

Supplementary material to "Density functional theory including dispersion corrections for intermolecular interactions in a large benchmark set of biologically relevant molecules"

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- [1] P. Jurecka, J. Sponer, J. Cerny, and P. Hobza, *Phys. Chem. Chem. Phys.* **8**, 1985 (2006).

TABLE SI: DFT-D/TZV(2d,2p) intermolecular interaction energies (kcal mol⁻¹) for the small dataset.

No.	Complex (symmetry)	B97-D			PBE-D		B-LYP-D		ΔE_{ref}^a
		ΔE^b	CP ^c	dev. ^d	ΔE^b	dev. ^d	ΔE^b	dev. ^d	
Hydrogen bonded complexes (7)									
1	(NH ₃) ₂ (<i>C</i> _{2h})	-3.76	-0.45	-0.59	-4.56	-1.39	-4.19	-1.02	-3.17
2	(H ₂ O) ₂ (<i>C</i> _s)	-5.16	-0.69	-0.14	-6.41	-1.39	-5.89	-0.87	-5.02
3	Formic acid dimer (<i>C</i> _{2h})	-18.37	-0.69	0.24	-20.93	-2.32	-19.44	-0.83	-18.61
4	Formamide dimer (<i>C</i> _{2h})	-15.43	-0.61	0.53	-17.57	-1.61	-16.52	-0.56	-15.96
5	Uracil dimer (<i>C</i> _{2h})	-19.55	-0.49	1.10	-21.56	-0.91	-20.81	-0.16	-20.65
6	2-pyridoxine·2-aminopyridine	-17.23	-0.63	-0.52	-19.08	-2.37	-18.12	-1.41	-16.71
7	Adenine·thymine WC	-16.32	-0.65	0.05	-18.24	-1.87	-17.27	-0.90	-16.37
Complexes with predominant dispersion contribution (8)									
8	(CH ₄) ₂ (<i>D</i> _{3d})	-0.57	-0.02	-0.04	-0.73	-0.20	-0.36	0.17	-0.53
9	(C ₂ H ₄) ₂ (<i>D</i> _{2d})	-1.57	-0.07	-0.06	-2.01	-0.50	-1.57	-0.06	-1.51
10	Benzene·CH ₄ (<i>C</i> ₃)	-1.53	-0.06	-0.03	-1.78	-0.28	-1.40	0.10	-1.50
11	Benzene dimer (<i>C</i> _{2h})	-2.68	-0.28	0.05	-2.64	0.09	-2.38	0.35	-2.73
12	Pyrazine dimer (<i>C</i> _s)	-4.08	-0.28	0.34	-4.17	0.25	-4.08	0.34	-4.42
13	Uracil dimer (<i>C</i> ₂)	-10.12	-0.70	0.00	-10.23	-0.11	-10.62	-0.50	-10.12
14	Indole·benzene	-4.74	-0.49	0.48	-4.58	0.64	-4.61	0.61	-5.22
15	Adenine·thymine stack	-12.21	-0.90	0.02	-12.15	0.08	-12.98	-0.75	-12.23
Mixed complexes (7)									
16	Ethene·ethine (<i>C</i> _{2v})	-1.77	-0.08	-0.24	-2.06	-0.53	-1.66	-0.13	-1.53
17	Benzene·H ₂ O (<i>C</i> _s)	-4.28	-0.75	-1.00	-4.71	-1.43	-4.29	-1.01	-3.28
18	Benzene·NH ₃ (<i>C</i> _s)	-2.83	-0.38	-0.48	-3.12	-0.77	-2.74	-0.39	-2.35
19	Benzene·HCN (<i>C</i> _s)	-5.02	-0.10	-0.56	-5.46	-1.00	-4.99	-0.53	-4.46
20	Benzene dimer (<i>C</i> _{2v})	-3.01	-0.17	-0.27	-3.12	-0.38	-2.84	-0.10	-2.74
21	Indole·benzene T-shape	-6.47	-0.36	-0.74	-6.66	-0.93	-6.34	-0.61	-5.73
22	Phenol dimer	-6.67	-0.58	0.38	-7.63	-0.58	-7.41	-0.36	-7.05

^aEstimated CCSD(T)/CBS [1]. ^bNo CP correction. ^cCounterpoise correction. ^d $\Delta E - \Delta E_{\text{ref}}$.

TABLE SII: DFT/TZV(2df,2pd) intermolecular interaction energies without dispersion correction (kcal mol⁻¹) for the small dataset.

