

Supporting Information:

Reliable prediction of association (free) energies of supramolecular complexes with heavy main group elements - the HS13L benchmark set

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S1 Statistical error measures

Statistical measures for a set of data points x_1, \dots, x_n with references r_1, \dots, r_n are:

- Average:

$$\bar{x} = \frac{1}{n} \sum_i^n x_i$$

- Mean deviation(MD):

$$MD = \frac{1}{n} \sum_i^n (x_i - r_i)$$

- Mean absolute deviation(MAD):

$$MAD = \frac{1}{n} \sum_i^n |x_i - r_i|$$

- relative Mean absolute deviation(relMAD):

$$relMAD = \frac{1}{n} \sum_i^n \frac{|x_i - r_i|}{|r_i|}$$

- standard deviation (SD):

$$SD = \sqrt{\frac{1}{n-1} \sum_i^n (x_i - r_i - MD)^2}$$

S2 Revised D4 parameter

In the development of another project in our group, revised D4 parameter were developed for ω B97X.^{S1} The respective parameter are given in the following Table.

Table S1: Revised D4 parameter for the ω B97X DFA. Details can be found in the respective publication.^{S1}

s6	s8	s9	a1	a2
1.0	0.4485	1.0	0.3306	4.2790

S3 Convergence Problems

Due to convergence problems in the geometry optimization and frequency calculation of the guest of complex **11**, the respective calculations with GFN-FF and GFN2 were performed with the GBSA solvation model instead of the ALPB solvation model. In the SPH approach for GFN2-xTB, this problem did not occur. For the same reason, PM6-D3H4X frequencies for **11**.CI could not be obtained and the respective values calculated for **11** were taken instead.

S4 Effect of the solvent model in the geometry optimization

Table S2: root-mean-square deviation (RMSD) of the heavy atoms of host, guest, and complex of **8** of r²SCAN-3c optimized geometries with SMD, COSMO and CPCM solvation model with respect to r²SCAN-3c[DCOSMO-RS] optimized geometries in Å. Association free energies ΔG_a computed with the default workflow (r²SCAN-3c + GFN2-xTB-SPH + COSMO-RS(16) normal) on the respective geometries are given in kcal mol⁻¹.

	SMD	COSMO	CPCM	DCOSMO-RS
RMSD(host)	4.00E-02	4.76E-02	4.90E-02	-
RMSD(guest)	7.06E-04	2.77E-04	2.77E-04	-
RMSD(complex)	1.12E-01	5.21E-02	9.12E-01	-
ΔG	-4.91	-5.31	-5.32	-5.44

S5 Influence of conformers

For the default workflow (r²SCAN-3c + GFN2-xTB-SPH + COSMO-RS(16) normal) the ensemble free energy \overline{G} was computed as Boltzmann average from all remaining conformers in the 3.5 kcal mol⁻¹ window after *Part2* of CENSO.

$$G_{\text{Bw}} = \sum_i^N p_i G_i$$

$$p_i = \frac{e^{-G_i/kT}}{\sum_i^N e^{-G_i/kT}}$$

Table S3: Experimental and calculated association free energies at the default level of theory (r²SCAN-3c energies, GFN2-xTB[ALPB]-SPH thermostistical contributions, and COSMO-RS(16)-normal(r²SCAN-3c) solvation free energies) for the lowest conformer of each complex of the HS13L set, as well as Boltzmann-weighted average ΔG_{Bw} of all conformers found below the threshold of 3.5 kcal mol⁻¹.

complex	ΔG_{EXP}	ΔG_{calc}	ΔG_{Bw}
1	-8.4	-7.2	-7.2
2	-5.8	-4.4	-4.5
3	-4.7	-12.5	-12.4
4	-5.7	-5.1	-5.2
5	-1.9	-4.5	-4.5
6	-6.8	-1.9	-1.6
7	-6.7	-4.0	-4.1
8	-5.0	-4.9	-4.8
9	-5.5	-4.7	-4.7
10	-9.2	-5.4	-5.1
11	-8.1	-12.2	-12.3
12	-5.2	1.8	1.1
13	-7.5	-2.5	-3.0

S6 Counterpoise correction

Table S4: Boys Bernardi Counterpoise correction E_{CP} in kcal mol⁻¹ for complex **1** for best-performing DFAs of each class with respect to the backcorrected experimental values.

