



**Figure 9.** Model for the action of Swi/Snf-type nucleosome remodelers at promoters, and their regulation by acetylation. (A) SAGA or other histone acetyltransferase (HAT) complexes can be recruited to gene promoters by interacting with sequence-specific DNA-binding transcription activators (TA). Once recruited these HATs acetylate (blue Ac flag) nucleosomes in proximity of the activator recognition site. (B) The Swi/Snf or RSC nucleosome remodeling complexes (remodeler) can be recruited to promoters by interactions with transcription activators. Bromodomains (bromo) within subunits of these complexes then interact with the acetylated (Ac) nucleosomes at the promoter. (C) ATP-dependent remodeling and/or displacement (gray arrows) are preferentially directed at the acetylated nucleosomes bound by the bromodomains in the remodeling complex. (D) SAGA or other Gcn5-containing complexes acetylate specific lysines within subunits of the remodeling complex. These acetylated lysines compete for interaction with the bromodomains, which (E) leads to dissociation of the remodeler from the acetylated nucleosomes (gray arrow). (Adapted from Suganuma and Workman 2011.)