No.	Complex (symmetry)	PBE			B-LYP			ΔE_{ref}^a
		ΔE^b	CP ^c	dev. ^d	ΔE^b	CP ^c	dev. ^d	
Hydrogen bonded complexes (7)								
1	(NH ₃) ₂ (<i>C</i> _{2h})	-3.49	-0.48	-0.32	-2.50	-0.52	0.67	-3.17
2	(H ₂ O) ₂ (<i>C</i> _s)	-5.73	-0.75	-0.71	-4.87	-0.81	0.15	-5.02
3	Formic acid dimer (<i>C</i> _{2h})	-18.93	-0.70	-0.32	-16.32	-0.73	2.29	-18.61
4	Formamide dimer (<i>C</i> _{2h})	-15.43	-0.64	0.53	-13.20	-0.67	2.76	-15.96
5	Uracil dimer (<i>C</i> _{2h})	-18.96	-0.48	1.69	-16.73	-0.51	3.92	-20.65
6	2-pyridoxine-2-aminopyridine	-16.01	-0.63	0.70	-13.28	-0.67	3.43	-16.71
7	Adenine-thymine WC	-14.95	-0.62	1.42	-12.11	-0.66	4.26	-16.37
Complexes with predominant dispersion contribution (8)								
8	(CH ₄) ₂ (<i>D</i> _{3d})	-0.11	-0.02	0.42	0.63	-0.02	1.16	-0.53
9	(C ₂ H ₄) ₂ (<i>D</i> _{2d})	-0.39	-0.05	1.12	1.02	-0.05	2.53	-1.51
10	Benzene·CH ₄ (<i>C</i> ₃)	-0.12	-0.05	1.38	1.25	-0.06	2.75	-1.50
11	Benzene dimer (<i>C</i> _{2h})	1.65	-0.25	4.38	4.51	-0.28	7.24	-2.73
12	Pyrazine dimer (<i>C</i> _s)	0.48	-0.28	4.90	3.40	-0.30	7.82	-4.42
13	Uracil dimer (<i>C</i> ₂)	-3.38	-0.69	6.74	0.32	-0.72	10.44	-10.12
14	Indole·benzene	1.82	-0.43	7.04	5.69	-0.46	10.91	-5.22
15	Adenine-thymine stack	-2.17	-0.88	10.06	3.01	-0.92	15.24	-12.23
Mixed complexes (7)								
16	Ethene·ethine (<i>C</i> _{2v})	-1.27	-0.08	0.26	-0.42	-0.09	1.11	-1.53
17	Benzene·H ₂ O (<i>C</i> _s)	-2.82	-0.79	0.46	-1.36	-0.83	1.92	-3.28
18	Benzene·NH ₃ (<i>C</i> _s)	-1.33	-0.39	1.02	0.07	-0.41	2.42	-2.35
19	Benzene·HCN (<i>C</i> _s)	-3.00	-0.10	1.46	-1.15	-0.11	3.31	-4.46
20	Benzene dimer (<i>C</i> _{2v})	-0.31	-0.15	2.43	1.62	-0.16	4.36	-2.74
21	Indole·benzene T-shape	-2.48	-0.35	3.25	0.21	-0.36	5.94	-5.73
22	Phenol dimer	-4.50	-0.61	2.55	-2.45	-0.64	4.60	-7.05

^aEstimated CCSD(T)/CBS [1]. ^bNo CP correction. ^cCounterpoise correction. ^d $\Delta E - \Delta E_{\text{ref}}$.

TABLE III: DFT-D/TZV(2df,2pd) intermolecular interaction energies (kcal mol⁻¹) for the large dataset.

No. ^a	Complex	B97-D			PBE-D		B-LYP-D		ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	dev. ^e	ΔE^c	dev. ^e	
Hydrogen-bonded DNA base pairs (38)									
1	G···C WC	-30.10	-0.72	1.96	-32.81	-0.75	-31.67	0.39	-32.06
2	mG···mC WC	-30.40	-0.74	1.19	-33.18	-1.59	-31.96	-0.37	-31.59
3	A···T WC	-16.20	-0.58	0.66	-18.12	-1.26	-17.19	-0.33	-16.86
4	mA···mT H	-17.15	-0.65	1.01	-19.35	-1.19	-18.33	-0.17	-18.16
5	8oG···C WC pl	-31.47	-0.73	1.83	-34.31	-1.01	-33.03	0.27	-33.30
6	I···C WC pl	-23.65	-0.61	1.25	-25.80	-0.90	-24.71	0.19	-24.90
7	G···U wobble	-17.80	-0.56	1.30	-19.96	-0.86	-19.05	0.05	-19.10
8	CCH+	-50.54	-0.60	0.86	-53.60	-2.20	-52.09	-0.69	-51.40
9	U···U Calcutta pl	-9.23	-0.47	1.07	-10.91	-0.61	-10.28	0.02	-10.30
10	U···U pl	-12.44	-0.49	1.26	-14.52	-0.82	-13.72	-0.02	-13.70
11	6tG···C WC pl	-28.73	-0.77	0.77	-31.70	-2.20	-29.86	-0.36	-29.50
12	A···4tU WC	-13.84	-0.54	0.36	-15.53	-1.33	-14.60	-0.40	-14.20
13	2-aminoA···T	-19.55	-0.68	-0.05	-22.12	-2.62	-21.02	-1.52	-19.50
14	2-aminoA···T pl	-19.59	-0.65	0.11	-22.18	-2.48	-21.11	-1.41	-19.70
15	A···F	-4.84	-0.43	0.36	-5.83	-0.63	-5.53	-0.33	-5.20
16	G···4tU	-16.22	-0.56	1.58	-18.28	-0.48	-17.50	0.30	-17.80
17	G···2tU	-14.92	-0.57	1.68	-17.18	-0.58	-15.67	0.93	-16.60
18	A···C pl	-17.94	-0.55	-0.34	-19.72	-2.12	-18.70	-1.10	-17.60
19	G···G pl	-20.52	-0.63	0.78	-22.39	-1.09	-21.70	-0.40	-21.30
20	G···6tG pl	-20.66	-0.63	1.14	-22.87	-1.07	-21.80	0.00	-21.80
21	6tG···G pl	-21.51	-0.71	1.19	-23.76	-1.06	-22.62	0.08	-22.70
22	G···A 1	-19.71	-0.70	-0.31	-21.70	-2.30	-20.76	-1.36	-19.40
23	G···A 1 pl	-19.32	-0.57	-0.42	-21.28	-2.38	-20.53	-1.63	-18.90
24	G···A 2	-13.77	-0.64	0.63	-15.39	-0.99	-14.60	-0.20	-14.40
25	G···A 2 pl	-12.90	-0.52	-0.10	-14.54	-1.74	-13.75	-0.95	-12.80

TABLE SIII: (continued)

