



Figure 8. Structures of expanded and paired modules bound to methylated arginine histone marks. (A) NMR solution structure of the complex containing the SMN Tudor domain (green ribbon representation) bound to a symmetrical Rme2s-containing peptide (yellow) (PDB: 4A4E). The methyl groups are illustrated with magenta spheres and the aromatic-lined cage in orange. (B) 2.8-Å crystal structure of the complex containing the SND1 extended Tudor module bound to the amino-terminal PIWI peptide, traced from R10 to R17, with the R14me2s modification (PDB: 3NTI). The core fold of the Tudor domain is shown in green, whereas the extensions are shown in blue. (C) Enlargement of B showing the positioning of R14me2s in the aromatic-lined cage of the SND1 Tudor domain in the complex.