



**Figure 4.** Autoacetylation regulation of HAT proteins. Close-up views of the autoacetylation site of HAT proteins. (A) Model for p300 activation by autoacetylation. The black loop and green acetylated lysine balls are modeled on the p300/Lys-CoA crystal structure. (B) Structure of the K290 autoacetylation site of Rtt109, highlighting the environment around acetylated K290. The acetylated lysine and other side chains that interact with the acetylated lysine are indicated in stick figure in CPK coloring with carbon in green and the hydrogen bond is shown as a dotted orange line. The AcCoA molecule is shown as a stick figure in CPK coloring with carbon atoms in yellow. (C) Structure of the  $\gamma$ Esa1/H4K16CoA complex is shown, highlighting the environment around acetylated K262 (green). The corresponding K274 of hMOF is superimposed in the unacetylated (yellow) and acetylated (orange) conformations showing that the unacetylated conformation would clash with binding of the cognate substrate lysine (as represented by the lysine of the H4K16CoA bisubstrate inhibitor shown in purple).