No. ^a	Complex	B97-D			PBE-D		B-LYP-D		ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	dev. ^e	ΔE^c	dev. ^e	
26	G···A 3	-18.50	-0.74	0.30	-20.62	-1.82	-19.70	-0.90	-18.80
27	G···A 4	-13.84	-0.55	-0.34	-15.46	-1.96	-14.61	-1.11	-13.50
28	A···A 1 pl	-14.95	-0.52	-0.45	-16.69	-2.19	-15.73	-1.23	-14.50
29	A···A 2 pl	-13.86	-0.55	-0.16	-15.66	-1.96	-14.73	-1.03	-13.70
30	A···A 3 pl	-12.11	-0.59	0.09	-13.85	-1.65	-13.02	-0.82	-12.20
31	8oG···G	-21.28	-0.63	1.52	-23.69	-0.89	-22.60	0.20	-22.80
32	2tU···2tU pl	-10.70	-0.54	1.90	-12.91	-0.31	-11.51	1.09	-12.60
33	mA···mT WC ^f	-16.44	-0.60	-0.04	-18.31	-1.91	-17.39	-0.99	-16.40
34	mG···mC WC ^{*f,g}	-33.39	-0.79	2.41	-36.15	-0.35	-34.93	0.87	-35.80
35	mA···mT WC ^f	-18.24	-0.63	0.16	-19.99	-1.59	-19.10	-0.70	-18.40
36	G···A HB	-13.80	-0.70	-2.50	-15.59	-4.29	-14.64	-3.34	-11.30
37	C···G WC	-30.89	-0.75	-0.19	-33.91	-3.21	-32.55	-1.85	-30.70
38	G···C WC	-30.55	-0.74	0.85	-33.60	-2.20	-32.25	-0.85	-31.40
Interstrand base pairs (32)									
39	GG0/3.36 CGis036	-4.21	-0.45	-0.53	-4.07	-0.39	-3.89	-0.21	-3.68
40	GG0/3.36 GCis036	-4.03	-0.91	0.79	-3.48	1.34	-4.18	0.64	-4.82
41	AA20/3.05 TAis2005 ^h	-2.56	-0.34	-0.40	-2.79	-0.63	-2.60	-0.44	-2.16
42	AA20/3.05 ATis2005 ^h	-4.66	-0.55	-2.32	-4.48	-2.14	-4.83	-2.49	-2.34
43	GC0/3.25 C//Cis	2.80	-0.13	-0.29	2.90	-0.19	2.94	-0.15	3.09
44	GC0/3.25 G//Gis	1.46	-0.57	-0.47	1.51	-0.42	1.81	-0.12	1.93
45	CG0/3.19 C//Cis ⁱ	0.82	-0.18	-0.42	0.88	-0.36	1.05	-0.19	1.24
46	CG0/3.19 G//Gis ⁱ	-5.00	-0.81	-1.09	-4.84	-0.93	-4.79	-0.88	-3.91
47	GA10/3.15 A//Cis	-0.26	-0.32	0.05	-0.22	0.09	0.01	0.32	-0.31
48	GA10/3.15 T//Gis	0.51	-0.24	-0.07	0.53	-0.05	0.75	0.17	0.58
49	AG08/3.19 T//Gis	-0.89	-0.46	-0.42	-1.02	-0.55	-0.81	-0.34	-0.47
50	AG08/3.19 A//Cis	-0.60	-0.33	-0.42	-0.58	-0.40	-0.37	-0.19	-0.18
51	TG03.19 A//Gis	-4.83	-0.59	-0.61	-4.65	-0.43	-4.63	-0.41	-4.22

TABLE SIII: (continued)

No. ^a	Complex	B97-D			PBE-D		B-LYP-D		ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	dev. ^e	ΔE^c	dev. ^e	
52	TG03.19 T//Cis	-1.45	-0.15	-0.30	-1.34	-0.19	-1.25	-0.10	-1.15
53	GT10/3.15 T//Cis	0.02	-0.14	-0.28	0.12	-0.18	0.21	-0.09	0.30
54	GT10/3.15 A//Gis	-4.48	-0.49	-0.42	-4.59	-0.53	-4.42	-0.36	-4.06
55	AT10/3.26 T//Tis	0.54	-0.17	-0.34	0.64	-0.24	0.82	-0.06	0.88
56	AT10/3.26 A//Ais	-1.42	-0.45	-0.50	-1.40	-0.48	-1.21	-0.29	-0.92
57	TA08/3.16 A//Ais	-1.53	-0.39	0.02	-1.55	-0.00	-1.58	-0.03	-1.55
58	TA08/3.16 T//Tis	0.54	-0.14	-0.16	0.62	-0.08	0.72	0.02	0.70
59	AA0/3.24 A//Tis	-2.06	-0.22	-0.35	-1.87	-0.16	-1.70	0.01	-1.71
60	AA0/3.24 T//Ais	-1.79	-0.26	-0.49	-1.67	-0.37	-1.48	-0.18	-1.30
61	mA···mA IS ^f	-1.12	-0.52	-0.42	-1.20	-0.50	-1.01	-0.31	-0.70
62	mT···mT IS ^f	0.63	-0.20	-0.37	0.72	-0.28	0.90	-0.10	1.00
63	mG···mG IS ^f	-5.47	-0.82	-0.97	-5.04	-0.54	-5.14	-0.64	-4.50
64	mC···mC IS ^f	0.89	-0.26	-0.51	0.83	-0.57	0.99	-0.41	1.40
65	mA···mG IS ^f	-5.23	-0.50	-0.43	-5.26	-0.46	-4.98	-0.18	-4.80
66	mT···mC IS ^f	-0.43	-0.18	-0.33	-0.30	-0.20	-0.21	-0.11	-0.10
67	C···A IS	-2.58	-0.45	0.42	-2.96	0.04	-2.74	0.26	-3.00
68	G···G IS	-5.78	-0.38	-0.58	-5.77	-0.57	-5.61	-0.41	-5.20
69	G···G IS	0.30	-0.72	-0.50	0.05	-0.75	0.41	-0.39	0.80
70	C···C IS	2.79	-0.11	-0.31	2.89	-0.21	2.91	-0.19	3.10
Stacked base pairs (54)									
71	G···C S	-18.57	-0.98	0.45	-19.20	-0.18	-19.78	-0.76	-19.02
72	mG···mC S	-19.08	-1.09	1.27	-19.67	0.68	-20.59	-0.24	-20.35
73	A···T S	-12.11	-0.80	0.19	-12.08	0.22	-12.85	-0.55	-12.30
74	mA···mT S	-14.55	-0.95	0.02	-14.80	-0.23	-16.01	-1.44	-14.57
75	CC1	2.09	-0.66	-0.36	2.09	-0.36	2.12	-0.33	2.45
76	CC2	-3.85	-0.71	-0.00	-3.81	0.04	-3.97	-0.12	-3.85
77	CC3	-8.39	-0.77	0.49	-8.46	0.42	-8.71	0.17	-8.88

