Electronic Supplementary Material (ESI) for Physical Chemistry Chemical Physics.

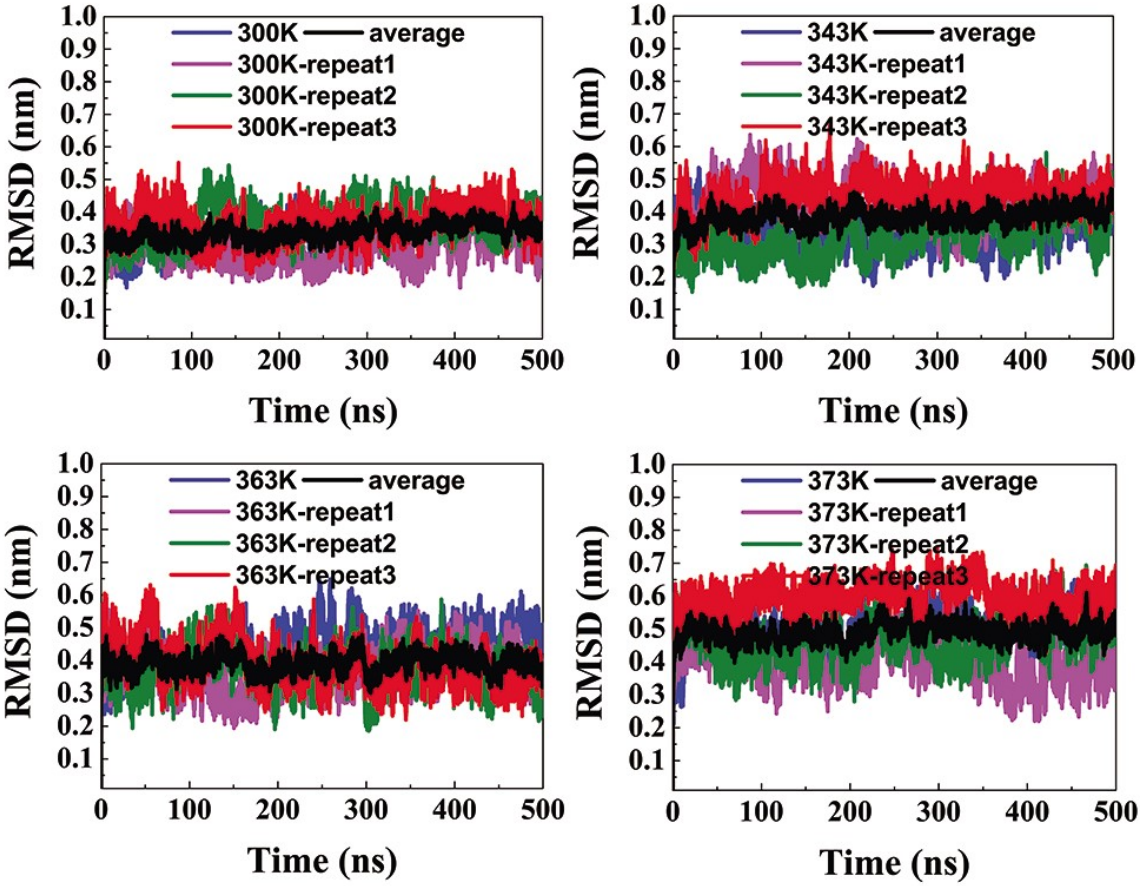

Fig. S1. Root-mean-square deviation (RMSD) as a function of time for Ape10b2-dsDNA complex.

