- Most transposable elements are **retrotransposons**, which move by an RNA intermediate.
  - Retrotransposons always leave a copy at the original site during transposition because they are initially transcribed into an RNA intermediate.
- Retroviruses, which use reverse transcriptase to produce their DNA, may have evolved from retrotransposons.

Gene-related DNA makes up about 25% of the human genome.

- In most eukaryotic genomes, solitary genes make up less than half the total transcribed DNA.
  - The rest of the transcribed DNA occurs in **multigene families**, collections of two or more identical or very similar genes.
- The classic examples of multigene families of *nonidentical* genes are two related families of genes that encode globins, a group of proteins that include the **α and β polypeptide subunits of hemoglobin**.
  - One family, located on chromosome 16 in humans, encodes various forms of α-globin; the other, on chromosome 11, encodes forms of β-globin.
  - The different forms of each globin subunit are expressed at different times in development, allowing hemoglobin to function effectively in the changing environment of the developing animal.
  - In humans, embryonic and fetal forms of hemoglobin have a higher affinity for oxygen than the adult forms, thus ensuring the efficient transfer of oxygen from mother to fetus.

<u>Concept 21.6 Comparing genome sequences provides clues to evolution and development</u>

Comparisons of genome sequences from different species tell about the evolutionary history of life.

- The more similar in sequence the genes and genomes of two species, the more closely related those species are in their evolutionary history.
- Comparing the genomes of closely related species provides information about recent evolutionary events; comparing the genomes of distantly related species sheds light on ancient evolutionary history.
- Analyzing **highly conserved** genes in distantly related species can help clarify evolutionary relationships among species that diverged long ago.
  - Comparisons of the complete genome sequences of bacteria, archaea, and eukaryotes strongly support the theory that these groups are the fundamental domains of life.

Comparative studies of the genetic programs that direct embryonic development clarify mechanisms that have generated the great diversity of life.

- Biologists in the field of evolutionary developmental biology, or **evo-devo**, compare the developmental processes of multicellular organisms.
  - Their goal is to understand how these processes have evolved and how changes in them can modify existing organismal features or lead to new ones.
- **Homeotic genes** in *Drosophila* specify the identity of body segments in the fruit fly.
  - Molecular analysis has shown that these genes all include a 180-nucleotide sequence called a **homeobox**, specifying a 60-amino-acid **homeodomain** in the encoded proteins.
- ***An identical or very similar nucleotide sequence has been discovered in the homeotic genes of many invertebrates and vertebrates (therefore they are "highly conserved" in evolution.)***
  - The sequences are so similar between humans and fruit flies that one researcher has whimsically referred to flies as "little people with wings."
- Homeotic genes in animals were named ***Hox* genes**, short for *h*omeob*ox*-containing genes, because homeotic genes were the first genes found to have this sequence.
  - Most of these genes are associated with development, suggesting their ancient and fundamental importance in that process.
- In some cases, small changes in the regulatory sequences of particular genes cause changes in gene expression patterns that can lead to major changes in body form.