TABLE SIII: (continued)

No. ^a	Complex	B97-D			PBE-D		B-LYP-D		ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	dev. ^e	ΔE^c	dev. ^e	
78	CC4	-9.17	-0.79	0.75	-9.08	0.84	-9.42	0.50	-9.92
79	CC5	0.27	-0.75	-0.05	0.15	-0.17	0.14	-0.18	0.32
80	CC6	0.50	-0.78	-0.14	0.36	-0.28	0.40	-0.24	0.64
81	CC7	-1.18	-0.61	-0.20	-1.24	-0.26	-1.12	-0.14	-0.98
82	CC8	-8.14	-0.77	0.96	-8.13	0.97	-8.43	0.67	-9.10
83	CC9	-8.67	-0.73	0.44	-8.50	0.61	-8.76	0.35	-9.11
84	CC10	-7.98	-0.82	0.29	-7.82	0.45	-8.11	0.16	-8.27
85	CC11	-8.68	-0.69	0.75	-8.57	0.86	-8.89	0.54	-9.43
86	CC12	-6.62	-0.62	0.81	-6.63	0.80	-6.84	0.59	-7.43
87	CC13	-8.39	-0.76	0.41	-8.33	0.47	-8.43	0.37	-8.80
88	CC14	-8.45	-0.76	0.66	-8.42	0.69	-8.80	0.31	-9.11
89	AAst	-8.55	-0.77	0.03	-8.11	0.47	-8.62	-0.04	-8.58
90	GGst	-12.55	-0.91	0.12	-12.04	0.63	-12.77	-0.10	-12.67
91	ACst	-9.80	-0.71	0.42	-9.53	0.69	-9.86	0.36	-10.22
92	GAst	-11.06	-0.79	0.32	-10.56	0.82	-11.19	0.19	-11.38
93	CCst	-9.43	-0.68	0.59	-9.28	0.74	-9.54	0.48	-10.02
94	AUst	-9.63	-0.67	0.16	-9.45	0.34	-9.76	0.03	-9.79
95	GCst	-10.82	-0.82	-0.22	-10.60	0.00	-10.84	-0.24	-10.60
96	CUst	-9.85	-0.63	0.57	-9.91	0.51	-10.12	0.30	-10.42
97	UUst	-7.53	-0.50	-0.07	-7.46	-0.00	-7.51	-0.05	-7.46
98	GUst	-11.85	-0.74	0.24	-11.66	0.43	-12.10	-0.01	-12.09
99	GG0/3.36 CCs036 ^j	-1.93	-0.67	-0.31	-1.90	-0.28	-1.96	-0.34	-1.62
100	GG0/3.36 GGs036 ^j	-5.09	-0.23	-1.55	-4.91	-1.37	-4.79	-1.25	-3.54
101	AA20/3.05 AAs2005	-6.22	-0.78	-0.16	-5.77	0.29	-6.47	-0.41	-6.06
102	AA20/3.05 TTs2005	-2.28	-0.28	1.90	-2.53	1.65	-2.34	1.84	-4.18
103	GC0/3.25 G//Cs	-11.11	-0.86	-0.31	-10.85	-0.05	-11.46	-0.66	-10.80

TABLE SIII: (continued)

