



**Figure 6.** Bromodomains as acetyllysine-binding domains. In all structures, the histone peptide is in yellow and the main and side chains of the protein residues are color-coded by atom type. (A) The three-dimensional solution structure of the PCAF bromodomain bound to an H3K36ac peptide (PDB code: 2RNX) is illustrated as a ribbon diagram (*left*) and a surface electrostatic representation (*right*) of the protein with red and blue colors representing negatively or positively charged amino acid residues, respectively. (B) The acetyllysine-binding pocket is depicted from the crystal structure of the GCN5 bromodomain (green) in complex with an H4K16ac peptide (PDB code: 1E6I). This stick diagram shows key residues and bound water molecules (magenta spheres) contributing to acetyllysine recognition. Hydrogen bonding interactions are indicated by dotted lines. (C) The crystal structure of the tandem bromodomains of uncomplexed human TAF1 (PDB code: 1EQF). (D) The crystal structure of the first bromodomain of Brdt bound to an H4K5acK8ac peptide (PDB code: 2WP2).