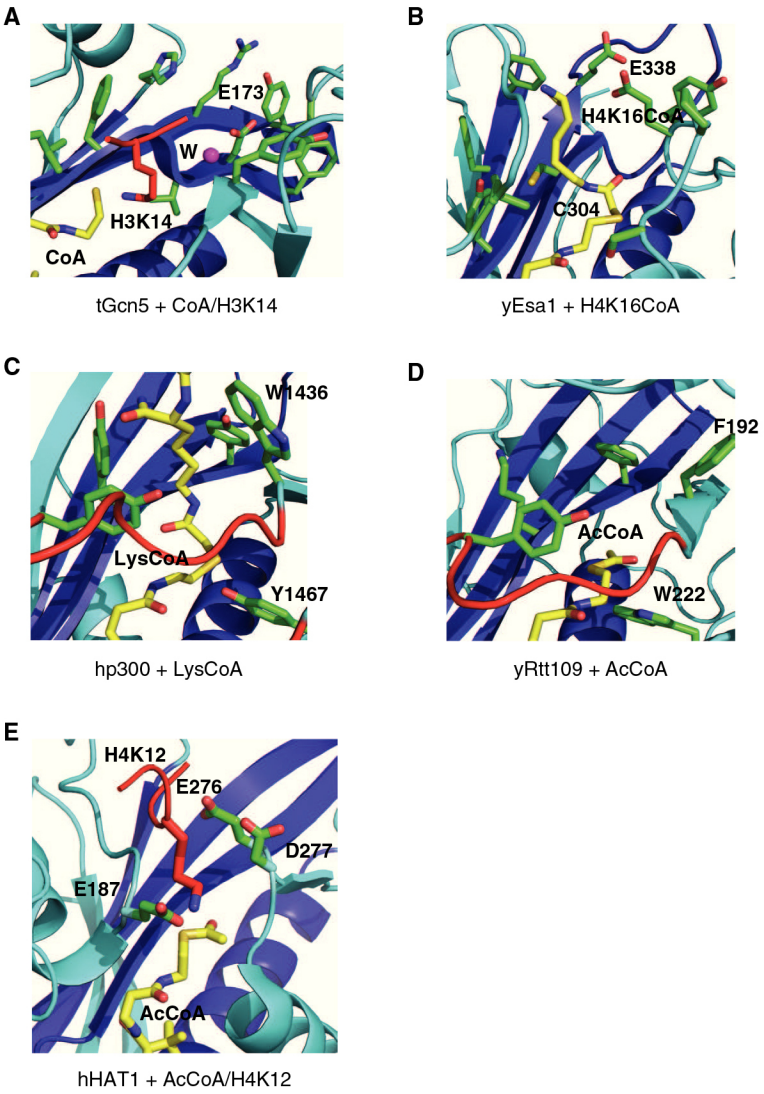


Figure 2. Catalytic mechanism of HAT proteins. Active sites of representative members of the HAT subfamilies are illustrated highlighting the relevant side chains on a backbone cartoon of the active site. (*A*) *Tetrahymena* Gcn5/CoA/histone H3. Key catalytic residues are labeled and hydrophobic residues of the active site that likely raise the pKa of Glu 173 are shown in stick figure in CPK coloring with carbon in green. A segment of the histone H3 peptide is shown in red. W indicates a well-ordered water molecule that participates in catalysis. The numbering is for yeast Gcn5. (*B*) Yeast Esa1 bound to the H4K16CoA bisubstrate inhibitor (stick figure and CPK coloring with carbon atoms in yellow). Key catalytic residues are labeled and hydrophobic residues of the active site that likely raise the pKa of Glu 338 are shown. Residues flanking K16 in the peptide are disordered in the structure. (*C*) Human p300 bound to the Lys-CoA bisubstrate inhibitor (stick figure and CPK coloring with carbon atoms in yellow). Residues shown to play catalytic roles are labeled with other potential catalytic residues shown in stick figure. The substrate-binding loop is shown in red. (*D*) Yeast Rtt109/CoA. Potential catalytic residues in the corresponding position of hp300 are shown. The CoA molecule is shown in stick figure in CPK coloring with carbon atoms in yellow. The substrate-binding loop is shown in red. (*E*) hHAT1/AcCoA/histone H4. The three general base candidate residues are represented as green stick figures and a segment of the histone H4 peptide is shown in red.