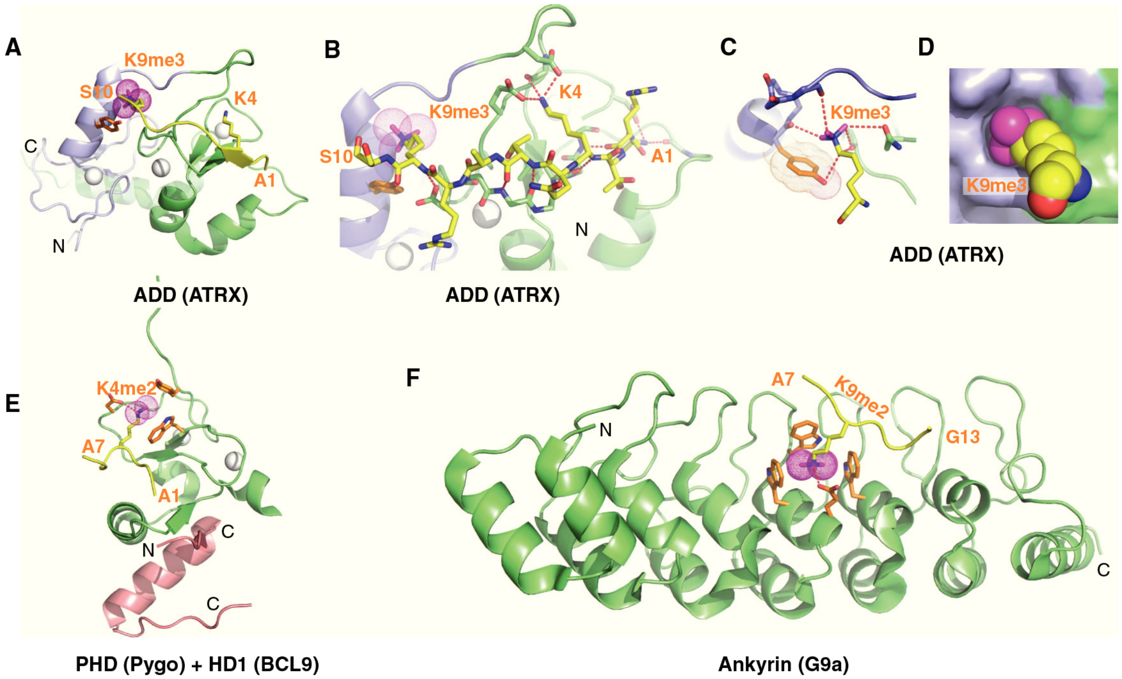

Figure 7. Structures of expanded and paired modules bound to methylated lysine histone marks. (*A*) 1.6-Å crystal structure of the complex containing the ADD domain of ATRX bound to the H3(1-15)K9me3 peptide (PDB: 3QLA). The ADD GATA-1 and PHD fingers are colored in blue and green, respectively. Bound Zn ions are shown as silver balls. The H3 peptide containing K9me3 is traced from A1 to S10. (*B*) Enlargement of *A* showing intermolecular contacts between the K9me3-containing H3 peptide, traced from A1 to S10, complexed with the ADD domain. The me3 are shown as magenta spheres. (*C*) Ribbon and stick representation of K9me3 positioned to interact with the GATA-1 and PHD finger domains in the complex. (*D*) Surface and space-filling representation of surface complementarity between K9me3 and the walls of the pocket lined by the GATA-1 and PHD finger domains in the complex. (*E*) 1.7-Å crystal structure of the ternary complex of the Pygo PHD finger (in green) bound to H3(1-7)K4me2 peptide (in yellow) in the presence of the HD1 domain of BCL9 (in pink) (PDB: 2VPE). (*F*) 2.99-Å crystal structure of the complex consisting of the G9a ankyrin repeats (green) bound to an H3(1-15)K9me2 peptide traced from A7 to G13 in yellow (PDB: 3B95). The K9me2 aromatic-lined binding pocket is positioned between the fourth and fifth ankyrin repeats of G9a.

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