Supplementary Material

Table S1. Mean interaction energies (kcal/mol) of all base pairs of the DNA molecules presented in the two binary complexes from different MD simulations.

	alone				complexed				
1BNZ	300K	360K	420K	480K	300K	360K	360K-1	420K	480K
T2A7	-5.405	-5.164	-1.032	-0.05	-5.361	-5.329	-5.342	-0.665	0.081
A3T6	-5.429	-5.118	-0.632	0.126	-5.517	-5.520	-5.186	-1.502	0.075
A4T5	-5.327	-5.123	-1.816	0.300	-5.173	-5.530	-5.544	-0.174	0.069
T5A4	-5.272	-5.057	-1.457	0.092	-5.495	-5.163	-5.162	-3.158	0.017
T6A3	-5.307	-4.906	-0.881	0.062	-5.322	-4.996	-4.981	-2.203	0.061
A7T2	-5.306	-3.227	-1.197	-0.09	-5.454	-5.238	-5.242	-1.952	-1.570
1BF4	300K	360K	420K	480K	300K	360K	360K-1	420K	480K
C2G7	-10.994	-10.715	-6.755	-1.594	-11.536	-11.211	-11.108	-9.981	-4.247
G3C6	-11.124	-10.712	-11.111	-1.932	-11.691	-11.185	-11.238	-10.958	-1.230
T4A5	-5.282	-5.152	-4.917	-0.10	-5.347	-5. 230	-5.234	-5.307	-0.204
T5A4	-5.400	-5.169	-4.957	-0.310	-5. 509	-5.237	-5.198	-4.483	-2.769
C6G3	-10.748	-10.614	-10.993	-4.293	-11.372	-10.784	-10.818	-9.109	-2.297
G7C2	-10.770	-10.605	-10.424	-3.828	-11.130	-10.432	-10.423	-2.304	-1.917

Table S2. Binding free energies (kcal/mol) contributed by enthalpy and entropy at 300 K and 360 K in single-trajectory/triplet- trajectory analysis for 1BNZ complex using different solute dielectric constants (ε_{in} = 1, ε_{in} = 4, and ε_{in} = 8).

A: The binding free energies in single-trajectory analysis

ε	1.0		4.0		8.0	
	300K	360K	300 K	360K	300K	360 K
E_{ele}	-2412.7	-2580.5	-2412.7	-2580.5	-2412.7	-2580.5
E_{vdw}	-101.9	-101.2	-101.9	-101.2	-101.9	-101.2
G_{nonp}	-13.3	-12.6	-13.3	-13.4	-13.2	-13.1
G_{pb}	2429.7	2587.2	588.9	622.4	277.0	294.0
ΔG_{np}	-115.2	-113.8	-115.2	-114.6	-115.1	-114.3
ΔG_{pb}	17.0	6.7	-1823.8	-1958.1	-2135.7	-2286.5
ΔE_{MM}	-2514.6	-2681.7	-2514.6	-2681.7	-2514.7	-2681.7
ΔG_{solv}	2416.4	2574.6	575.6	609.0	263.8	280.9
ΔH	-98.3	-107.1	-1939.0	-2072.7	-2250.9	-2400.8
$-T\Delta S$	30.0	50.1	32.7	71.3	61.4	81.3
ΔG_{bind}	-68.3	-57.0	-1877.6	-1999.4	-2189.5	-2319.5

B: The binding free energies from triplet-trajectory analysis

ε	1.0		4.0		8.0	
	300K	360K	300 K	360K	300K	360 K
E_{ele}	-2393.2	-2481.8	-2393.2	-2481.8	-2393.2	-2481.8
E_{vdw}	-88.9	-86.5	-88.9	-86.5	-88.9	-86.5
G_{nonp}	-8.8	-8.7	-8.7	-8.7	-8.8	-8.7
G_{pb}	2426.8	2509.8	584.0	603.3	276.5	285.4
ΔG_{np}	-97.7	-95.2	-97.6	-95.2	-97.7	-95.2
ΔG_{pb}	33.6	28.0	-1809.2	-1878.5	-2116.7	-2196.4
ΔE_{MM}	-2488.8	-2581.5	-2482.1	-2568.3	-2482.1	-2568.3
ΔG_{solv}	2418.0	2501.1	575.2	595.2	267.8	276.7
ΔH	-70.8	-80.4	-1906.8	-1973.1	-2214.4	-2291.6
$-T\Delta S$	39.4	45.8	62.4	97.9	82.5	117.9
ΔG_{bind}	-31.4	-34.6	-1844.4	-1875.2	-2133.9	-2173.7

Table S3. Binding free energies (kcal/mol) contributed by enthalpy and entropy at 300 K and 360 K in single-trajectory analysis for 1BNZ and 1BF4 complexes.

