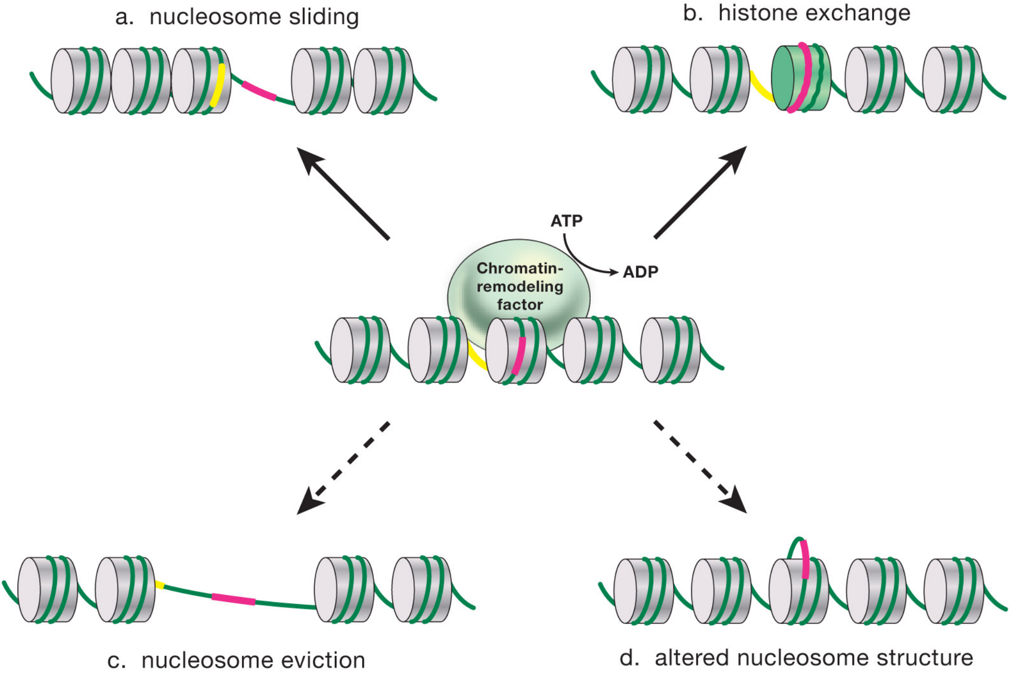

Figure 6. Mechanisms for ATP-dependent Remodeling

Models for chromatin remodeling are illustrated by showing the change in position or composition of nucleosomes relative to the DNA wrapped around it. The central panel indicates a starting chromatin region where linker DNA is indicated in yellow and nucleosomal DNA in red. (*a*) Movement of a nucleosome translationally along the DNA (sliding) to expose a region (marked in *red*) that was previously occluded; (*b*) exchange of a variant histone for a standard histone to create a variant nucleosome; (*c*) eviction of nucleosomes to open a large region of DNA. This mechanism might depend on other proteins, such as histone chaperones or DNA-binding factors, in addition to remodeling proteins; (*d*) creating a loop on the surface of the nucleosome. Remodelers in the SWI/SNF family have been hypothesized to use alternative mechanisms, such as creating stable loops of DNA on the surface of the nucleosome, to make sites available that are central to the nucleosome.

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