DFA	$E_{\text{CP}} / \text{kcal mol}^{-1}$
PBE-NL	0.08
B97M-V	0.03
PW6B95-NL	0.15
ω B97X-V	0.02
PWPB95-NL	1.25

S7 Magnitude of the ATM term

Table S5: Magnitude of the non-additive ATM term contribution (which is the same for each DFA) in kcal mol⁻¹ to the association energy for each complex of HS13L and HS13L-CI. The CI denotes that the complex was docked with counterions to neutralize its global charge.

complex	ATM / kcal mol⁻¹
1	1.11
2	1.95
3	3.93
4	2.86
5	-0.02
6	3.42
7	2.76
8	1.27
9	1.33
10	2.91
11	1.45
12	1.55
13	1.30
10_CI	3.00
11_CI	1.34
12_CI	1.62
13_CI	1.55

S8 DFT frequencies

Table S6: Comparison of ΔG_{mRRHO} obtained with SQM methods to those obtained from r²SCAN-3c-SPH calculations for the 5 smallest complexes of the HS13L. The MD and MAD is given with respect to r²SCAN-3c-SPH. Note that GFN1-xTB, GFN2-xTB, and GFN-FF were used with the ALPB implicit solvation model and PM6 and PM7 with the COSMO implicit solvation model.

complex	GFN-FF	GFN1	GFN2	PM6]	PM7	GFN2-xTB-SPH	r2scan-3c
1	13.90	10.57	13.54	12.70	12.52	11.67	9.98
2	16.46	16.31	15.76	16.35	16.67	15.69	16.10
5	11.58	11.73	11.15	11.87	16.09	11.89	13.06
8	14.14	14.05	13.71	13.96	14.75	14.29	14.37
9	14.83	14.48	14.62	14.01	15.53	14.73	13.94
MD	0.6	-0.2	0.2	0.3	1.6	0.0	
MAD	1.5	0.6	1.6	1.1	1.6	0.8	

Table S7: Symmetry numbers for optimized geometries of the lowest conformer of host, guest, and complex, respectively of the HS13L. Charged systems which were attributed with counterions (**10_B**, **10_AB**, **11_B**, **11_AB**, **12_B**, **12_AB**, **13_B**, **13_AB**) in the HS13L-CI have symmetry number 1.

complex	A	B	AB
1	12	2	2
2	1	4	1
3	1	10	1
4	1	1	1
5	3	2	1
6	1	3	1
7	14	1	1
8	2	2	1
9	2	2	1
10	12	1	1
11	2	60	1
12	1	1	1
13	1	1	1
10_CI	12	1	1
11_CI	2	1	1
12_CI	1	1	1
13_CI	1	1	1

S9 Statistical evaluation of HS13L without counterions

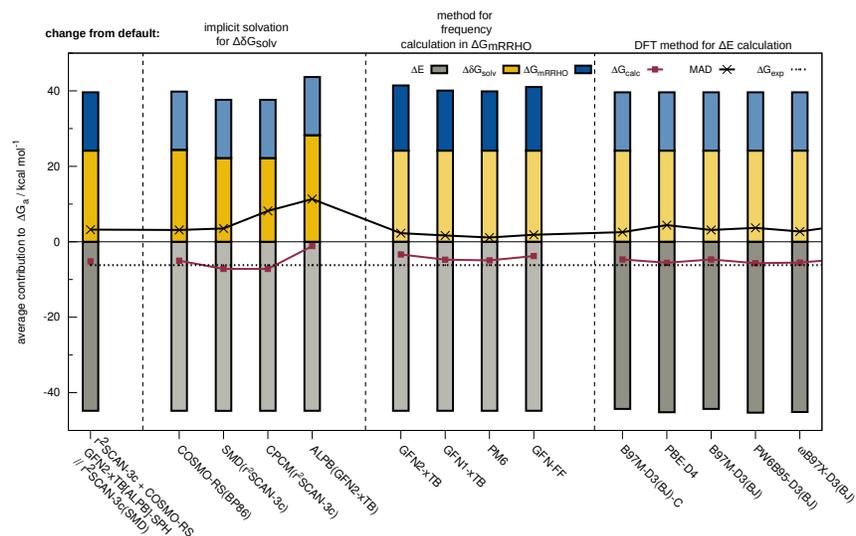


Figure S1: Contributions to the calculated ΔG_{calc} averaged over all complexes of the HS13L set. The leftmost bar illustrates the default approach used in this work, while the others illustrate the effect of using a different model or level of theory for the calculation of the solvation contribution, the thermostatical correction and the electronic energy. Contributions that are not affected by these variations are depicted in brighter colors.

