosine and guanine. Since cytosine and guanine bind to each other, there must be 35% cytosine and 35% guanine. If we multiply 5.8×10^7 times 0.35, we get

$$(5.8 \times 10^7)(0.35) = 2.0 \times 10^7 \text{ cytosines, or about 20 million cytosines}$$

C33. Yes, as long as there are sequences that are complementary and antiparallel to each other. It would be similar to the complementary double-stranded regions observed in RNA molecules (e.g., see Figures 9.23 and 9.24).

C34. The methyl group is not attached to one of the atoms that hydrogen bonds with guanine, so methylation would not directly affect hydrogen bonding. It could indirectly affect hydrogen bonding if it perturbed the structure of DNA. Methylation may affect gene expression because it could alter the ability of proteins to recognize DNA sequences. For example, a protein might bind into the major groove by interacting with a sequence of bases that includes one or more cytosines. If the cytosines are methylated, this may prevent a protein from binding into the major groove properly. Alternatively, methylation could enhance protein binding. In chapter 7, we considered DNA-binding proteins that were influenced by the methylation of DMRs (differentially methylated regions) that occur during genomic imprinting.

C35. Region 1 cannot form a stem-loop with region 2 and region 3 at the same time. Complementary regions of RNA form base pairs, not base triplets. The region 1/region 2 interaction would be slightly more stable than the region 1/region 3 interaction because it is one nucleotide longer, and it has a higher amount of GC base pairs. Remember that GC base pairs form three hydrogen bonds compared to AU base pairs, which form two hydrogen bonds. Therefore, helices with a higher GC content are more stable.