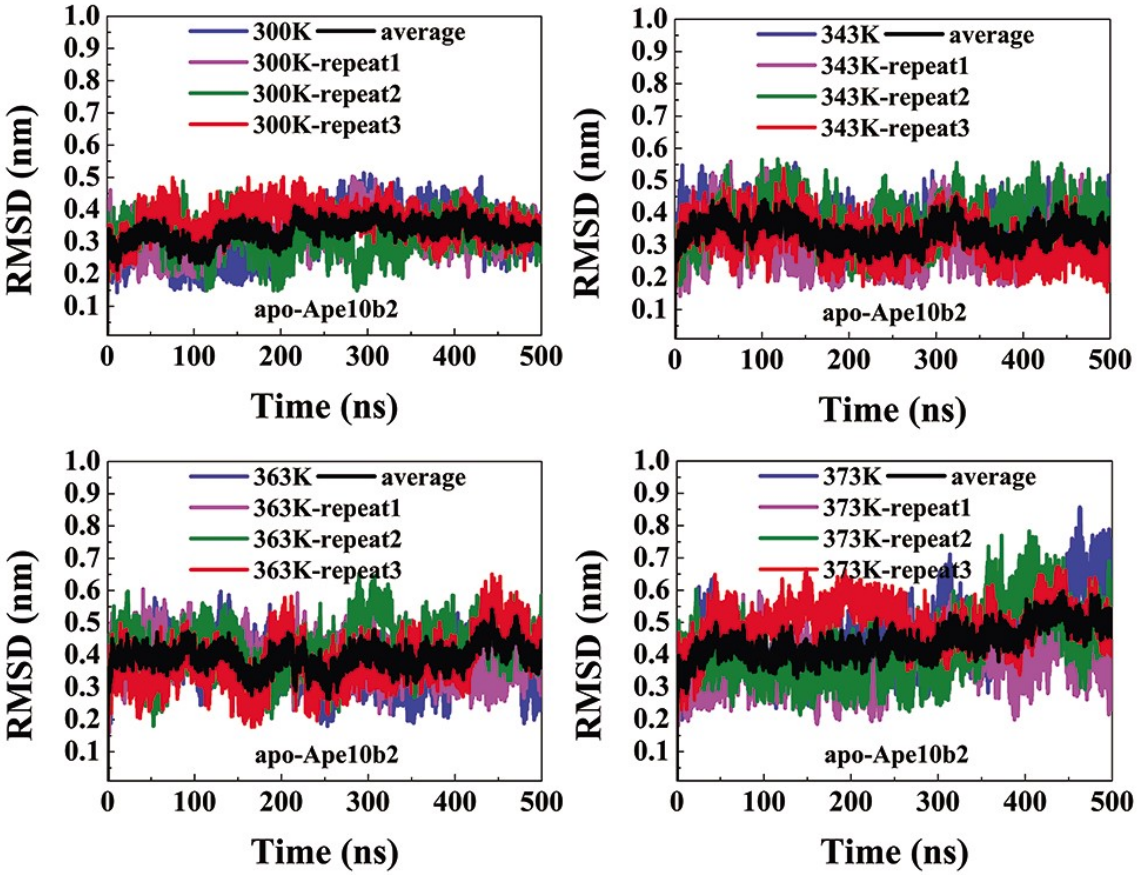

Fig. S2. Root-mean-square deviation (RMSD) as a function of time for apo-Ape10b2.

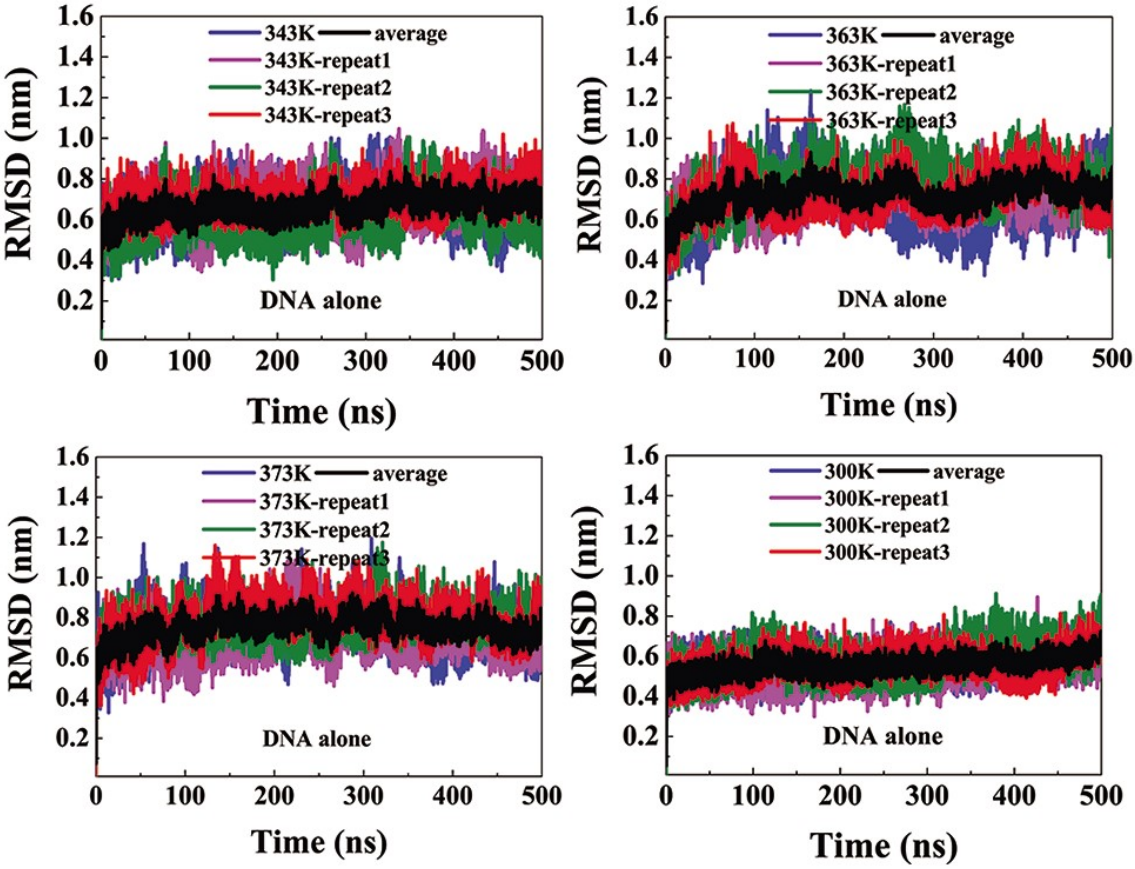

Fig. S3. Root-mean-square deviation (RMSD) as a function of time for alone dsDNA.

