



Figure 10. Structures of PHD finger and chromodomains bound to unmodified arginines. (A) 1.8-Å crystal structure of the complex of the PHD finger of UHRF1 bound to H3(1-9) peptide (PDB: 3SOU). The bound H3 peptide can be traced from A1 to R8. Zinc ions are shown by silver balls. (B) 3.18-Å crystal structure of the complex of the chromodomains and Ankyrin repeats of *A. thaliana* chloroplast signal recognition particle (cpSRP)43 bound to an RRKR (Arg-Arg-Lys-Arg)-containing peptide (yellow) (PDB: 3UI2). The side chains of R536 and R537 of the bound RRKR-containing peptide are positioned in adjacent pockets at the interface between the fourth Ankyrin repeat (purple) and the second chromodomain (green) in the complex. (C) Positioning of Arg536 of the RRKR-containing peptide within an aromatic-lined cage in the complex. (D) Positioning of Arg537 of the RRKR-containing peptide in a pocket lined by a Trp and two acidic side chains in the complex.