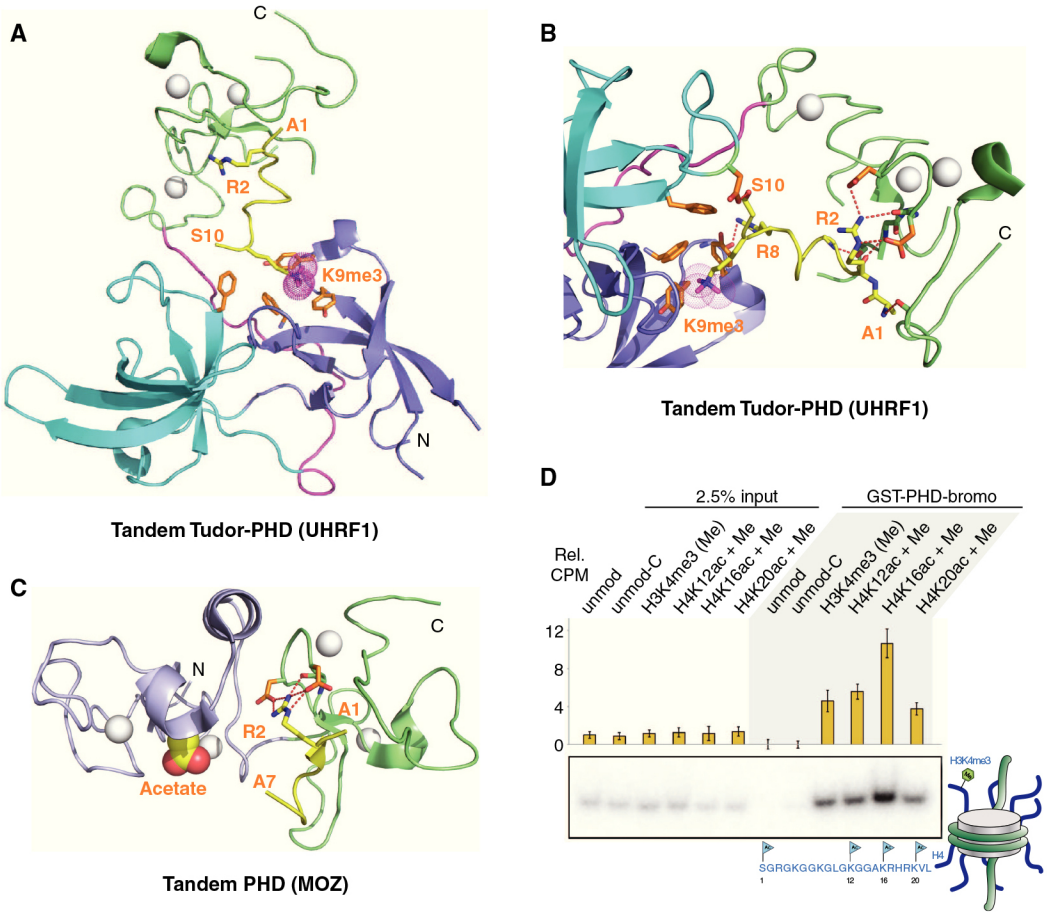

Figure 12. Structures of linked binding modules involved in multivalent readout at the peptide and nucleosomal levels. (*A*) 2.9-Å crystal structure of the UHRF1 tandem Tudor-PHD finger cassette bound to H3(1-13)K9me3 peptide (PDB: 3ASK). The tandem Tudor domains are shown in cyan and purple, whereas the PHD finger is shown in green. Zinc ions are shown as silver balls. The bound H3(1-13)K9me3-containing peptide can be traced from A1 to S10. (*B*) Enlargement of *A*, showing details of the intermolecular contacts between H3(1-13)K9me3-containing peptide (A1 to S10) and the tandem Tudor-PHD finger cassette of UHRF1. (*C*) 1.47-Å crystal structure of the complex of the tandem PHD finger cassette of MOZ bound to H3(1-18)K14ac peptide (PDB: 3V43). There is a bound acetate (in space-filling representation) from buffer bound in a pocket in the amino-terminal PHD finger (in blue). The bound H3(1-18)K14ac-containing peptide can be traced from A1 to A7, in which it is bound to the carboxy-terminal PHD finger (in green). (*D*) glutathione S-transferase (GST) pull-down of modified nucleosomes with semisynthetic histones produced by expressed protein ligation. Nucleosomes containing dual marks involving H4K12ac, H4K16ac, or H4K20ac in combination with H3K4me3 are pulled down with resin bound GST-BPTF PHD-bromo cassette and detected by autoradiography after native gel electrophoresis. (*D*, Reprinted from Ruthenburg et al. 2011.)