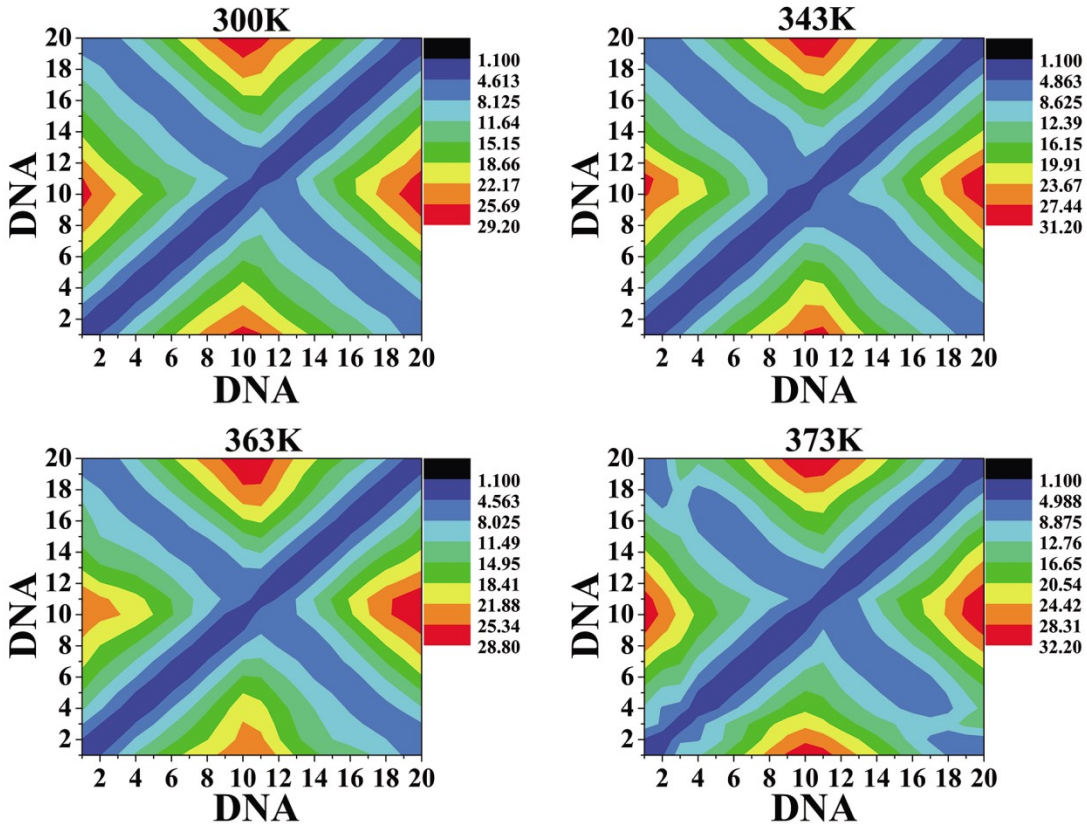

Fig. S4 Contact maps were calculated and plotted over the simulations on DNA in complex at four different temperatures (300, 343, 363, and 373 K).

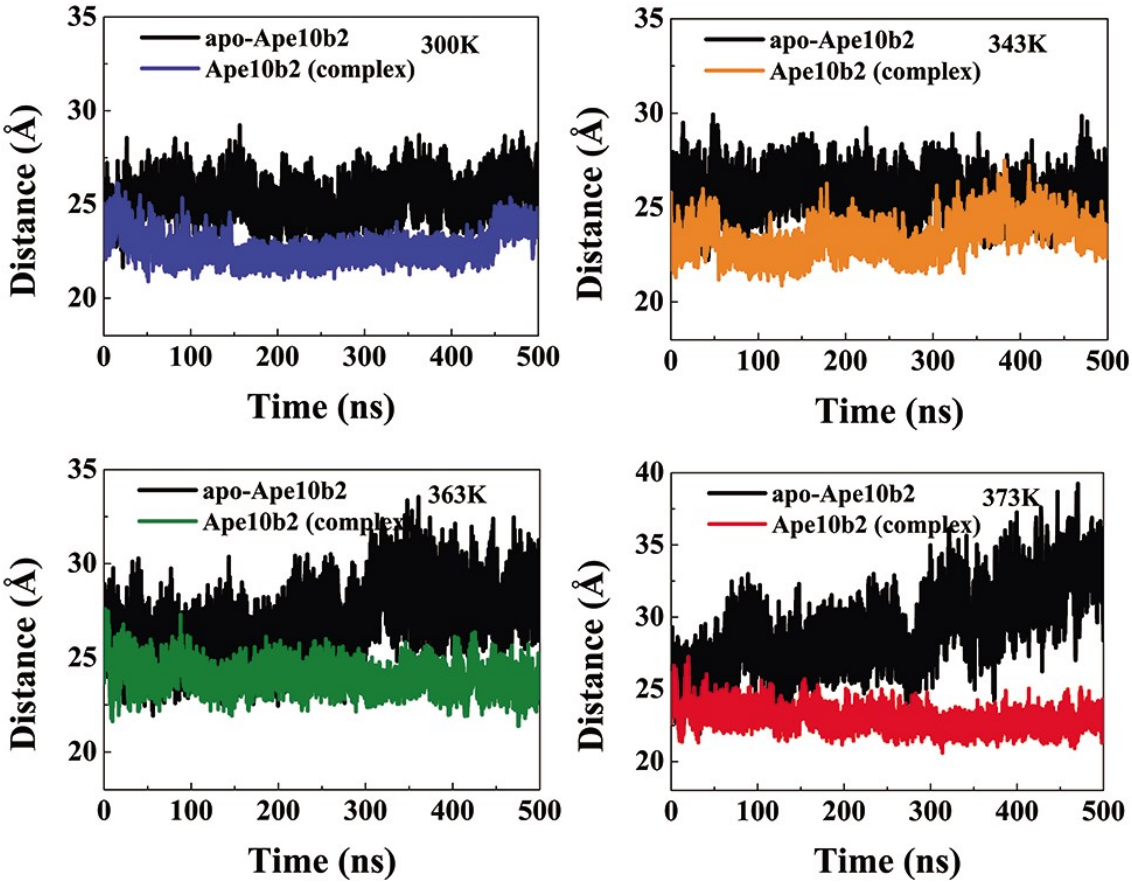

Fig. S5. Distance evolution values of loop1 (residues 10 to 16) region in apo-Ape10b2 (black) and Ape10b2 in complex at 300 K (blue) , 343 K (orange), 363 K (olive), and 373 K (red).

