

Figure S1. Superposition of the Trm4p model with two related structures: A) putative archaeal RNA:m⁵C MTase PH1374 (1ixk); RMSD = 0.75 Å for 286 pairs of spatially equivalent residues (distance between C- α atoms < 2.75 Å), B) DNA:m⁵C MTase M.HhaI (3mht); RMSD = 1.74 Å for 86 pairs of spatially equivalent residues. The C- α trace of all proteins is shown in the wireframe representation, with the ligands and side-chains of the catalytic Cys and carboxylate residues (Asp or Glu) shown in full-atom representation. Trm4p is shown in green (side-chains in yellow), PH1374 in red (side-chains in magenta), and M.HhaI in violet (side-chains in cyan). The following regions were omitted for the sake of clarity: aa 22-148 (N-terminus) and 349-379 (insertion) in Trm4, and aa 176-302 (target-recognition domain) in M.HhaI.