	1BNZ			1BF4		
	300K	360K	360K-1	300K	360K	360K-1
E_{ele}	-2412.7	-2580.5	-2591.7	-2319.5	-2431.4	-2439.2
E_{vdw}	-101.9	-101.2	-99.9	-100.1	-98.6	-98.5
G_{nonp}	-13.3	-12.6	-13.5	-11.2	-11.8	-9.1
G_{pb}	2429.7	2587.2	2596.9	2340.6	2445.5	2450.3
$\Delta G_{np}{}^{*}$	-115.2	-113.8	-113.4	-111.3	-110.4	-107.6
$\Delta G_{pb}{}^{+}$	17.0	6.7	5.2	21.1	14.1	11.1
ΔE_{MM}	-2514.6	-2681.7	-2691.6	-2419.6	-2530.0	-2537.7
ΔG_{solv}	2416.4	2574.6	2583.5	2329.3	2433.7	2441.2
ΔH	-98.3	-107.1	-108.2	-90.3	-96.2	-96.5
$-T\Delta S$	30.0	50.1	50.9	36.9	47.6	48.3
$\Delta G_{bind}{}^{\#}$	-68.3	-57.0	-57.3	-53.4	-48.6	-48.2

Notes: * $\Delta G_{np} = E_{vdw} + G_{nonp}$

$^{+}$ $\Delta G_{pb} = E_{ele} + G_{pb}$

$^{\#}$ $\Delta G_{bind} = \Delta G_{np} + \Delta G_{pb} + E_{int} - T\Delta S$

Table S4. Interaction energies (kcal/mol) of Sso7d-DNA-base and Sso7d-DNA-backbone.

	1BNZ			1BF4		
	300K	360K	360K-1	300K	360K	360K-1
Sso7d-D2a-base	-9.7	-14.5	-13.8	-7.5	-8.2	-8.7
Sso7d-D2a-bkb	-43.8	-49.7	-49.1	-51.8	-53.6	-53.2
Sso7d-D3a-base	-10.2	-10.6	-10.9	-9.2	-9.9	-9.8
Sso7d-D3a-bkb	-58.3	-57.6	-56.9	-67.4	-68.9	-67.5
Sso7d-D4a-base	-14.5	-16.2	-16.9	-13.8	-14.9	-14.5
Sso7d-D4a-bkb	-69.7	-60.4	-62.6	-89.9	-82.3	-83.4
Sso7d-D5a-base	-11.7	-15.9	-15.8	-18.9	-18.4	-17.9
Sso7d-D5a-bkb	-97.1	-83.1	-82.4	-87.9	-85.6	-85.9
Sso7d-D6a-base	-16.8	-16.9	-16.9	-13.8	-12.3	-12.9
Sso7d-D6a-bkb	-92.1	-88.9	-89.1	-77.4	-89.1	-88.3
Sso7d-D7a-base	-14.5	-10.9	-11.7	-8.5	-6.4	-6.7
Sso7d-D7a-bkb	-89.4	-88.1	-87.3	-76.2	-85.8	-84.6
Sso7d-D2b-base	-9.7	-15.1	-15.9	-12.1	-11.2	-11.9
Sso7d-D2b-bkb	-69.3	-50.2	-52.1	-83.1	-92.7	-90.9
Sso7d-D3b-base	-13.5	-14.9	-14.3	-12.7	-11.9	-12.3
Sso7d-D3b-bkb	-80.6	-96.7	-93.1	-89.6	-101.2	-100.8
Sso7d-D4b-base	-11.8	-15.6	-15.7	-13.0	-14.8	-13.4
Sso7d-D4b-bkb	-92.1	-97.6	-98.2	-76.0	-93.4	-92.7
Sso7d-D5b-base	-11.4	-12.9	-13.7	-10.5	-12.1	-12.9
Sso7d-D5b-bkb	-82.3	-87.6	-85.9	-58.2	-54.9	-55.4
Sso7d-D6b-base	-12.1	-13.4	-12.5	-8.4	-9.9	-10.3
Sso7d-D6b-bkb	-54.7	-58.7	-59.1	-42.4	-53.5	-50.9
Sso7d-D7b-base	-11.1	-11.1	-12.7	-5.2	-6.3	-7.0
Sso7d-D7b-bkb	-47.1	-43.5	-46.7	-42.4	-48.9	-47.6

Table S5. Relative binding free energies (kcal/mol) contributed by important residues ($|\Delta G_{bind}| \geq 3.5$ kcal mol^{-1}) in 1BNZ complex.