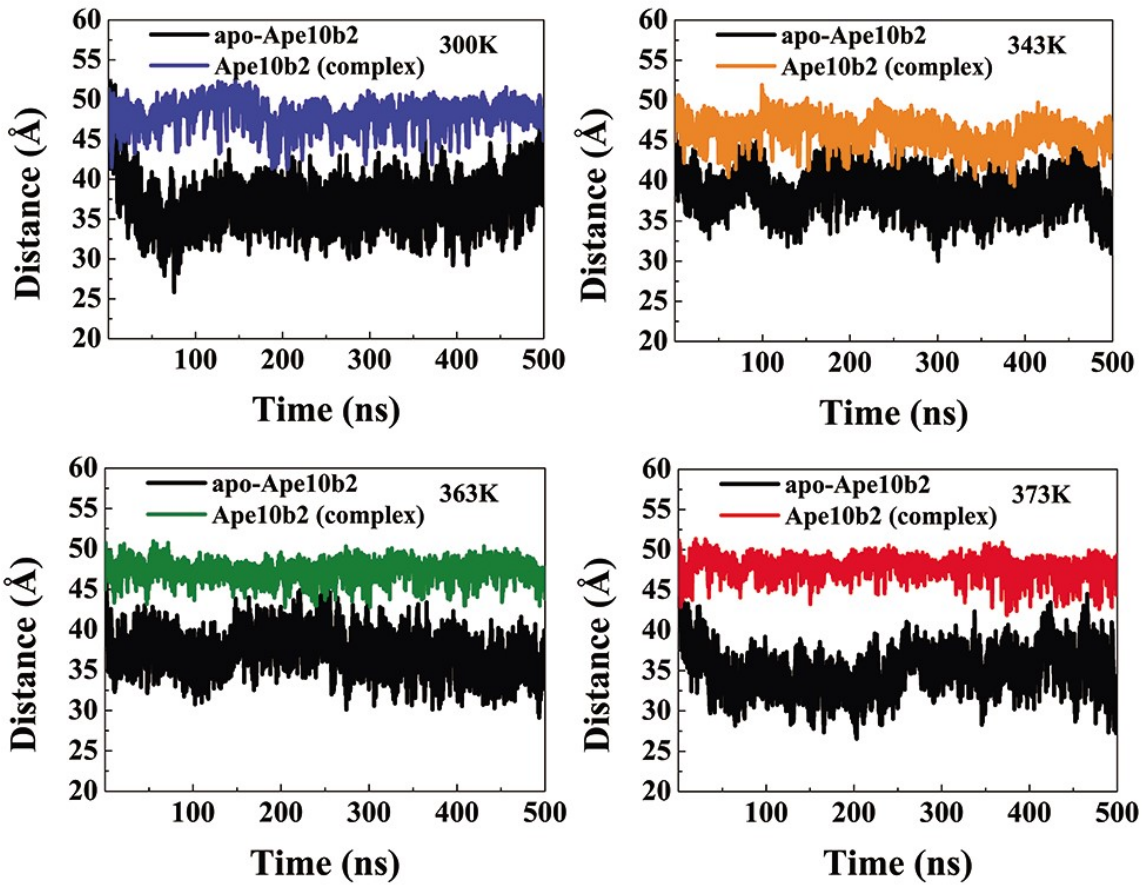

Fig. S6. Distance evolution values of loop5 (residues 75 to 86) region in apo-Ape10b2 (black) and Ape10b2 in complex at 300 K (blue) , 343 K (orange), 363 K (olive), and 373 K (red).

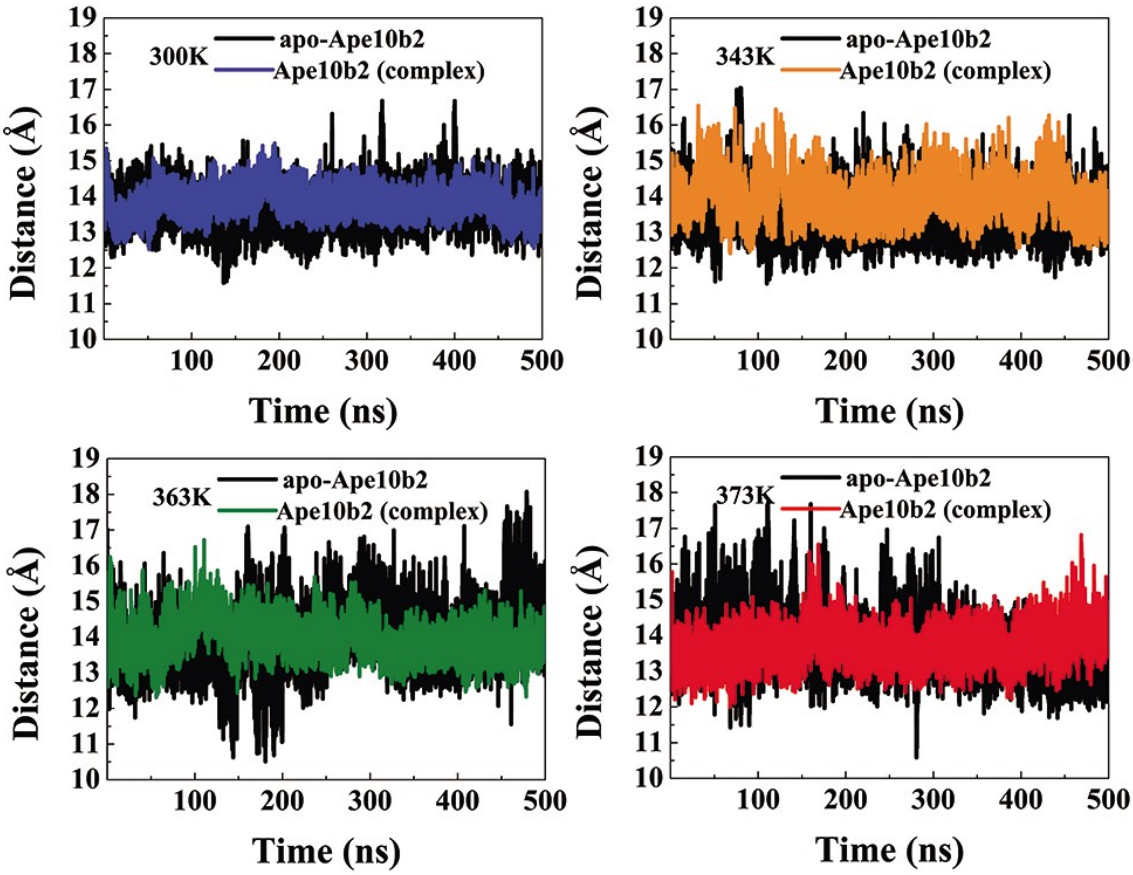

Fig. S7. Distance evolution values of residues 40-43 in apo-Ape10b2 (black) and Ape10b2 in complex at 300 K (blue) , 343 K (orange), 363 K (olive), and 373 K (red).

