



Figure 1. Overall structure of HAT proteins. Representative members of the five HAT subfamilies are illustrated as cartoons highlighting the structurally conserved core region (blue) and flanking amino- and carboxy-terminal regions (aqua). The cofactor is shown in stick figure in CPK coloring (carbon, yellow; oxygen, red; nitrogen, blue; phosphorous, orange; sulfur, brown): (A) yeast HAT1/AcCoA (PDB 1BOB), (B) *Tetrahymena* Gcn5/CoA/histone H3 (PDB code: 1PUA) with the histone H3 peptide shown in red, (C) yeast Esa1/H4K16-CoA (PDB code: 3TO6), (D) human p300/Lys-CoA (PDB code: 3BIY) with the substrate-binding loop shown in red, (E) yeast Rtt109/CoA (PDB code: 3D35) with the substrate-binding loop shown in red.