No. ^a	Complex	B97-D			PBE-D		B-LYP-D		ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	dev. ^e	ΔE^c	dev. ^e	
104	CG0/3.19 G//Cs	-7.25	-0.68	0.63	-7.22	0.66	-7.78	0.10	-7.88
105	GA10/3.15 A//Gs	-9.86	-0.99	-0.72	-9.38	-0.24	-10.19	-1.05	-9.14
106	GA10/3.15 T//Cs	-5.18	-0.65	-0.49	-5.08	-0.39	-5.21	-0.52	-4.69
107	AG08/3.19 A//Gs	-7.77	-0.67	-0.19	-7.23	0.35	-7.89	-0.31	-7.58
108	AG08/3.19 T//Cs	-6.38	-0.56	-0.31	-6.23	-0.16	-6.50	-0.43	-6.07
109	TG03.19 T//Gs	-5.47	-0.59	0.20	-5.40	0.27	-5.84	-0.17	-5.67
110	TG03.19 A//Cs	-4.83	-0.78	0.13	-4.82	0.14	-5.29	-0.33	-4.96
111	GT10/3.15 T//Gs	-5.49	-0.70	-0.53	-5.22	-0.26	-5.84	-0.88	-4.96
112	GT10/3.15 A//Cs	-5.52	-0.71	-0.08	-5.20	0.24	-5.62	-0.18	-5.44
113	AT10/3.26 A//Ts	-7.14	-0.55	-0.50	-6.71	-0.07	-7.21	-0.57	-6.64
114	TA08/3.16 A//Ts	-5.10	-0.74	0.97	-4.93	1.14	-5.78	0.29	-6.07
115	AA0/3.24 A//As	-6.40	-0.75	-0.15	-5.96	0.29	-6.64	-0.39	-6.25
116	AA0/3.24 T//Ts	-4.36	-0.55	-0.50	-4.37	-0.51	-4.80	-0.94	-3.86
117	mA...mT S ^f	-8.54	-0.63	-0.44	-7.94	0.16	-8.51	-0.41	-8.10
118	mG...mC S ^f	-7.76	-0.61	0.14	-7.30	0.60	-7.67	0.23	-7.90
119	mA...mC S ^f	-6.57	-0.79	0.13	-6.11	0.59	-6.51	0.19	-6.70
120	mT...mG S ^f	-7.04	-0.69	-0.84	-6.32	-0.12	-6.80	-0.60	-6.20
121	G...C S	-7.79	-0.81	-0.09	-7.42	0.28	-7.86	-0.16	-7.70
122	A...G S	-7.09	-0.90	-0.59	-6.69	-0.19	-7.40	-0.90	-6.50
123	C...G S	-10.92	-0.80	1.48	-10.68	1.72	-11.11	1.29	-12.40
124	G...C S	-11.14	-0.81	0.46	-10.90	0.70	-11.25	0.35	-11.60
Amino acid pairs (19)									
125	F30-K46	-3.63	-0.25	-0.53	-3.47	-0.37	-3.24	-0.14	-3.10
126	F30-L33	-5.53	-0.60	-0.53	-5.97	-0.97	-6.03	-1.03	-5.00
127	F30-Y13	-4.66	-0.31	-0.76	-4.49	-0.59	-4.39	-0.49	-3.90
128	F30-F49	-3.17	-0.11	0.13	-2.94	0.36	-2.88	0.42	-3.30
129	F30-Y4	-5.81	-0.29	1.19	-5.04	1.96	-5.38	1.62	-7.00

TABLE SIII: (continued)

No. ^a	Complex	B97-D			PBE-D		B-LYP-D		ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	dev. ^e	ΔE^c	dev. ^e	
130	F49-C39	-2.50	-0.16	-0.40	-2.60	-0.50	-2.59	-0.49	-2.10
131	F49-C6	-4.88	-0.41	0.12	-4.55	0.45	-4.43	0.57	-5.00
132	F49-K46	-4.72	-0.56	0.08	-5.23	-0.43	-5.17	-0.37	-4.80
133	F49-V5	-6.25	-0.61	0.45	-7.00	-0.30	-6.94	-0.24	-6.70
134	F49-W37 ^k	-2.19	-0.09	0.31	-2.16	0.34	-1.97	0.53	-2.50
135	F49-Y4	-4.03	-0.25	-0.93	-3.85	-0.75	-3.81	-0.71	-3.10
136	F49-PB (Y4-V5)	-3.62	-0.33	-0.82	-3.31	-0.51	-3.14	-0.34	-2.80
137	F49-PB (V5-C6)	-7.62	-0.63	0.58	-8.06	0.14	-8.12	0.08	-8.20
138	E47-K6 (1IU5)	-78.77	-1.02	1.96	-80.21	0.52	-80.03	0.70	-80.73
139	E49-K6 (1BQ9)	-110.34	-1.11	3.01	-111.19	2.16	-110.86	2.49	-113.35
140	E54-K2 (1SMM)	-93.45	-0.83	-5.16	-93.80	-5.51	-93.87	-5.58	-88.29
141	E50-K30 (1BRF)	-61.26	-0.35	-0.90	-61.57	-1.21	-62.00	-1.64	-60.36
142	E50-K52 (1BRF)	-94.36	-1.43	2.78	-95.52	1.62	-95.42	1.72	-97.14
143	E49-K6 (1BRF)	-71.00	-0.95	3.24	-72.17	2.07	-71.76	2.48	-74.24

^aThe calculated ΔE values are in the same sequence as the structures in the database.

^bEstimated CCSD(T)/CBS. The reference ΔE values of No. 41 and 42, No. 45 and 46, as well as No. 100 and 102 from Table 1 of Ref. [1] are interchanged. This is justified by a RI-MP2/aug-cc-pVDZ calculation and a comparison of the resulting ΔE values with the first column of Table 1 in Ref. [1]. In the discussion and the statistical analysis, the results for complexes No. 40, 42, 100, and 102 (after the interchange described above) are omitted, because the structures in the database disagree with their description given in Table 1 of Ref. [1]. Under the assumption, that the last pair of capital letters in the name describes the complex, No. 40 should be GC, but the 40th complex of the database is GG. Similarly, No. 42 (after interchange) has the name AT, while the 42nd coordinates in the database are TT, No. 100 (after interchange) is named GG, whereas the 100th complex in the database is CG, and the name of No. 102 is TT, but the 102nd coordinates in the database are AT. ^cNo CP correction. ^dCounterpoise correction. ^e $\Delta E - \Delta E_{\text{ref}}$. ^fBase pair methylated. ^gThe * is missing in the database. ^hRows 41 and 42 of

Table 1 in Ref. [1] are interchanged. ⁱRows 45 and 46 of Table 1 in Ref. [1] are interchanged.
^jRows 99 and 100 of Table 1 in Ref. [1] are interchanged. ^kResidue 37 of 1RB9 is tryptophan
(W), not tyrosine (Y).

TABLE SIV: DFT/TZV(2df,2pd) intermolecular interaction energies without dispersion correction (kcal mol⁻¹) for the large dataset.

