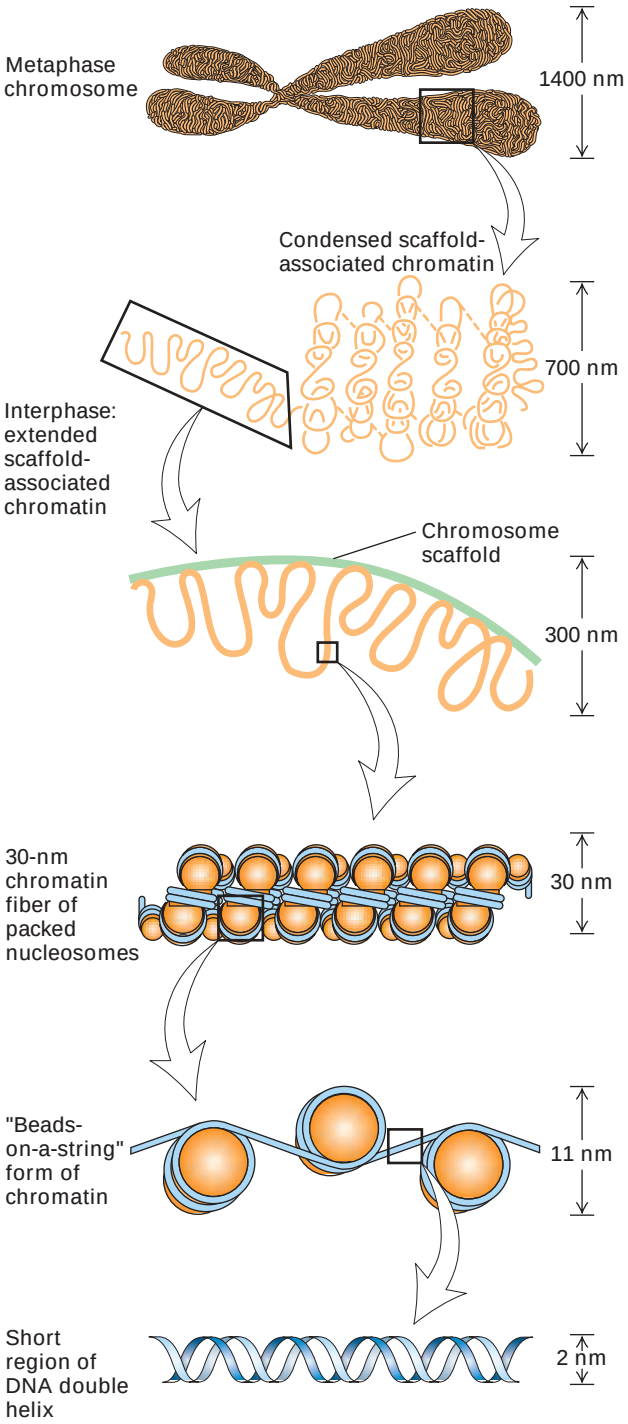
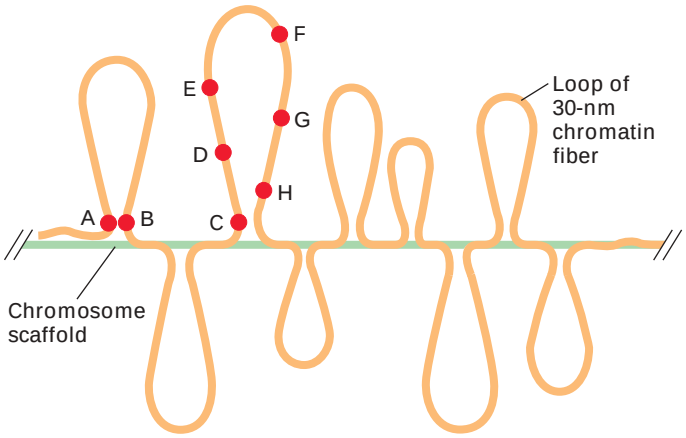


▲ FIGURE 10-24 **Model for the packing of chromatin and the chromosome scaffold in metaphase chromosomes.** In interphase chromosomes, long stretches of 30-nm chromatin loop out from extended scaffolds. In metaphase chromosomes, the scaffold is folded further into a highly compacted structure, whose precise geometry has not been determined.

In situ hybridization experiments with several different fluorescent-labeled probes to DNA in human interphase cells support the loop model shown in Figure 10-24. In these experiments, some probe sequences separated by millions of base pairs in linear DNA appeared reproducibly very close to one another in interphase nuclei from different cells (Figure 10-25). These closely spaced probe sites are postulated to lie close to specific sequences in the DNA, called *scaffold-associated regions (SARs)* or *matrix-attachment regions (MARs)*, that are bound to the chromosome scaffold. SARs have been mapped by digesting histone-depleted chromosomes with restriction enzymes and then recovering the fragments that are bound to scaffold proteins.

In general, SARs are found between transcription units. In other words, genes are located primarily within chromatin loops, which are attached at their bases to a chromosome scaffold. Experiments with transgenic mice indicate that in some cases SARs are required for transcription of neighboring genes. In *Drosophila*, some SARs can insulate transcription units from each other, so that proteins regulating transcription of one gene do not influence the transcription of a neighboring gene separated by a SAR.



▲ EXPERIMENTAL FIGURE 10-25 **Fluorescent-labeled probes hybridized to interphase chromosomes demonstrate chromatin loops and permit their measurement.** In situ hybridization of interphase cells was carried out with several different probes specific for sequences separated by known distances in linear, cloned DNA. Lettered circles represent probes. Measurement of the distances between different hybridized probes, which could be distinguished by their color, showed that some sequences (e.g., A, B, and C), separated from one another by millions of base pairs, appear located near one another within nuclei. For some sets of sequences, the measured distances in nuclei between one probe (e.g., C) and sequences successively farther away initially appear to increase (e.g., D, E, and F) and then appear to decrease (e.g., G and H). The measured distances between probes are consistent with loops ranging in size from 1 million to 4 million base pairs.
[Adapted from H. Yokota et al., 1995, *J. Cell Biol.* **130**:1239.]

MEDIA CONNECTIONS
Focus Animation: Three-Dimensional Packing of Nuclear Chromosomes