



Figure 4. Structures of single Royal Family modules bound to methylated lysine histone peptides. (A) 2.4-Å crystal structure of the complex containing an HP1 chromodomain bound to H3(1-15)K9me3 peptide (PDB: 1KNE). The bound K9me3-containing H3 peptide can be traced from Q5 to S10. The HP1 residues in orange illustrate the aromatic cage that captures K9me3. (B) 2.35-Å crystal structure of the complex between the male-specific lethal (MSL)3 chromodomain bound to a H4(9-31)K20me1 peptide in the presence of duplex DNA (in surface representation) (PDB: 3OA6). The bound K20me1-containing H4 peptide can be traced from H18 to L22. (C) 1.85-Å crystal structure of the complex containing the PHF1 (a Polycomb-like protein) Tudor domain bound to H3(31-40)K36me3 peptide (PDB: 4HCZ). The bound K36me3-containing H3 peptide can be traced from S31 to R40. (D) 1.5-Å crystal structure of the complex of Brf1 PWWP domain bound to H3(22-42)K36me3 peptide complex (PDB: 2X4W). The bound K36me3-containing H3 peptide can be traced from S28 to R40.