No. ^a	Complex	PBE			B-LYP			ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	CP ^d	dev. ^e	
Hydrogen-bonded DNA base pairs (38)								
1	G...C WC	-29.00	-0.76	3.06	-25.57	-0.81	6.49	-32.06
2	mG...mC WC	-29.16	-0.79	2.43	-25.52	-0.84	6.07	-31.59
3	A...T WC	-14.95	-0.62	1.91	-12.11	-0.66	4.75	-16.86
4	mA...mT H	-16.07	-0.70	2.09	-13.08	-0.75	5.08	-18.16
5	8oG...C WC pl	-30.33	-0.78	2.97	-26.66	-0.83	6.64	-33.30
6	I...C WC pl	-22.36	-0.66	2.54	-19.20	-0.70	5.70	-24.90
7	G...U wobble	-16.95	-0.60	2.15	-14.22	-0.64	4.88	-19.10
8	CCH+	-49.46	-0.64	1.94	-45.46	-0.68	5.94	-51.40
9	U...U Calcutta pl	-8.93	-0.51	1.37	-7.11	-0.54	3.19	-10.30
10	U...U pl	-12.17	-0.52	1.53	-9.97	-0.56	3.73	-13.70
11	6tG...C WC pl	-28.16	-0.83	1.34	-24.19	-0.91	5.31	-29.50
12	A...4tU WC	-12.59	-0.58	1.61	-9.91	-0.63	4.29	-14.20
13	2-aminoA...T	-17.91	-0.73	1.59	-14.29	-0.77	5.21	-19.50
14	2-aminoA...T pl	-18.21	-0.69	1.49	-14.76	-0.73	4.94	-19.70
15	A...F	-3.75	-0.46	1.45	-2.20	-0.49	3.00	-5.20
16	G...4tU	-15.45	-0.60	2.35	-12.98	-0.65	4.82	-17.80
17	G...2tU	-14.32	-0.61	2.28	-11.09	-0.67	5.51	-16.60
18	A...C pl	-16.53	-0.59	1.07	-13.59	-0.63	4.01	-17.60
19	G...G pl	-19.21	-0.68	2.09	-16.61	-0.72	4.69	-21.30
20	G...6tG pl	-19.48	-0.67	2.32	-16.38	-0.72	5.42	-21.80
21	6tG...G pl	-20.20	-0.77	2.50	-16.91	-0.83	5.79	-22.70
22	G...A 1	-17.71	-0.75	1.69	-14.38	-0.80	5.02	-19.40
23	G...A 1 pl	-17.53	-0.61	1.37	-14.54	-0.65	4.36	-18.90
24	G...A 2	-12.37	-0.69	2.03	-9.78	-0.74	4.62	-14.40
25	G...A 2 pl	-11.50	-0.57	1.30	-8.89	-0.60	3.91	-12.80

TABLE SIV: (continued)

No. ^a	Complex	PBE			B-LYP			ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	CP ^d	dev. ^e	
26	G...A 3	-16.89	-0.80	1.91	-13.72	-0.85	5.08	-18.80
27	G...A 4	-12.28	-0.59	1.22	-9.54	-0.63	3.96	-13.50
28	A...A 1 pl	-13.70	-0.56	0.80	-10.95	-0.60	3.55	-14.50
29	A...A 2 pl	-12.74	-0.60	0.96	-10.06	-0.64	3.64	-13.70
30	A...A 3 pl	-10.97	-0.63	1.23	-8.41	-0.67	3.79	-12.20
31	8oG...G	-20.41	-0.68	2.39	-17.36	-0.72	5.44	-22.80
32	2tU...2tU pl	-10.44	-0.58	2.16	-7.55	-0.63	5.05	-12.60
33	mA...mT WC ^f	-14.97	-0.64	1.43	-12.04	-0.68	4.36	-16.40
34	mG...mC WC ^{*f,g}	-32.00	-0.84	3.80	-28.29	-0.90	7.51	-35.80
35	mA...mT WC ^f	-16.60	-0.67	1.80	-13.67	-0.72	4.73	-18.40
36	G...A HB	-11.93	-0.75	-0.63	-8.77	-0.79	2.53	-11.30
37	C...G WC	-29.83	-0.81	0.87	-26.02	-0.86	4.68	-30.70
38	G...C WC	-29.62	-0.79	1.78	-25.87	-0.85	5.53	-31.40
Interstrand base pairs (32)								
39	GG0/3.36 CGis036	-2.89	-0.48	0.79	-1.98	-0.51	1.70	-3.68
40	GG0/3.36 GCis036	3.57	-0.98	8.39	7.10	-1.03	11.92	-4.82
41	AA20/3.05 TAis2005 ^h	-1.54	-0.36	0.62	-0.61	-0.39	1.55	-2.16
42	AA20/3.05 ATis2005 ^h	1.87	-0.60	4.21	5.32	-0.63	7.66	-2.34
43	GC0/3.25 C//Cis	3.14	-0.13	0.05	3.33	-0.15	0.24	3.09
44	GC0/3.25 G//Gis	3.26	-0.60	1.33	4.60	-0.64	2.67	1.93
45	CG0/3.19 C//Cis ⁱ	1.38	-0.19	0.14	1.85	-0.21	0.61	1.24
46	CG0/3.19 G//Gis ⁱ	-0.01	-0.89	3.90	2.95	-0.92	6.86	-3.91
47	GA10/3.15 A//Cis	0.79	-0.33	1.10	1.63	-0.36	1.94	-0.31
48	GA10/3.15 T//Gis	1.18	-0.25	0.60	1.79	-0.27	1.21	0.58
49	AG08/3.19 T//Gis	0.77	-0.49	1.24	2.06	-0.52	2.53	-0.47
50	AG08/3.19 A//Cis	0.43	-0.35	0.61	1.23	-0.38	1.41	-0.18
51	TG03.19 A//Gis	-0.90	-0.64	3.32	1.37	-0.67	5.59	-4.22

TABLE SIV: (continued)