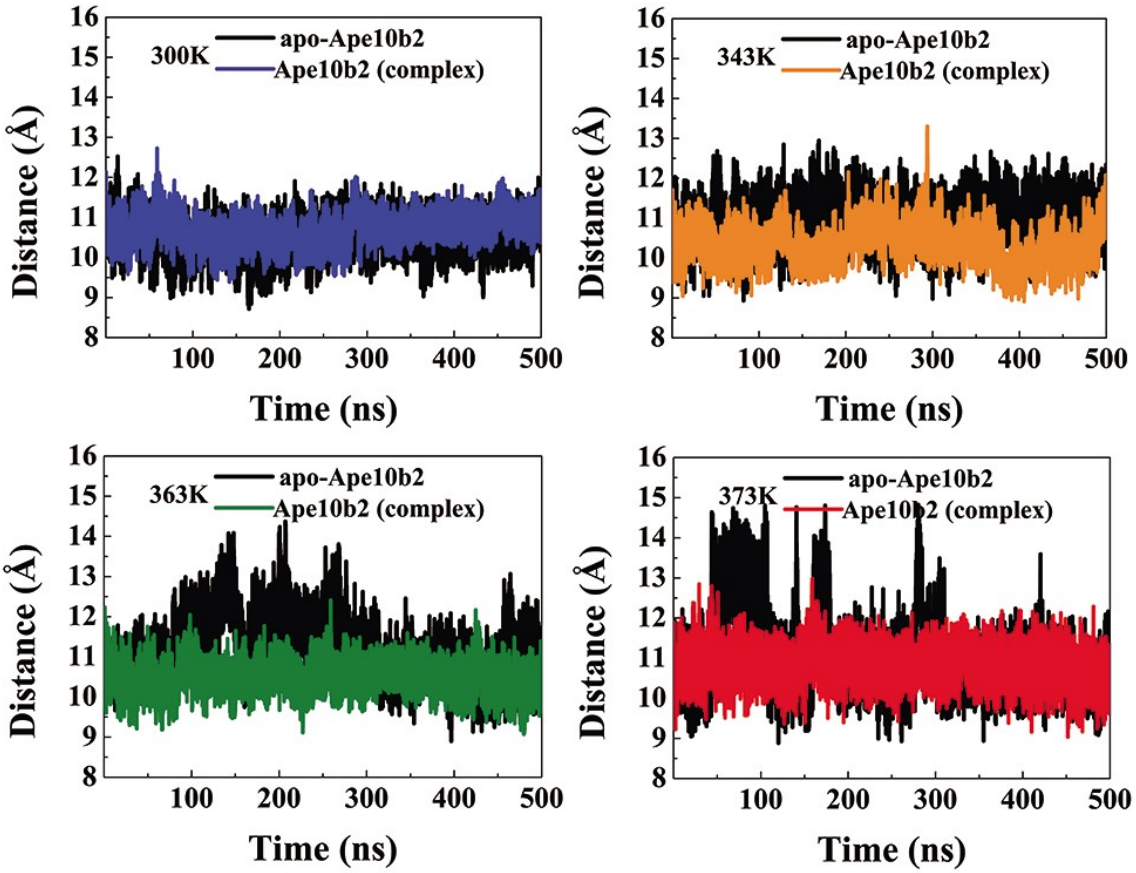

Fig. S8. Distance evolution values of residues 45-46 in apo-Ape10b2 (black) and Ape10b2 in complex at 300 K (blue) , 343 K (orange), 363 K (olive), and 373 K (red).

Table S1

Relative binding free energies (kcal/mol) contributed by important residues ($|\Delta G_{bind}| \geq 1.0$ kcal/mol) in Ape10b2-dsDNA complex at 300 K.

Residue	ELE	GB	VDW	SA	Total
Arg13(A)	-299.836	297.238	-1.010	-0.375	-3.982
Lys14(A)	-220.710	219.980	-0.452	-0.014	-1.196
Pro15(A)	-11.723	9.953	-1.814	-0.322	-3.905
Val16(A)	-11.376	9.108	-0.861	-0.148	-3.278
Arg40(A)	-251.676	248.554	-0.550	-0.245	-3.917
Gly41(A)	-9.649	7.395	-0.568	-0.123	-2.945
Arg42(A)	-341.987	340.574	-4.556	-0.765	-6.734
Arg46(A)	-316.925	310.427	-0.651	-0.222	-7.371
Lys56(A)	-265.544	264.209	-1.144	-0.305	-2.783
Arg57(A)	-249.861	247.932	-1.415	-0.347	-3.690
Val76(A)	-7.304	6.233	-2.995	-0.271	-4.337
Gln77(A)	-1.299	1.175	-2.849	-0.533	-3.506
Thr78(A)	-3.882	4.396	-2.627	-0.232	-2.344
Pro79(A)	-3.289	3.651	-1.935	-0.324	-1.897
Thr85(A)	-2.783	3.995	1.382	-0.238	-0.407
Arg86(A)	-306.290	305.743	-5.439	-0.993	-6.979
Arg13(C)	-323.890	317.809	-1.778	-0.402	-8.261
Arg40(C)	-285.419	280.829	-0.471	-0.284	-5.346
Arg42(C)	-340.517	338.177	-2.017	-0.529	-4.885
Asn45(C)	-13.329	10.579	-0.656	-0.143	-3.548
Arg46(C)	-299.964	295.518	-0.291	-0.233	-4.971
Ile74(C)	-2.210	2.197	-0.965	-0.119	-1.098
Val76(C)	-6.406	6.610	-2.221	-0.290	-2.308
Gln77(C)	-0.119	1.281	-3.217	-0.534	-2.588
Thr78(C)	-4.023	4.690	-2.315	-0.147	-1.794
Pro79(C)	-4.995	5.743	-4.052	-0.693	-3.997
Arg84(C)	-184.651	184.548	-0.874	-0.132	-1.109
Arg86(C)	-298.816	299.443	-4.419	-0.871	-4.664
Val88(C)	-7.365	6.931	-0.924	-0.101	-1.458
1G4	-159.281	161.038	-1.690	-0.419	-0.352
1C6	-185.193	186.645	-3.497	-0.847	-2.891
1G15	-104.244	106.706	-2.839	-0.434	-0.811
2G4	-159.281	161.038	-1.690	-0.419	-0.352
2C6	-185.193	186.645	-3.497	-0.847	-2.891
2C15	-104.244	106.706	-2.839	-0.434	-0.811

