**Chapter Review**

**Chapter 6: Genes and Genomes**

6.1

Most eukaryotic genes have a split structure in which segments of coding sequence (exons) are interrupted by noncoding sequences (introns). In mammals, introns account for more than ten times as much DNA as exons. Although they are removed from mRNAs, introns have multiple cellular functions. Some proteins or RNAs are encoded within introns of larger genes. In addition, introns contain transcriptional regulatory sequences and allow alternative splicing.

6.2

About two-thirds of mammalian genomes are composed of sequences other than protein-coding genes. Many genes encode regulatory RNAs, including miRNAs and lncRNAs. Mammalian genomes encode more lncRNAs than proteins. Over 50% of mammalian DNA consists of highly repetitive DNA sequences, some of which are present in 105–106 copies per genome. These sequences include simple-sequence repeats as well as transposable elements that have moved throughout the genome by either RNA or DNA intermediates. In addition, many eukaryotic genes are present in multiple copies, called gene families, which have arisen by duplication of ancestral genes. Many members of gene families (pseudogenes) have been inactivated by mutations and no longer represent functional genes.

6.3

The DNA of eukaryotic cells is wrapped around histones to form nucleosomes and chromatin fibers. Chromatin fibers are loosely packed in transcriptionally active euchromatin but tightly packed in heterochromatin and metaphase chromosomes of cells undergoing mitosis. Centromeres are specialized regions of eukaryotic chromosomes that serve as the sites where sister chromatids are joined and the sites of spindle fiber attachment during mitosis. Centromere function is determined by a variant H3-like histone, which is epigenetically maintained at cell division.