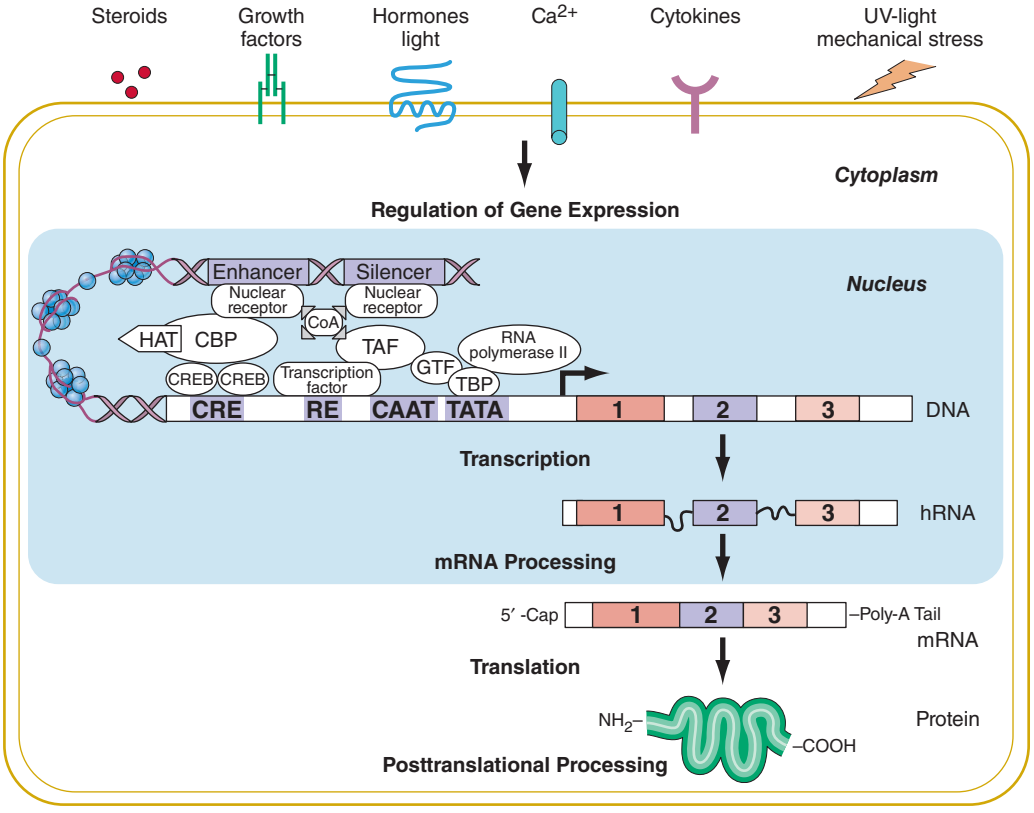

FIGURE 82-2 Flow of genetic information. Multiple extracellular signals activate intracellular signal cascades that result in altered regulation of gene expression through the interaction of transcription factors with regulatory regions of genes. RNA polymerase transcribes DNA into RNA that is processed to mRNA by excision of intronic sequences. The mRNA is translated into a polypeptide chain to form the mature protein after undergoing posttranslational processing. CBP, CREB-binding protein; CoA, co-activator; COOH, carboxyterminus; CRE, cyclic AMP responsive element; CREB, cyclic AMP response element–binding protein; GTF, general transcription factors; HAT, histone acetyl transferase; NH2, aminoterminus; RE, response element; TAF, TBP-associated factors; TATA, TATA box; TBP, TATA-binding protein.

sister chromatids ($2n \rightarrow 4n$) are formed for each chromosome pair and there is an exchange of DNA between homologous paternal and maternal chromosomes. This process involves the formation of *chiasmata*, structures that correspond to the DNA segments that cross over between the maternal and paternal homologues (Fig. 82-6). Usually there is at least one crossover on each chromosomal arm; recombination occurs more frequently in female meiosis than in male meiosis. Subsequently, the chromosomes segregate randomly. Because there are 23 chromosomes, there exist 2^{23} (>8 million) possible combinations of chromosomes. Together with the genetic exchanges that occur during recombination, chromosomal segregation generates tremendous diversity, and each gamete is genetically unique. The process of recombination and the independent segregation of chromosomes provide the foundation for performing linkage analyses, whereby one attempts to correlate the inheritance of certain chromosomal regions (or linked genes) with the presence of a disease or genetic trait (see below).

After the first meiotic division, which results in two daughter cells ($2n$), the two chromatids of each chromosome separate during a second meiotic division to yield four gametes with a haploid state ($1n$). When the egg is fertilized by sperm, the two haploid sets are combined, thereby restoring the diploid state ($2n$) in the zygote.

REGULATION OF GENE EXPRESSION

Regulation by Transcription Factors The expression of genes is regulated by DNA-binding proteins that activate or repress transcription. The number of DNA sequences and transcription factors that regulate transcription is much greater than originally anticipated. Most genes contain at least 15–20 discrete regulatory elements within 300 bp of the transcription start site. This densely packed promoter region often contains binding sites for ubiquitous transcription factors such as CAAT box/enhancer binding protein (C/EBP), cyclic AMP response element–binding (CREB) protein, selective promoter factor 1 (Sp-1), or activator protein 1 (AP-1). However, factors involved in cell-specific expression may also bind to these sequences. Key regulatory elements may also reside at a large distance from the proximal promoter. The globin and the immunoglobulin genes, for example, contain *locus control regions* that are several kilobases away from the structural sequences of the gene. Specific groups of transcription factors that bind to these promoter and enhancer sequences provide a combinatorial code for regulating transcription. In this manner, relatively ubiquitous factors interact with more restricted factors to allow each gene to be expressed and regulated in a unique manner that is dependent on developmental state, cell type, and numerous extracellular stimuli. Regulatory factors also bind within the gene itself, particularly in the intronic regions. The transcription factors that bind to DNA actually represent only the first level of regulatory control. Other proteins—*co-activators* and *co-repressors*—interact with the DNA-binding transcription factors to generate large regulatory complexes. These complexes are subject to control by numerous cell-signaling pathways and enzymes, leading to phosphorylation, acetylation, sumoylation, and ubiquitination. Ultimately, the recruited transcription factors interact with, and stabilize, components of the basal transcription complex that assembles at the site of the TATA box and initiator region. This basal transcription factor complex consists of >30 different proteins. Gene transcription occurs when RNA polymerase begins to synthesize RNA from the DNA template. A large number of identified genetic diseases involve transcription factors (Table 82-2).

The field of *functional genomics* is based on the concept that understanding alterations of gene expression under various physiologic and pathologic conditions provides insight into the underlying functional role of the gene. By revealing specific gene expression profiles, this knowledge may be of diagnostic and therapeutic relevance. The large-scale study of expression profiles, which takes advantage of microarray and bead array technologies, is also referred to as *transcriptomics*