Table S2

Relative binding free energies (kcal/mol) contributed by important residues ($|\Delta G_{bind}| \geq 1.0$ kcal/mol) in Ape10b2-dsDNA complex at 343 K.

Residue	ELE	GB	VDW	SA	Total
Arg10(A)	-272.022	264.895	-1.608	-0.535	-9.270
Gly12(A)	-5.411	5.084	-0.911	-0.067	-1.305
Arg13(A)	-362.752	354.758	-2.080	-0.591	-10.665
Lys14(A)	-335.459	337.546	-3.009	-0.844	-1.766
Pro15(A)	-0.203	0.062	-0.850	-0.066	-1.056
Val16(A)	-4.174	3.961	-0.829	-0.181	-1.223
Arg40(A)	-289.703	284.797	-1.148	-0.413	-6.466
Arg42(A)	-357.531	352.905	-4.303	-0.745	-9.674
Arg46(A)	-341.608	334.045	-0.750	-0.349	-8.662
Arg86(A)	-293.761	289.493	-0.607	-0.359	-5.234
Arg10(C)	-261.406	253.977	-0.972	-0.392	-8.792
Arg13(C)	-311.959	314.264	-6.818	-1.279	-5.792
Lys14(C)	-228.486	228.035	-0.685	-0.099	-1.235
Arg40(C)	-275.275	268.205	-2.795	-0.331	-10.196
Arg42(C)	-338.557	339.356	-7.069	-1.380	-7.650
Asn43(C)	-1.477	1.565	-1.522	-0.168	-1.603
Asn45(C)	-20.281	17.624	-0.451	-0.102	-3.209
Asn46(C)	-305.610	298.230	-0.039	-0.326	-7.745
Arg84(C)	-245.245	243.101	-0.230	-0.140	-2.515
Arg86(C)	-318.106	308.440	-1.418	-0.476	-11.560
Val88(C)	-6.769	6.354	-0.816	-0.007	-1.238
1G3	-123.570	127.226	-4.802	-0.825	-1.972
1G4	-163.706	165.512	-2.760	-0.610	-1.564
1C12	-143.319	143.380	-1.177	-0.134	-1.250
1C13	-194.271	190.149	-3.831	-0.537	-8.490
1G14	-195.866	191.483	-6.871	-1.182	-12.436
2C3	-108.160	105.579	-0.451	-0.039	-3.071
2G4	-100.552	100.317	-1.898	-0.171	-2.303
2G5	-121.616	124.603	-3.668	-0.387	-1.067
2C6	-182.811	182.755	-2.680	-0.575	-3.311
2G7	-203.439	205.846	-5.009	-0.919	-3.521
2T8	-193.770	191.636	-2.714	-0.734	-5.581
2G9	-165.993	165.590	-0.816	-0.314	-1.532
2G11	-95.278	94.596	-0.455	-0.076	-1.213
2G12	-85.075	83.024	-0.153	-0.074	-2.279

Table S3

Relative binding free energies (kcal/mol) contributed by important residues ($|\Delta G_{bind}| \geq 1.0$ kcal/mol) in Ape10b2-dsDNA complex at 363 K.

Residue	ELE	GB	VDW	SA	Total
Arg10(A)	-287.505	279.500	-0.471	-0.319	-8.794
Arg13(A)	-356.081	352.129	-4.243	-0.947	-9.142
Arg40(A)	-279.188	274.327	-2.875	-0.297	-8.033
Gly41(A)	-9.869	7.861	-1.163	-0.090	-3.261
Arg42(A)	-378.388	371.270	-4.045	-0.842	-12.005
Asn43(A)	-2.257	2.588	-1.440	-0.188	-1.297
Asn45(A)	-21.812	19.142	-0.580	-0.062	-3.311
Arg46(A)	-332.151	324.473	-0.433	-0.322	-8.434
Arg84(A)	-275.792	276.168	-2.557	-0.524	-2.705
Arg86(A)	-302.725	302.087	-3.391	-0.768	-4.797
Val88(A)	-6.756	6.577	-2.344	-0.419	-2.942
Arg13(C)	-321.675	316.984	-3.757	-0.812	-9.261
Arg40(C)	-255.055	249.423	-1.038	-0.412	-7.082
Gly41(C)	-7.749	6.792	-0.562	-0.040	-1.558
Arg42(C)	-327.495	323.657	-4.458	-0.840	-9.135
Arg46(C)	-327.701	318.588	0.155	-0.176	-9.134
Val76(C)	0.247	0.208	-1.746	-0.184	-1.475
Gln77(C)	0.693	-1.523	-0.453	-0.122	-1.406
Thr78(C)	-9.883	10.105	-1.672	-0.086	-1.537
Pro79(C)	-6.219	6.829	-2.953	-0.524	-2.866
Arg84(C)	-258.896	257.498	-1.394	-0.250	-3.042
Arg86(C)	-307.792	299.955	-3.809	-0.733	-12.378
1G2	-87.913	90.031	-3.906	-0.525	-2.314
1G4	-160.565	163.358	-6.093	-0.960	-4.259
1C13	-135.977	137.005	-1.808	-0.239	-1.018
1G14	-160.868	164.605	-5.297	-0.838	-2.397
1G15	-169.777	171.582	-4.433	-0.839	-3.467
1G16	-112.481	115.632	-5.716	-1.121	-3.686
2C2	-67.082	67.291	-1.982	-0.286	-2.058
2G5	-136.749	137.133	-2.484	-0.348	-2.447
2C6	-196.627	196.226	-3.595	-0.752	-4.747
2G7	-200.176	203.022	-3.846	-0.792	-1.791
2T8	-167.481	169.585	-3.074	-0.744	-1.714
2G9	-138.218	138.572	-0.683	-0.234	-0.564
2C13	-87.827	87.007	-0.294	-0.036	-1.150
2C14	-101.009	100.646	-1.842	-0.246	-2.450

