Supplementary Material

Figure Legend

Figure S1.

Backbone $^{15}$N relaxation rates at 600MHz field. (A) $R_1$, (B) $R_2$, (C) $^{15}$N-$^1$H heteronuclear NOE. The values for the free protein are represented by the black squares and for the TT-10 complex by gray squares.

All relaxation experiments were performed at 300 K. $R_1$ values of $^{15}$N were measured from spectra recorded with eleven different delays of $T = 10, 50, 100, 150, 200, 300, 400, 500, 700, 800, 1000$ ms with relaxation delays of 1.5 s. $R_2$ values were determined from spectra recorded with duration delays of 10, 30, 50, 70, 90, 110, 130, 150, 210 ms with relaxation delays of 1 s. The $^{15}$N-$^1$H NOE experiment was acquired with a 3 s presaturation period preceded by a 2 s relaxation delay. Data were processed using NMRPIPE and analyzed using SPARKY. The relaxation rate constants, $R_1$ and $R_2$, were obtained by fitting the resultant time profiles of the intensities to a monoexponential decay function.

In the absence of DNA, the relaxation data show that the N-terminal residues and C-terminal residues, as well as residues in the tip of L12 and L45 loops are flexible. Also 229, 230, 234 and 235 shows higher than the average value in $R_1$. Addition of ssDNA to scRPA70A is seen to reduce the internal motions of some regions of the protein that have above-average flexibility in the absence of DNA. The hetNOE values in the L12 and L45 are increased after ssDNA addition. For most residues except the two loops and the terminals, the relatively uniform- and high values of hetNOE indicates the backbone of the protein is essentially rigid all along its length. Residues 232 and 253 show elevated T1/T2 ratios, which indicates that there are motions on the micro- millisecond timescale. However, we do not think that these motions make an incorrect structural model by averaging RDC values.

Figure S1.