1BNZ	T	van der Waals	Electrostatic	Polar solvation	Non-Polar solv	TOTAL
Lys7	300K	-4.171	178.898	174.553	-0.651	-9.162
	360K	-2.264	-172.255	167.703	-0.290	-7.321
	360K-1	-2.547	-172.624	171.196	-0.438	-7.526
Tyr8	300K	-5.15	-2.776	2.994	-0.392	-4.988
	360K	-5.497	-5.572	5.942	-0.592	-5.619
	360K-1	-5.378	-8.114	5.621	-0.563	-5.546
Lys9	300K	-1.759	-188.575	184.147	-0.319	-5.483
	360K	-1.838	-183.579	179.237	-0.318	-5.020
	360K-1	-2.148	-181.728	178.764	-0.512	-5.217
Lys22	300K	-1.724	-190.117	186.791	-0.487	-5.936
	360K	-0.841	-175.791	171.351	-0.344	-5.643
	360K-1	-1.217	-175.326	172.421	-0.761	-5.789
Trp24	300K	-6.609	-4.537	5.426	-0.573	-6.377
	360K	-5.746	-3.547	4.522	-0.562	-5.344
	360K-1	-5.864	-3.107	4.211	-0.657	-5.113
Val26	300K	-5.173	3.525	-3.569	-0.637	-5.449
	360K	-4.944	1.731	-2.169	-0.640	-6.256
	360K-1	-4.764	1.523	-2.204	-0.542	-6.114
Lys28	300K	-1.867	-178.561	175.958	-0.391	-4.926
	360K	-4.161	-219.633	214.426	-0.800	-11.140
	360K-1	-4.106	-217.201	213.839	-0.896	-10.314
Met29	300K	-5.508	-0.079	1.670	-0.580	-4.077
	360K	-5.569	-0.617	1.660	-0.551	-4.427
	360K-1	-5.282	-0.479	1.519	-0.548	-4.326
Arg43	300K	-5.889	-208.259	206.336	-0.997	-8.829
	360K	-5.066	-204.224	202.597	-1.027	-8.476
	360K-1	-4.816	-205.102	203.251	-0.824	-8.312

Table S6. Relative binding free energies (kcal/mol) contributed by important residues ($|\Delta G_{bind}| \geq 3.5$ kcal mol^{-1}) in 1BF4 complex.

1BF4	T	van der Waals	Electrostatic	Polar solvation	Non-Polar solv	TOTAL
Lys7	300K	-2.104	-172.450	188.107	-0.414	-9.218
	360K	-2.003	-184.087	178.186	-0.164	-8.137
	360K-1	-2.089	-185.265	179.234	-0.174	-8.532
Tyr8	300K	-5.790	-10.179	10.684	-0.475	-6.917
	360K	-5.788	-9.739	10.443	-0.439	-7.941
	360K-1	-5.896	-9.692	10.002	-0.463	-7.899
Lys9	300K	-2.524	-167.803	174.260	-0.374	-6.382
	360K	-2.437	-170.919	168.348	-0.459	-6.024
	360K-1	-2.363	-170.563	164.241	-0.412	-5.971
Lys22	300K	-1.713	-181.744	178.260	-0.397	-5.693
	360K	-1.256	-182.708	179.817	-0.307	-4.537
	360K-1	-1.247	-181.636	178.720	-0.326	-4.616
Trp24	300K	-5.253	-5.603	5.232	-0.608	-6.650
	360K	-5.374	-4.284	4.214	-0.597	-6.136
	360K-1	-5.027	-4.986	4.928	-0.617	-6.256
Val26	300K	-4.901	3.408	-3.516	-0.543	-6.895
	360K	-4.622	3.089	-3.439	-0.428	-5.582
	360K-1	-4.789	2.925	-3.378	-0.427	-5.589
Met29	300K	-5.903	-0.957	1.127	-0.779	-7.246
	360K	-5.712	-0.676	0.352	-0.520	-6.938
	360K-1	-5.541	-0.624	1.304	-0.561	-6.747
Arg43	300K	-5.074	-201.312	199.397	-0.620	-8.615
	360K	-4.304	-203.465	202.638	-0.737	-6.745
	360K-1	-4.405	-203.383	203.519	-0.816	-6.519

