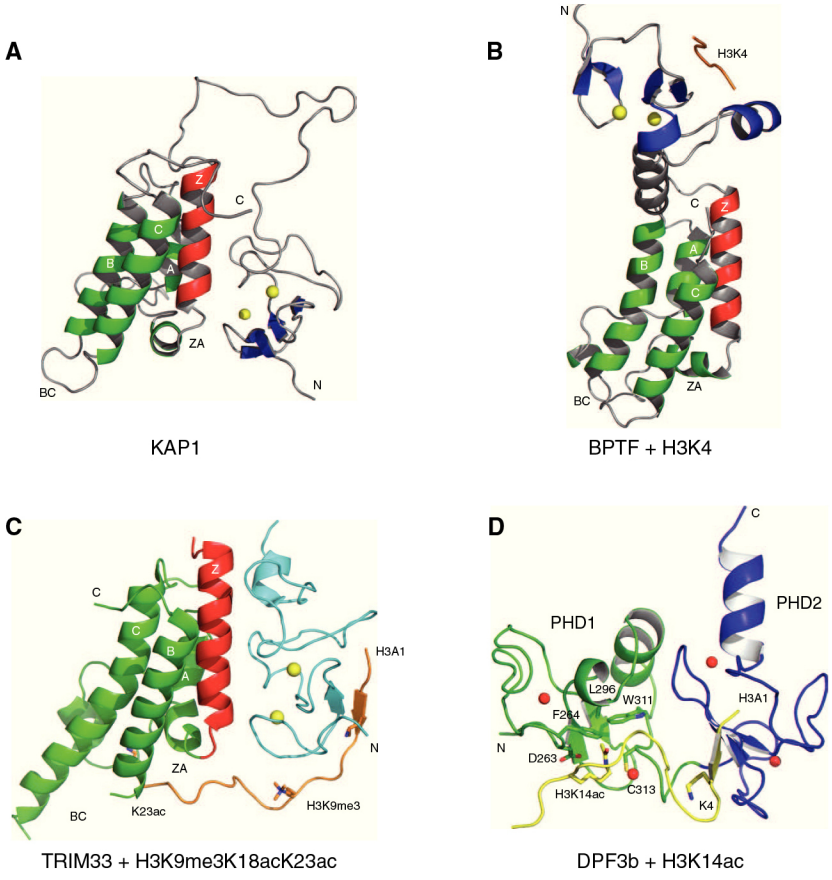

Figure 8. Interdomain interactions in tandem histone-binding modules. (*A*) The solution structure of the PHD (navy)–bromodomain (red and green) module of human KAP1 (PDB code: 2RO1). (*B*) The PHD–bromodomain module of human BPTF in complex with an H3K4 peptide (PDB code: 3QZV). (*C*) The crystal structure of the PHD–bromodomain module of human TRIM33 in complex with an H3K9me3K18acK23ac peptide (PDB code: 3U5P). Note that the second bromodomain in each of the above tandem modules are colored green, and each structure is oriented with respect to the α_Z helix (red) of this bromodomain. (*D*) The solution structure of the tandem PHD finger module of human DPF3b bound to an H3K14ac peptide (PDB code: 2KWJ). The zinc atoms are highlighted as red spheres, and the main and side chains of the protein residues involved in H3K14ac binding are color-coded by atom type with green, red, and blue for carbon, oxygen and nitrogen, respectively.