



Figure 5. Structures of tandem Royal Family modules bound to methylated lysine histone peptides. (A) 2.4-Å crystal structure of the complex of the human CDH1 tandem chromodomains bound to H3(1-19)K4me3 peptide (PDB: 2B2W). Chromodomains 1 and 2 are colored in green and blue, respectively, with the connecting helix-turn-helix linker in pink. The bound K4me3-containing H3 peptide can be traced from A1 to Q5. (B) 1.7-Å crystal structure of the complex of 53BP1 tandem Tudor domains bound to H4(15-24)K20me2 peptide (PDB: 2IG0). Tudor domains 1 and 2 are colored in green and blue, respectively. The bound K20me2-containing H4 peptide can be traced for the R19-K20me2 step. (C) 2.7-Å crystal structure of the complex of tandem Tudor domains of *A. thaliana* SHH1 protein bound to a H3(1-15)K9me2 peptide (PDB: 4IUT). A bound zinc ion is shown in a silver ball. Tudor domains 1 and 2 are colored in green and blue, respectively. The bound K9me2-containing H3 peptide can be traced from T3 to S10. (D) The enlargement shows details of the alignment of the K9me2-containing H3 peptide from T3 to S10 positioned on the *A. thaliana* SHH1 domain in the complex with intermolecular interactions formed with both Tudor domains. (E) 1.26-Å crystal structure of the complex of tandem Tudor domains of SGF29 bound to H3(1-11)K4me3 peptide (PDB: 3MEA). Tudor domains 1 and 2 are colored in blue and green, respectively. The bound K4me3-containing peptide can be traced from A1 to K4me3. (F) 2.1-Å crystal structure of the complex of tandem Tudor domains of JMJD2A bound to H3(1-10)K4me3 peptide (PDB: 2GFA). Individual Tudor domains are colored in green and blue, respectively. The bound K4me3-containing peptide can be traced from A1 to A7.