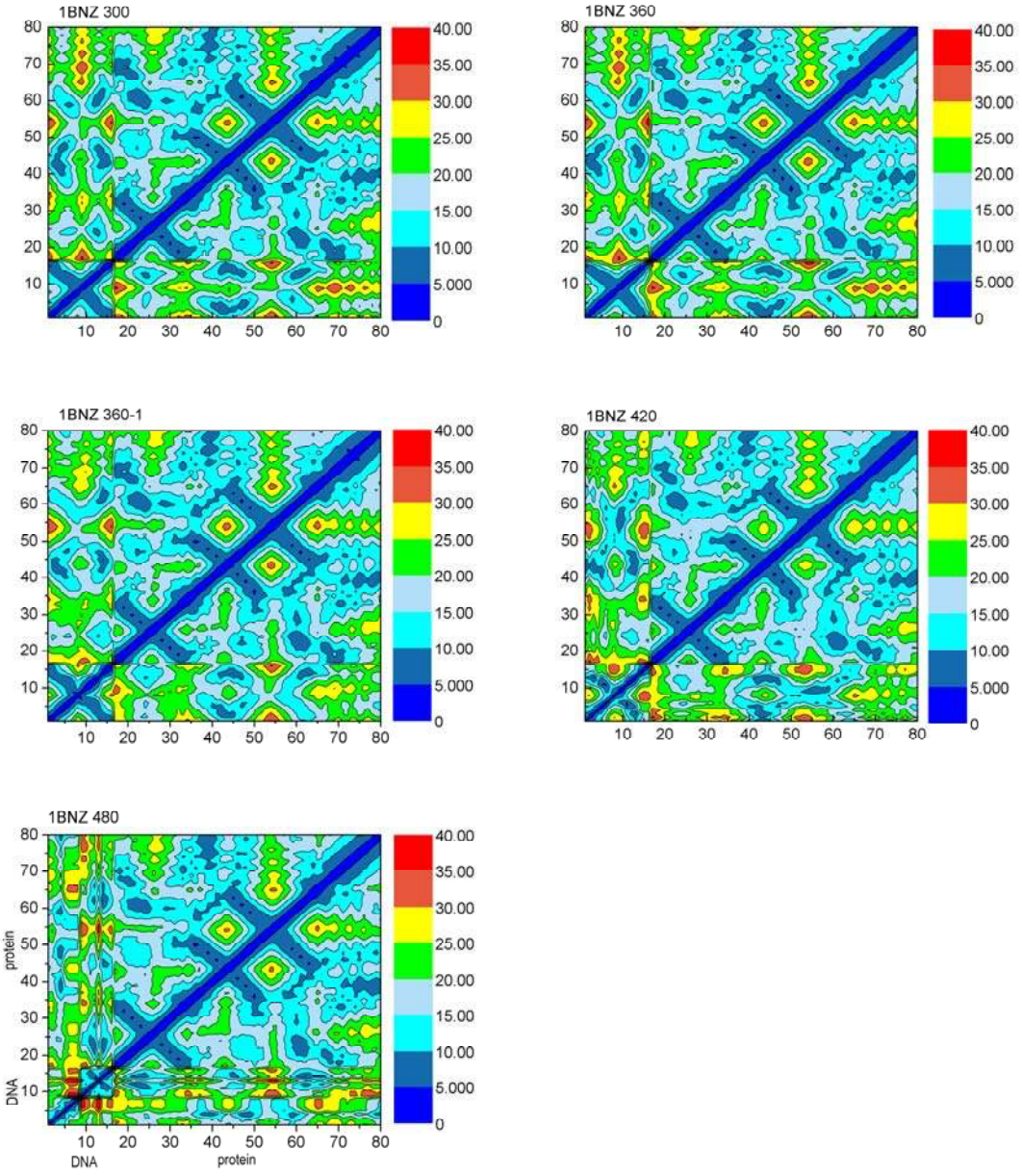

Figure S1. Contact maps showing the inter residue/nucleotide distances that were calculated and plotted over the last 20 ns of the simulations on the 1BNZ complex at different temperatures.