No. ^a	Complex	PBE			B-LYP			ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	CP ^d	dev. ^e	
52	TG03.19 T//Cis	-0.99	-0.15	0.16	-0.69	-0.17	0.46	-1.15
53	GT10/3.15 T//Cis	0.38	-0.14	0.08	0.62	-0.16	0.32	0.30
54	GT10/3.15 A//Gis	-2.61	-0.52	1.45	-1.26	-0.55	2.80	-4.06
55	AT10/3.26 T//Tis	1.10	-0.17	0.22	1.55	-0.19	0.67	0.88
56	AT10/3.26 A//Ais	0.02	-0.48	0.94	1.06	-0.51	1.98	-0.92
57	TA08/3.16 A//Ais	1.84	-0.41	3.39	3.86	-0.44	5.41	-1.55
58	TA08/3.16 T//Tis	0.90	-0.15	0.20	1.18	-0.17	0.48	0.70
59	AA0/3.24 A//Tis	-1.03	-0.23	0.68	-0.35	-0.25	1.36	-1.71
60	AA0/3.24 T//Ais	-0.92	-0.27	0.38	-0.29	-0.29	1.01	-1.30
61	mA...mA IS ^f	0.59	-0.55	1.29	1.86	-0.59	2.56	-0.70
62	mT...mT IS ^f	1.22	-0.21	0.22	1.70	-0.23	0.70	1.00
63	mG...mG IS ^f	0.04	-0.89	4.54	2.98	-0.93	7.48	-4.50
64	mC...mC IS ^f	1.72	-0.28	0.32	2.40	-0.30	1.00	1.40
65	mA...mG IS ^f	-3.47	-0.53	1.33	-2.11	-0.56	2.69	-4.80
66	mT...mC IS ^f	0.02	-0.19	0.12	0.30	-0.21	0.40	-0.10
67	C...A IS	-1.22	-0.48	1.78	0.05	-0.51	3.05	-3.00
68	G...G IS	-4.52	-0.40	0.68	-3.61	-0.43	1.59	-5.20
69	G...G IS	2.77	-0.78	1.97	4.75	-0.81	3.95	0.80
70	C...C IS	3.12	-0.11	0.02	3.29	-0.13	0.19	3.10
Stacked base pairs (54)								
71	G...C S	-10.04	-1.07	8.98	-5.13	-1.13	13.89	-19.02
72	mG...mC S	-7.24	-1.21	13.11	-0.69	-1.27	19.66	-20.35
73	A...T S	-2.17	-0.88	10.13	3.01	-0.92	15.31	-12.30
74	mA...mT S	-1.10	-1.06	13.47	5.91	-1.11	20.48	-14.57
75	CC1	7.72	-0.72	5.27	11.12	-0.77	8.67	2.45
76	CC2	2.40	-0.78	6.25	5.96	-0.83	9.81	-3.85
77	CC3	-2.23	-0.84	6.65	1.26	-0.89	10.14	-8.88

TABLE SIV: (continued)

No. ^a	Complex	PBE			B-LYP			ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	CP ^d	dev. ^e	
78	CC4	-2.93	-0.86	6.99	0.42	-0.91	10.34	-9.92
79	CC5	6.07	-0.81	5.75	9.61	-0.86	9.29	0.32
80	CC6	6.41	-0.86	5.77	10.09	-0.90	9.45	0.64
81	CC7	2.49	-0.66	3.47	4.84	-0.70	5.82	-0.98
82	CC8	-2.92	-0.83	6.18	-0.10	-0.87	9.00	-9.10
83	CC9	-2.30	-0.79	6.81	1.16	-0.84	10.27	-9.11
84	CC10	-1.90	-0.90	6.37	1.35	-0.95	9.62	-8.27
85	CC11	-2.83	-0.76	6.60	0.30	-0.79	9.73	-9.43
86	CC12	-3.50	-0.66	3.93	-1.82	-0.69	5.61	-7.43
87	CC13	-3.20	-0.83	5.60	-0.22	-0.87	8.58	-8.80
88	CC14	-2.15	-0.82	6.96	1.23	-0.88	10.34	-9.11
89	AAst	-0.77	-0.83	7.81	3.12	-0.88	11.70	-8.58
90	GGst	-3.86	-0.98	8.81	0.31	-1.02	12.98	-12.67
91	ACst	-2.75	-0.78	7.47	0.98	-0.82	11.20	-10.22
92	GAst	-2.77	-0.85	8.61	1.28	-0.90	12.66	-11.38
93	CCst	-3.30	-0.75	6.72	0.02	-0.79	10.04	-10.02
94	AUst	-2.49	-0.74	7.30	1.37	-0.77	11.16	-9.79
95	GCst	-4.03	-0.89	6.57	-0.33	-0.93	10.27	-10.60
96	CUst	-4.06	-0.69	6.36	-0.76	-0.73	9.66	-10.42
97	UUst	-2.14	-0.55	5.32	1.01	-0.58	8.47	-7.46
98	GUst	-4.57	-0.81	7.52	-0.76	-0.84	11.33	-12.09
99	GG0/3.36 Ccs036 ^j	2.63	-0.73	4.25	5.29	-0.77	6.91	-1.62
100	GG0/3.36 Gcs036 ^j	-4.30	-0.24	-0.76	-3.81	-0.26	-0.27	-3.54
101	AA20/3.05 AAs2005	2.01	-0.85	8.07	5.98	-0.90	12.04	-6.06
102	AA20/3.05 TTs2005	-0.98	-0.30	3.20	0.14	-0.32	4.32	-4.18
103	GC0/3.25 G//Cs	-3.16	-0.93	7.64	0.85	-0.99	11.65	-10.80

TABLE SIV: (continued)

