- 1. The DNA double helix is held together by two types of bonds, covalent and hydrogen. Covalent bonds occur within each linear strand and strongly bond the bases, sugars, and phosphate groups (both within each component and between components). Hydrogen bonds occur between the two strands and involve a base from one strand with a base from the second in complementary pairing. These hydrogen bonds are individually weak but collectively quite strong.
- **3.** A primer is a short segment of RNA that is synthesized by primase using DNA as a template during DNA replication. Once the primer is synthesized, DNA polymerase then adds DNA to the 3' end of the RNA. Primers are required because the major DNA polymerase involved with DNA replication is unable to initiate DNA synthesis and, rather, requires a 3' end. (It is the 3' -OH group that is required to create the next phosphodiester bond.) The RNA is subsequently removed and replaced with DNA so that no gaps exist in the final product.
- 4. Helicases are enzymes that disrupt the hydrogen bonds that hold the two DNA strands together in a double helix. This breakage is required for both RNA and DNA synthesis. Topoisomerases are enzymes that create and relax supercoiling in the DNA double helix. The supercoiling itself is a result of the twisting of the DNA helix that occurs when the two strands separate.
- 5. Because the DNA polymerase is capable of adding new nucleotides only at the 3' end of a DNA strand, and because the two strands are antiparallel, at least two molecules of DNA polymerase must be involved in the replication of any specific region of DNA. When a region becomes single-stranded, the two strands have an opposite orientation. Imagine a single-stranded region that runs from right to left. The 5' end is at the right, with the 3' end pointing to the left; synthesis can initiate and continue uninterrupted toward the right end of this strand. Remember: new nucleotides are added in a 5' \rightarrow 3' direction, so the template must be copied from its 3' end. The other strand has a 5' end at the left with the 3' end pointing right. Thus, the two strands are oriented in opposite directions (antiparallel), and synthesis (which is $5' \rightarrow 3'$) must proceed in opposite directions. For the leading strand (say, the top strand) replication is to the right, following the replication fork. It is continuous and may be thought of as moving "downstream." Replication on the bottom strand cannot move in the direction of the fork (to the right) because, for this strand, that would mean adding nucleotides to its 5' end. Therefore, this strand must replicate discontinuously: as the fork creates a new single-stranded stretch of DNA, this is replicated to the left (away from the direction of fork movement). For this lagging strand, the replication fork is always opening new single-stranded DNA for replication *upstream* of the previously replicated stretch, and a new fragment of DNA is replicated back to the previously created fragment. Thus, one (Okazaki) fragment follows the other in the direction of the replication fork, but each fragment is created in the opposite direction.
- **14.** d. Replication would take twice as long.
- 15. a. Prior to the S phase, each chromosome has two telomeres, so in the case of 2n = 14, there are 14 chromosomes and 28 telomeres.
 - **b.** After S, each chromosome consists of two chromatids, each with two telomeres, for a total of four telomeres per chromosome. So, for 14 chromosomes, there would be $14 \times 4 = 56$ telomeres.

- c. At prophase, the chromosomes still consist of two chromatids each, so there would be $14 \times 4 = 56$ telomeres.
- **d.** At telophase, there would be 28 telomeres in each of the soon-to-be daughter cells.
- 17. If the DNA is double stranded, G = C = 24% and A = T = 26%.
- **22.** The bottom strand will serve as the template for the Okazaki fragment so its sequence will be:

5'CCTTAAGACTAACTACTTACTGGGATC....3'

24. Sample A must be live S cells because it kills mice when injected and S cells are recovered from the mice.

Sample C must be live R cells because it has no effect on mice when injected but live R cells are recovered.

Sample B must be DNA from S cells as it transforms sample C when co-injected.