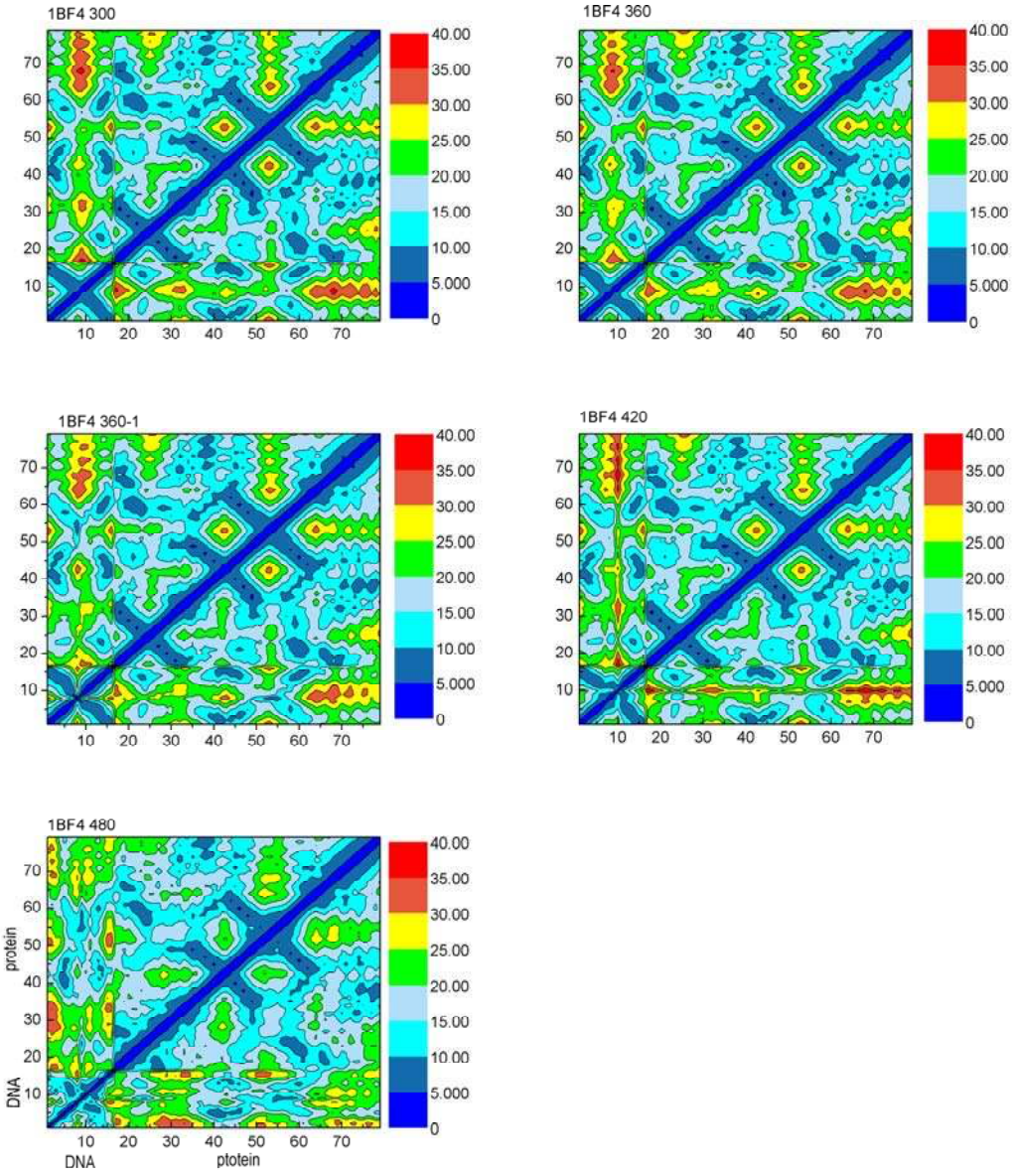

Figure S2. Contact maps showing the inter residue/nucleotide distances that were calculated and plotted over the last 20 ns of the simulations on the 1BF4 complex at different temperatures.

