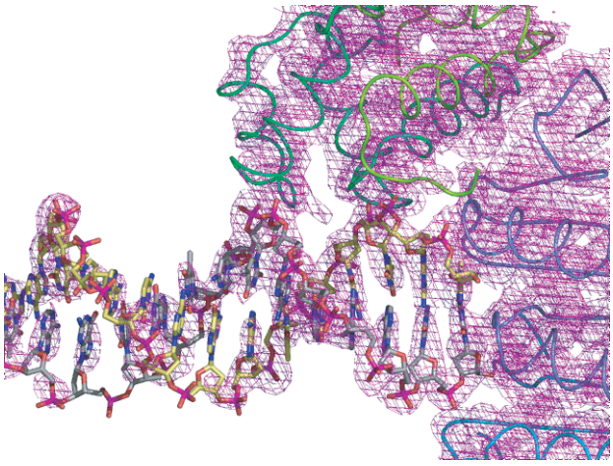
Figure S2: (A) Initial electron density map at 2.8Å calculated using phases from the molecular replacement solution of the nuclease domain. Superposed is the final refined model for ApeXPF-DNA. Density is apparent for both the dsDNA and the $(HhH)_2$ domain. The map was calculated after "prime-and-switch" phase improvement with RESOLVE and is contoured at 1.5σ.



(B) Initial electron density map at 3.2Å calculated using phases from the molecular replacement solution of full length ApeXPF from the DNA-bound structure. Superposed is the final refined model for apo-ApeXPF. The map was calculated after "prime-and-switch" phase improvement with RESOLVE and is contoured at 1.0σ.