Charged H-bonds data set

Complexes. The data set contains following hydrogen-bonded complexes:

- 1) anions: acetate water, acetate methanol, acetate methylamine
- 2) cations: methylammonium water, methylammonium methanol, methylammonium methylamine, methylammonium formaldehyde, guanidinium water, guanidinium methanol, guanidinium methylamine, guanidinium formaldehyde, imidazolium water, imidazolium methanol, imidazolium methylamine, imidazolium formaldehyde,

Methods. Geometries of the complexes had been optimized using MP2 in cc-pVTZ basis set with counterpoise correction. The CCSD(T)/CBS interaction energy consist of HF term calculated in aug-cc-pVQZ basis set, MP2/CBS term extrapolated from aug-cc-pVTZ and aug-cc-pVQZ and CCSD(T) correction calculated in aug-cc-pVDZ basis set. All the interaction energies are counterpoise corrected; MP2 calculations use density fitting.

Benchmark results. Table S1 lists the CCSD(T)/CBS interaction energies.

Table S1. CCSD(T)/CBS interaction energies in the data set of charged H-bonds.

complex	ΔE (kcal/mol)
acetate methanol	-19.753
acetate water	-21.062
acetate methylamine	-11.455
methylammonium formaldehyde	-19.096
methylammonium methylamine	-28.560
methylammonium methanol	-21.225
methylammonium water	-18.514
guanidinium formaldehyde	-18.090
guanidinium methylamine	-20.196
guanidinium methanol	-19.788
guanidinium water	-17.467
imidazolium formaldehyde	-16.410
imidazolium methylamine	-25.977
imidazolium methanol	-18.914
imidazolium water	-16.485

Structures. Here we list the structures of the complexes in XYZ format:

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Supplementary error measures

Table S2. Mean unsigned errors (in kcal/mol) of the studied methods in multiple benchmark data sets.

	S66	S66x8	S66a8	S22	HB104	Charged HB	HC12	AA24
PM6	2.67	1.99	1.89	3.34	2.67	3.40	2.56	3.07
PM6-DH2	0.64	0.51	0.50	0.39	1.14	1.69	0.62	0.74
PM6-DH+	0.62	0.55	0.49	0.60	1.20	1.51	0.62	1.00
PM6-D3H4	0.47	0.45	0.48	0.61	0.84	0.88	0.58	0.59
DFTB	2.74	2.10	2.12	3.05	2.68	4.29	2.80	2.87
DFTB-D	1.25	1.07	0.98	1.35	1.81	3.85	0.41	1.41
DFTB-D,γ	0.98	0.89	0.79	1.01	1.44	3.16	0.39	1.13
DFTB-DH2	1.08	0.76	0.69	1.32	1.11	1.80	0.41	0.90
DFTB-D3H4	0.52	0.46	0.43	0.79	0.57	1.10	0.48	0.50
RM1	4.75	3.43	3.54	5.84	5.12	4.99	3.53	4.13
RM1-D3H4	0.67	0.64	0.55	0.76	0.70	1.50	0.18	0.46
RM1-D3H4*	0.67	0.64	0.56	0.75	0.70	1.63	0.18	0.50
OM3	3.08	2.22	2.29	3.56	2.69	2.57	3.78	3.83
OM3-DH2	0.63	0.61	0.46	0.67	0.65	1.42	0.97	0.86
OM3-D3H4	0.37	0.39	0.31	0.43	0.44	1.16	0.57	1.10
AM1	5.15	3.76	3.40	6.77	5.10	6.57	3.49	4.65
AM1-DH2	1.39	1.19	1.13	0.69	1.56	2.45	3.23	2.49
AM1-D3H4	0.96	1.08	0.99	1.25	1.72	2.35	0.76	1.18
PM3	4.29	3.32	3.17	5.88	4.75	6.38	1.51	3.25
PM3-D3H4	0.94	0.76	0.67	1.45	0.67	1.53	0.29	0.72

Table S3. Maximum unsigned errors (in kcal/mol) of the studied methods in multiple benchmark data sets.

	S66	S66x8	S66a8	S22	HB104	Charged HB	HC12	AA24
PM6	7.99	9.14	6.00	7.61	8.96	7.29	4.01	9.93
PM6-DH2	3.53	4.80	3.46	1.47	4.67	6.45	1.00	4.53
PM6-DH+	2.47	3.09	2.39	1.79	3.37	4.82	1.00	5.82
PM6-D3H4	2.45	3.16	2.76	2.16	3.09	3.06	1.34	4.06
DFTB	5.17	5.31	4.03	7.44	4.71	9.64	4.15	6.82
DFTB-D	3.17	4.36	3.84	2.88	3.86	8.93	1.60	5.50
DFTB-D,γ	2.52	3.14	3.35	2.38	3.35	8.39	1.50	4.45
DFTB-DH2	4.60	6.67	3.83	5.53	5.32	5.29	1.60	4.70
DFTB-D3H4	2.36	2.47	2.51	2.00	1.70	5.09	1.03	2.64
RM1	12.50	13.31	11.69	13.18	12.99	10.52	5.46	11.84
RM1-D3H4	2.95	4.50	3.25	2.89	2.53	6.99	0.53	1.96
RM1-D3H4 no s	2.95	4.50	3.25	2.89	2.53	6.60	0.53	3.63
OM3	7.21	8.31	6.95	8.56	7.41	6.15	6.23	12.76
OM3-DH2	2.26	4.91	2.65	2.26	2.45	6.22	1.94	5.31
OM3-D3H4	1.29	3.06	1.46	1.54	1.41	4.55	1.23	8.10
AM1	20.02	28.20	13.42	20.29	23.05	17.93	6.25	15.77
AM1-DH2	5.27	9.70	5.08	2.08	7.34	11.60	7.14	11.38
AM1-D3H4	3.97	12.67	7.63	4.63	7.14	10.29	1.16	5.52
PM3	16.09	22.86	11.49	19.22	10.99	16.05	5.12	10.08
PM3-D3H4	7.06	9.96	4.33	7.72	2.17	10.39	1.06	2.68

Table S4. Coefficients of the polynomial radial function used in the H-bond correction.

power	c
7	-0.00303407407407313510
6	0.07357629629627092382
5	-0.70087111111082800452
4	3.25309629629461749545
3	-7.20687407406838786983
2	5.31754666665572184314
1	3.40736000001102778967
0	-4.68512000000450434811

Figure S1. The repulsive H-H correction (E_{rep}) and its effect on the PM6-D3H4 dissociation curve of T-shaped dimer of hydrogen molecules.