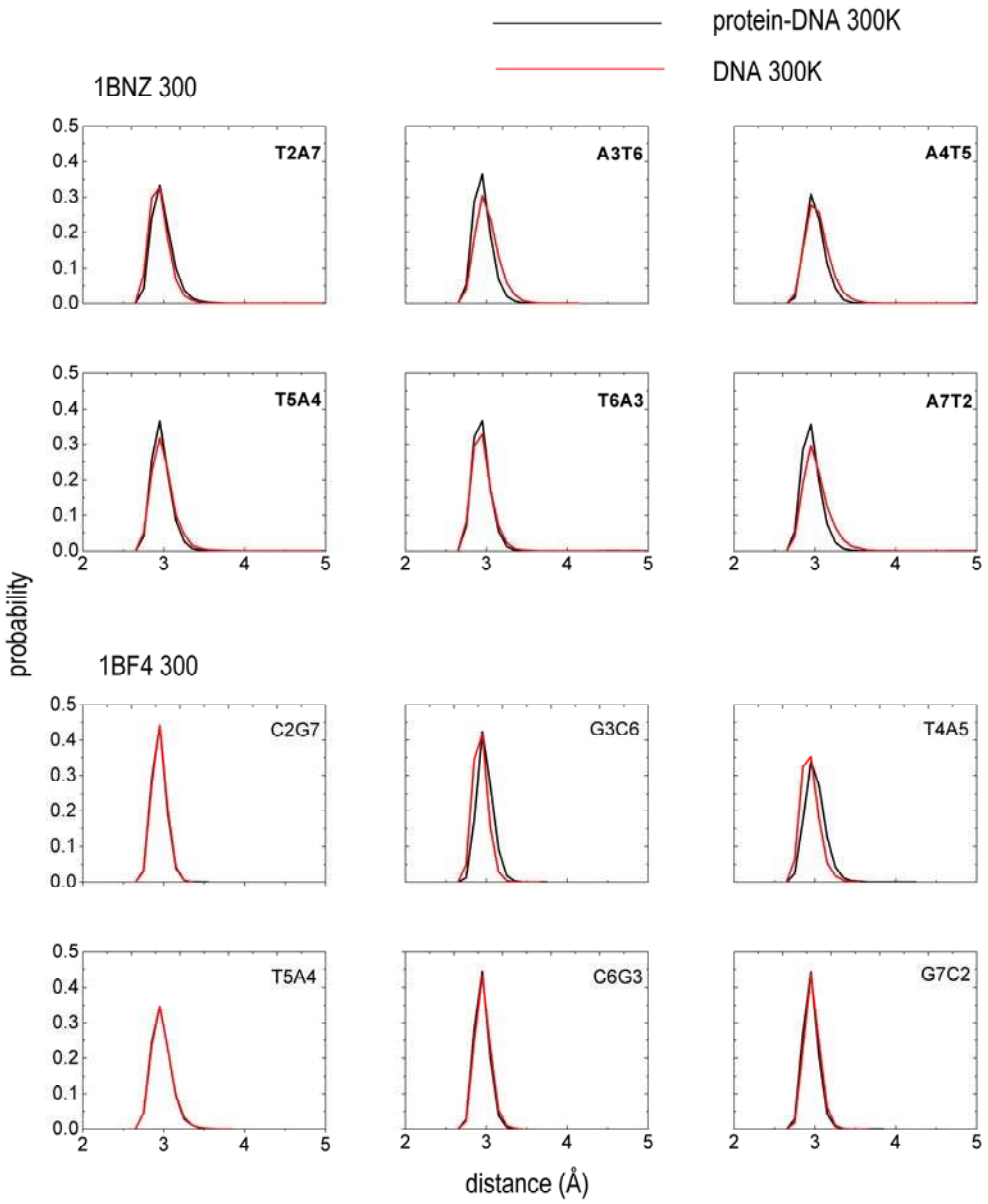

Figure S3. Probability distributions of the N1(G/A)-N3(C/T) distances in the central six base pairs of the unbound DNA and bound DNA systems at 300K.