Table S4

Relative binding free energies (kcal/mol) contributed by important residues ($|\Delta G_{bind}| \geq 1.0$ kcal/mol) in Ape10b2-dsDNA complex at 373 K.

Residue	ELE	GB	VDW	SA	Total
Arg13(A)	-318.229	313.803	-2.211	-0.706	-7.343
Lys14(A)	-222.508	221.892	-0.389	-0.037	-1.042
Arg40(A)	-292.610	283.220	-0.289	-0.254	-9.933
Gly41(A)	-8.653	8.042	-0.963	-0.071	-1.646
Arg42(A)	-359.345	353.595	-4.008	-0.741	-10.499
Arg46(A)	-319.983	313.375	-0.556	-0.317	-7.481
Gln77(A)	-8.481	7.859	-1.160	-0.260	-2.043
Pro79(A)	3.666	-3.208	-1.413	-0.205	-1.160
Gln82(A)	-1.198	1.562	-4.445	-0.600	-4.680
Arg84(A)	-245.352	244.143	-5.146	-0.750	-7.106
Thr85(A)	1.823	0.379	-4.792	-0.613	-3.203
Arg86(A)	-280.752	271.988	-2.422	-0.309	-11.495
Arg87(A)	-298.998	291.347	-1.847	-0.405	-9.904
Val88(A)	-9.072	6.425	-3.445	-0.425	-6.517
Arg10(C)	-234.432	230.588	-3.098	-0.592	-7.533
Ile11(C)	2.233	-1.281	-1.510	-0.049	-0.607
Gly12(C)	-5.382	3.222	-1.551	-0.143	-3.853
Arg13(C)	-328.609	321.704	-4.023	-0.797	-11.726
Lys14(C)	-267.498	266.706	-0.751	-0.041	-1.583
Pro15(C)	-7.092	7.052	-1.949	-0.384	-2.372
Ala39(C)	-9.550	7.367	-0.916	-0.038	-3.137
Arg40(C)	-259.454	254.879	-3.133	-0.617	-8.326
Gly41(C)	-5.260	4.231	-0.521	-0.042	-1.592
Arg42(C)	-363.362	353.125	-4.315	-0.934	-15.487
Asn43(C)	1.945	-3.570	-1.766	-0.203	-3.594
Asn45(C)	-8.450	5.869	-0.957	-0.079	-3.617
Arg46(C)	-334.746	327.185	-0.954	-0.084	-8.598
Arg57(C)	-251.717	250.637	-0.583	-0.089	-1.752
Ile74(C)	-2.681	2.666	-2.182	-0.254	-2.451
Val76(C)	-6.799	6.739	-3.574	-0.340	-3.975
Gln77(C)	2.631	-0.450	-3.201	-0.441	-1.461
Thr78(C)	-4.997	5.323	-1.778	-0.131	-1.583
Pro79(C)	-5.062	5.276	-1.230	-0.236	-1.253
Arg84(C)	-234.810	233.872	-4.698	-0.626	-6.262
Thr85(C)	-2.555	3.647	-2.068	-0.280	-1.255
Arg86(C)	-323.188	312.985	-3.856	-0.809	-14.867

Arg87(C)	-222.253	220.935	-1.010	-0.139	-2.467
1G2	-66.532	65.809	-2.528	-0.304	-3.556
1G3	-87.926	89.774	-2.907	-0.168	-1.227
1G4	-139.354	139.764	-4.908	-0.605	-5.104
1C5	-166.496	161.799	-3.415	-0.613	-8.726
1C6	-175.528	179.548	-7.133	-1.028	-4.141
1G7	-195.716	194.127	-4.797	-0.929	-7.314
1G14	-99.312	104.004	-6.857	-0.820	-2.984
1G15	-131.331	136.011	-8.333	-1.119	-4.772
2C3	-146.994	153.616	-11.972	-1.752	-7.102
2G4	-168.154	171.878	-4.723	-0.620	-1.619
2G5	-184.713	189.742	-5.039	-0.701	-0.711
2C6	-182.553	183.814	-2.867	-0.589	-2.194
2G7	-197.769	196.489	-1.595	-0.540	-3.416
2T8	-149.200	149.381	-1.455	-0.409	-1.683
2G9	-124.307	123.923	-0.268	-0.114	-0.766

Table S5

Ape10b2 salt bridges with the DNA backbone (columns 1-3) and hydrogen bonds with the DNA bases (columns 4-6) with occupancy over 20% are highly dynamic at 300K.

protein	DNA backbone	Occupancy (%)	protein	DNA base	Occupancy (%)
Arg46(C)@NH2	1C6@O2P	96.50	Asn45(C)(ND2)	1C6(O1P)	96.80
Arg13(C)@NH2	1G7@O1P	81.00	Arg86(A)(NH1)	2C14(O2)	78.50
Arg46(A)@NE	2G7@O1P	43.80	Arg86(C)(NH1)	2C3(O2)	31.10
Arg42(C)@NH2	2C6@O1P	30.70	Thr85(A)(OG1)	2C15(O3')	24.90
Arg40(A)@NH2	1G4@O2P	30.60			
Arg40(C)@NH2	2G5@O1P	28.50			
Arg57(A)@NH2	1G15@O2P	27.00			
Arg40(C)@NH1	2G4@O2P	26.50			
Arg42(C)@NE	2G5@O1P	25.10			

