



Figure 8. Models for the Involvement of Chromatin Remodeling and Histone Exchange in Transcriptional Processes

In Model 1, the Swi/Snf family of ATPase binds chromatin through bromodomain recognition of acetylated histones and acts to alter the local chromatin structure. Model 2 depicts the reported octamer eviction that occurs at certain loci such as *PHO5* by an unknown mechanism. In Model 3, the ATPase SWR1 catalyzes the replacement of histone H2A with H2AZ, which poises chromatin for transcription. Model 4 focuses on the involvement of FACT in transcriptional elongation, assisting in nucleosome unraveling by the displacement of an H2A/H2B dimer. Concomitantly, histone H3 may be exchanged with H3.3 during the process.