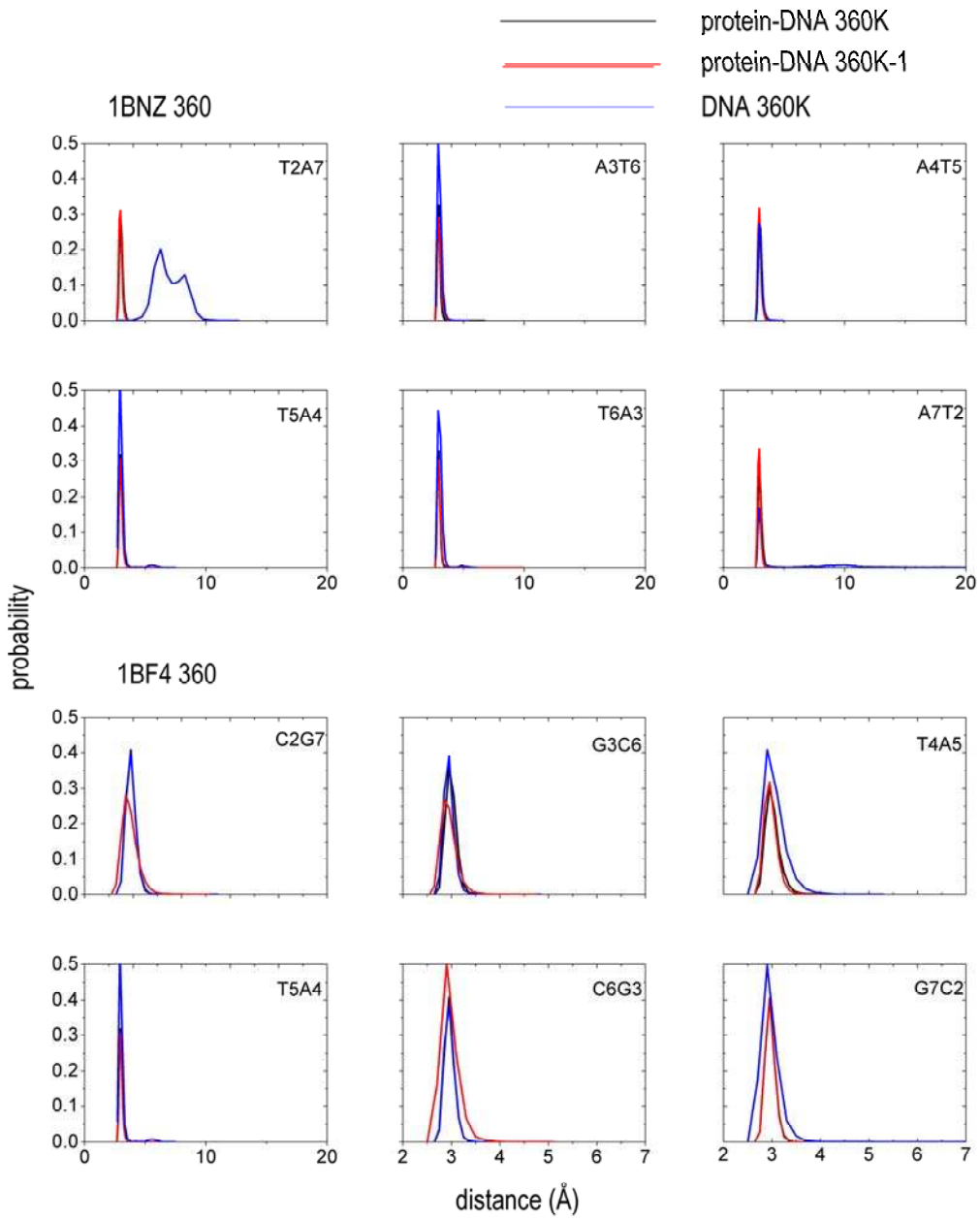

Figure S4. Probability distributions of the N1(G/A)-N3(C/T) distances in the central six base pairs of the unbound DNA and bound DNA systems at 360 K..

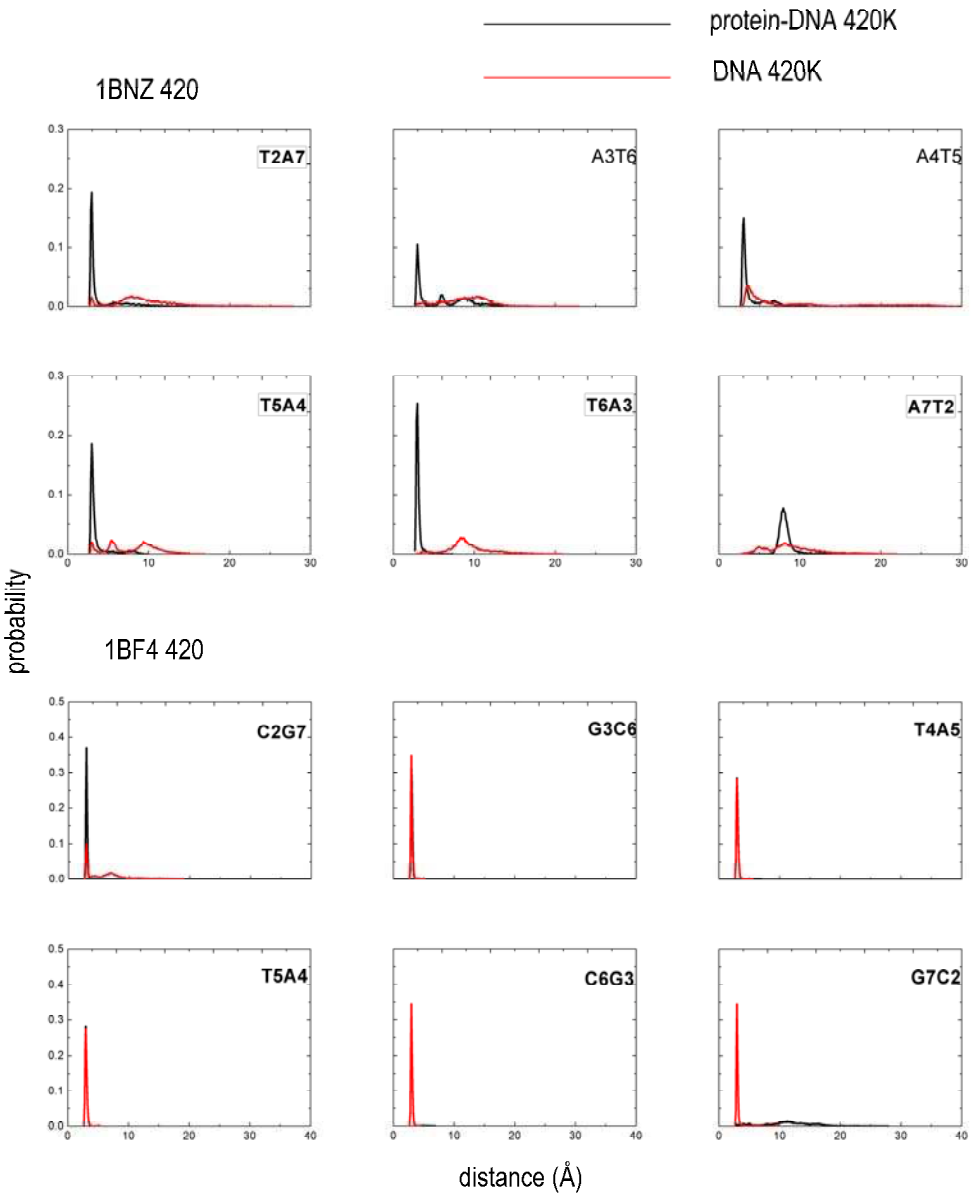

Figure S5. Probability distributions of the N1(G/A)-N3(C/T) distances in the central six base pairs of the unbound DNA and bound DNA systems at 420 K.