Table S6

Ape10b2 salt bridges with the DNA backbone (columns 1-3) and hydrogen bonds with the DNA bases (columns 4-6) with occupancy over 20% are highly dynamic at 343K.

protein	DNA backbone	Occupancy (%)	protein	DNA base	Occupancy (%)
Arg86(C)@NH1	1G14@O1P	93.30	Arg42(C)@NH2	1C13@O2	88.70
Arg40(C)@NH2	1G14@O1P	92.40	Arg13(C)@NH1	2G4@N3	62.10
Arg42(A)@NH2	2G7@O1P	88.40	Arg13(C)@NH2	2C3@O2	60.00
Arg46(C)@NH2	2C6@O2P	87.90	Asn45(C)@ND2	2G7@O2P	58.40
Arg13(A)@NH2	2T8@O1P	78.60	Arg42(C)@NH1	1C12@O2	20.60
Arg10(C)@NH2	1G15@O1P	65.40			
Arg46(A)@NH2	2G9@O1P	50.90			
Arg46(A)@NH2	2T8@O2P	50.50			
Arg10(A)@NH2	1G3@O2P	42.40			
Arg84(C)@NH2	1C13@O1P	26.50			
Arg10(A)@NH2	1G4@O2P	22.80			
Arg86(A)@NH1	1C6@O2P	21.70			
Arg40(A)@NH2	1C5@O1P	20.80			

Table S7

Ape10b2 salt bridges with the DNA backbone (columns 1-3) and hydrogen bonds with the DNA bases (columns 4-6) with occupancy over 20% are highly dynamic at 363K.

protein	DNA backbone	Occupancy (%)	protein	DNA base	Occupancy (%)
Arg46(C)@NH1	2C6@O2P	86.00	Asn45(A)@ND2	2G7@O1P	46.10
Arg86(C)@NH1	1G14@O1P	82.10	Arg46(A)@NH2	2G7@O3’	26.80
Arg46(A)@NH1	2T8@O2P	70.60	Glu80(C)@OE2	2C2@N4	24.00
Arg42(C)@NH1	2G7@O2P	68.50	Arg86(C)@NE	1G15@N7	23.90
Arg40(A)@NH1	1G3@O2P	67.30	Arg86(A)@NH2	2C13@O2	20.40
Arg10(A)@NH2	1G4@O2P	56.40			
Arg10(A)@NH2	1G3@O2P	50.00			
Arg13(C)@NH2	1G15@O2P	36.10			
Arg40(C)@NH1	1G15@O2P	36.00			
Arg13(C)@NH1	2C6@O2P	32.20			
Arg42(A)@NE	1C5@O1P	31.20			
Arg42(A)@NE	2G7@O1P	26.80			
Arg13(A)@NH1	2G9@O1P	24.70			

Table S8

Ape10b2 salt bridges with the DNA backbone (columns 1-3) and hydrogen bonds with the DNA bases (columns 4-6) with occupancy over 20% are highly dynamic at 373K.

protein	DNA backbone	Occupancy (%)	protein	DNA base	Occupancy (%)
Arg40(A)@NH1	1C5@O1P	98.10	Asn45(C)@ND2	1G7@O1P	89.40
Arg46(C)@NH1	1G7@O1P	95.60	Asn43(C)@ND2	2C3@O2	81.00
Arg86(A)@NH2	1G4@O2P	90.60	Gln82(A)@NE2	1G2@N3	68.90
Arg42(A)@NE	1G7@O1P	90.50	Thr85(C)@OG1	1G15@N2	62.50
Arg13(C)@NE	2G4@O2P	82.90	Arg13(A)@NH2	2T8@O5’	31.70
Arg86(C)@NH2	2C6@O2P	76.20	Arg42(A)@NH2	1G7@O5’	22.30
Arg87(A)@NE	1C6@O1P	57.60	Arg13(C)@NE	2G4@O5’	20.40
Arg42(C)@NH1	2C6@O1P	57.40	Arg10(C)@NE	2C3@O5’	20.30
Arg13(A)@NE	2T8@O1P	56.10			
Arg42(C)@NH2	2G7@O1P	48.40			
Arg86(C)@NH1	2G5@O3’	39.80			
Arg10(C)@NH1	2C3@O2P	36.90			
Arg13(A)@NH2	2G9@O1P	36.70			
Arg42(C)@NH2	2G5@O1P	34.50			
Arg46(A)@NH1	2G7@O2P	34.10			
Arg42(A)@NE	1C6@O3’	32.40			
Arg86(C)@NH1	1G15@O2P	29.30			
Arg84(C)@NE	1G15@O5’	23.70			

Table S9

Hydrophobic interactions analyses for Ape10b2-dsDNA complex at 300, 343, 363, and 373K.

300K	343K	363K	373K
Val76(A)/2C15	Gly12(A)/1G3	Val88(A)/1C5	Val88(A)/1C6
Ile74(C)/2G4	Pro15(A)/1G3	Gly41(A)/1G4	Ile11(C)/2C3
Pro15(A)/2G7	Gly41(C)/1G14	Val88(A)/1G4	Gly12(C)/2C3
Val76(C)/2C3	Gly12(C)/1G15	Val76(C)/1G15	Val88(A)/1C5
Val76(C)/2G4	Val16(A)/1G2	Pro79(C)/2C2	Pro15(C)/1G7
Val88(C)/2G4	Pro79(A)/1C6	Val88(A)/1G3	Val76(C)/1G15
Ile74(C)/2C3			Val76(C)/1G14
Val76(C)/2C2			Pro79(C)/1G14
Val16(A)/2C6			Gly41(A)/1C6
			Gly81(A)/1G2