No. ^a	Complex	PBE			B-LYP			ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	CP ^d	dev. ^e	
104	CG0/3.19 G//Cs	-2.54	-0.72	5.34	-0.30	-0.77	7.58	-7.88
105	GA10/3.15 A//Gs	-0.68	-1.07	8.46	3.73	-1.12	12.87	-9.14
106	GA10/3.15 T//Cs	0.18	-0.71	4.87	3.21	-0.75	7.90	-4.69
107	AG08/3.19 A//Gs	-0.98	-0.71	6.60	2.11	-0.76	9.69	-7.58
108	AG08/3.19 T//Cs	-1.28	-0.60	4.79	1.43	-0.64	7.50	-6.07
109	TG03.19 T//Gs	-0.57	-0.63	5.10	1.88	-0.66	7.55	-5.67
110	TG03.19 A//Cs	0.65	-0.84	5.61	3.45	-0.89	8.41	-4.96
111	GT10/3.15 T//Gs	2.63	-0.76	7.59	6.72	-0.80	11.68	-4.96
112	GT10/3.15 A//Cs	1.34	-0.77	6.78	4.83	-0.82	10.27	-5.44
113	AT10/3.26 A//Ts	0.09	-0.59	6.73	3.68	-0.63	10.32	-6.64
114	TA08/3.16 A//Ts	4.80	-0.82	10.87	9.79	-0.85	15.86	-6.07
115	AA0/3.24 A//As	1.40	-0.81	7.65	5.15	-0.86	11.40	-6.25
116	AA0/3.24 T//Ts	2.33	-0.60	6.19	5.92	-0.63	9.78	-3.86
117	mA...mT S ^f	0.09	-0.69	8.19	4.34	-0.73	12.44	-8.10
118	mG...mC S ^f	-3.70	-0.65	4.20	-1.91	-0.70	5.99	-7.90
119	mA...mC S ^f	0.73	-0.85	7.43	4.42	-0.91	11.12	-6.70
120	mT...mG S ^f	0.80	-0.76	7.00	4.59	-0.80	10.79	-6.20
121	G...C S	-0.81	-0.89	6.89	2.71	-0.93	10.41	-7.70
122	A...G S	1.11	-0.99	7.61	5.08	-1.03	11.58	-6.50
123	C...G S	-4.09	-0.86	8.31	-0.57	-0.91	11.83	-12.40
124	G...C S	-4.57	-0.87	7.03	-1.13	-0.92	10.47	-11.60
Amino acid pairs (19)								
125	F30-K46	-1.28	-0.28	1.82	0.26	-0.29	3.36	-3.10
126	F30-L33	-0.88	-0.66	4.12	2.12	-0.70	7.12	-5.00
127	F30-Y13	-1.30	-0.34	2.60	0.71	-0.36	4.61	-3.90
128	F30-F49	-0.34	-0.13	2.96	1.26	^k	4.56	-3.30
129	F30-Y4	0.57	-0.33	7.57	3.60	-0.35	10.60	-7.00

TABLE SIV: (continued)

No. ^a	Complex	PBE			B-LYP			ΔE_{ref}^b
		ΔE^c	CP ^d	dev. ^e	ΔE^c	CP ^d	dev. ^e	
130	F49-C39	0.13	-0.18	2.23	1.78	-0.18	3.88	-2.10
131	F49-C6	0.26	-0.45	5.26	3.27	-0.49	8.27	-5.00
132	F49-K46	-1.58	-0.61	3.22	0.66	-0.63	5.46	-4.80
133	F49-V5	-1.08	-0.66	5.62	2.55	-0.70	9.25	-6.70
134	F49-W37 ^l	-0.28	-0.10	2.22	1.05	^k	3.55	-2.50
135	F49-Y4	0.80	-0.29	3.90	3.62	-0.29	6.72	-3.10
136	F49-PB (Y4-V5)	-0.94	-0.37	1.86	0.66	-0.38	3.46	-2.80
137	F49-PB (V5-C6)	-2.73	-0.69	5.47	0.41	-0.73	8.61	-8.20
138	E47-K6 (1IU5)	-75.95	-1.11	4.78	-73.22	-1.17	7.51	-80.73
139	E49-K6 (1BQ9)	-107.19	-1.19	6.16	-104.44	-1.26	8.91	-113.35
140	E54-K2 (1SMM)	-92.29	-0.88	-4.00	-91.45	-0.94	-3.16	-88.29
141	E50-K30 (1BRF)	-61.37	-0.37	-1.01	-61.69	-0.41	-1.33	-60.36
142	E50-K52 (1BRF)	-91.10	-1.53	6.04	-88.35	-1.63	8.79	-97.14
143	E49-K6 (1BRF)	-67.96	-1.04	6.28	-65.02	-1.08	9.22	-74.24

^aThe calculated ΔE values are in the same sequence as the structures in the database.

^bEstimated CCSD(T)/CBS. The reference ΔE values of No. 41 and 42, No. 45 and 46, as well as No. 100 and 102 from Table 1 of Ref. [1] are interchanged. This is justified by a

RI-MP2/aug-cc-pVDZ calculation and a comparison of the resulting ΔE values with the first column of Table 1 in Ref. [1]. ^cNo CP correction. ^dCounterpoise correction. ^e $\Delta E - \Delta E_{\text{ref}}$. ^fBase pair methylated. ^gThe * is missing in the database. ^hRows 41 and 42 of Table 1 in Ref. [1] are interchanged. ⁱRows 45 and 46 of Table 1 in Ref. [1] are interchanged. ^jRows 99 and 100 of Table 1 in Ref. [1] are interchanged. ^kCalculation of a fragment with the full basis set of the complex did not converge to an energy below the fragment energy obtained with the fragment basis alone.

^lResidue 37 of 1RB9 is tryptophan (W), not tyrosine (Y).