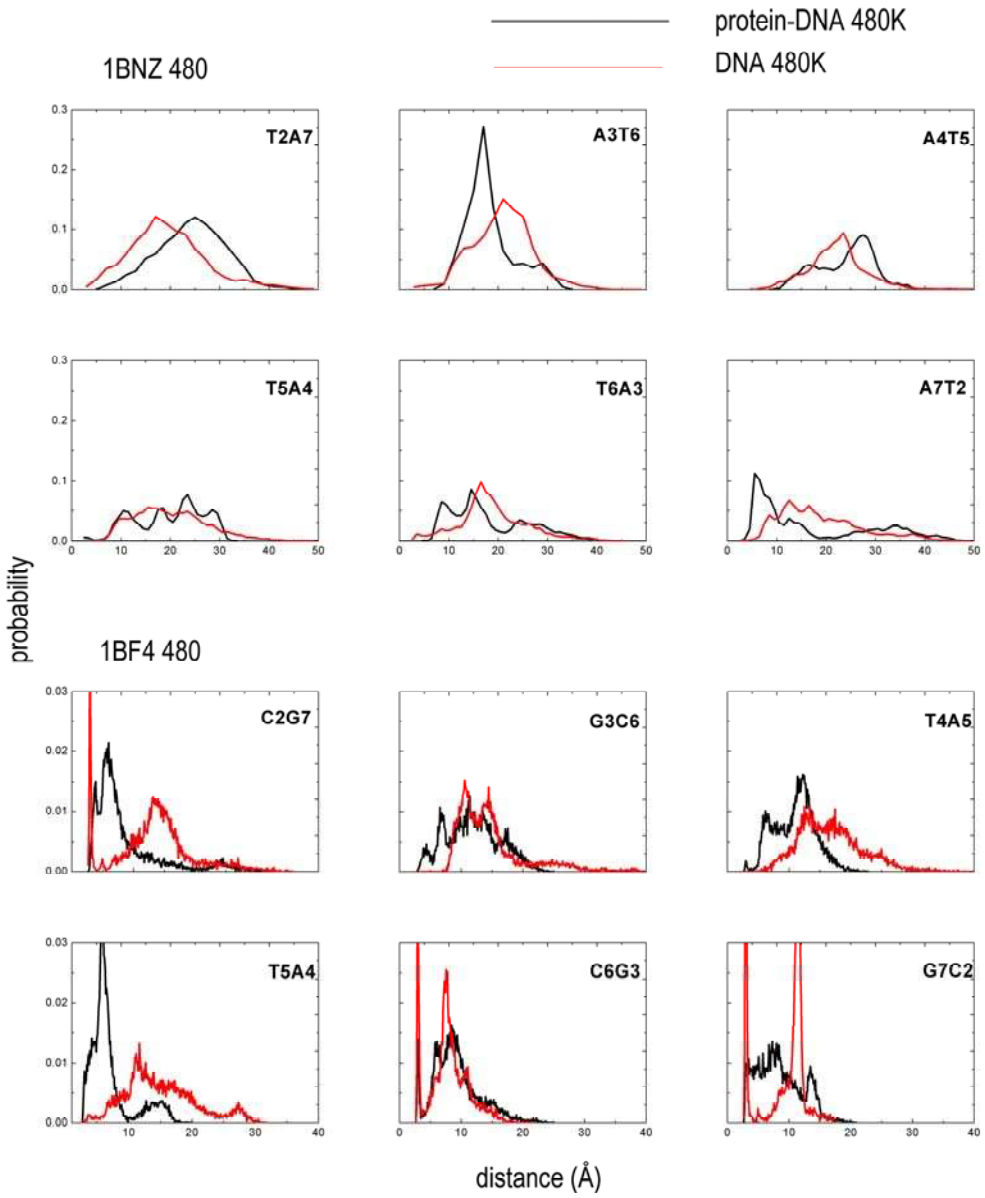

Figure S6. Probability distributions of the N1(G/A)-N3(C/T) distances in the central six base pairs of the unbound DNA and bound DNA systems at 480 K.