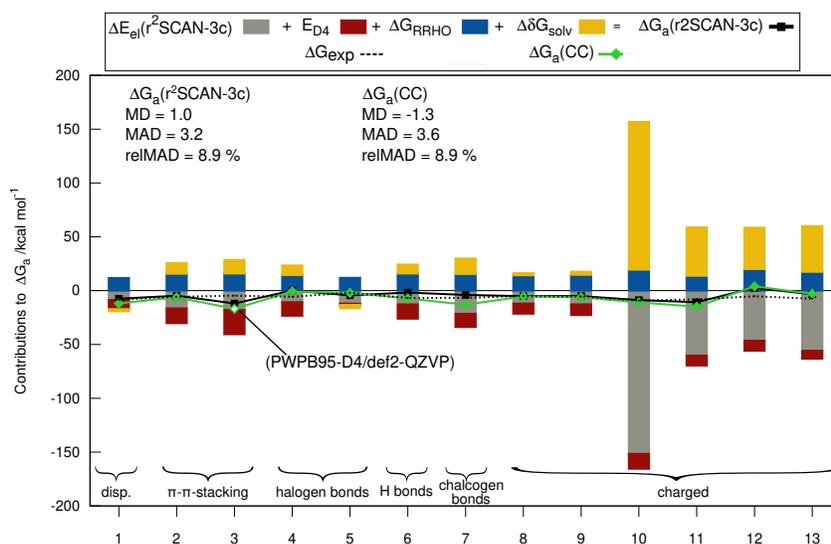


Figure S2: Contributions to the association free energy ΔG_a for each complex of the HS13L set in kcal mol^{-1} . MD, MAD, and relMAD are also given. For comparison, ΔG_a when using DLPNO-CCSD(T1)/CBS instead of $r^2\text{SCAN-3c}$ are also given. For complex **3** only PWPB95-D4/def2-QZVP values could be obtained and are shown instead.

Table S8: MDs, MADs and SDs in kcal mol⁻¹ to the DLPNO-CCSD(T1)/CBS reference values of all assessed DFAs in def2-QZVP basis in combination with their best dispersion correction and composite methods for the HS13L. For complex **3** PWPB95-D4/def2-QZVP values were used as reference, as no DLPNO-CCSD(T1)/CBS reference value could be obtained for this complex.*:downscaled s9.

	MD	MAD	SD
r²SCAN-3c	2.27	2.91	3.19
PBEh-3c	5.92	6.81	7.91
B97-3c	2.86	4.67	9.95
B97M-V-C	-1.31	2.87	3.45
PBE-NL	-0.42	2.81	3.63
RPBE-NL	-2.22	3.25	3.55
R²SCAN-D4	1.63	2.39	3.16
M06L-D3(0)	-1.52	3.78	4.85
B97M-V	-0.77	1.90	2.57
PW6B95-NL	0.05	2.46	3.55
B3LYP-D4	-1.43	2.65	2.78
M06-2X-D3(0)	1.23	3.13	4.27
PBE0-D4	1.22	2.30	3.35
ωB97X-V	-1.43	2.87	3.32
ωB97M-V	-2.54	3.47	3.18
PWPB95-D3	0.15	2.30	3.03
rev-DSDPBEP86-D4	2.86	3.77	3.74
rev-DSDPBEP86-D4*	0.51	2.62	4.08
MP2-CBS	-13.1	13.1	12.4

Table S9: Mean deviation (MD), mean absolute deviation (MAD), and standard deviation (SD) to the DLPNO-CCSD(T1)/CBS reference values of tested semiempirical methods for the HS13L in kcal mol⁻¹. The average root-mean square deviation of the heavy atom positions (\overline{RMSD}) between the with implicit solvation (ALPB for the GFN methods and COSMO for the PM methods) optimized geometries with respect to the r²SCAN-3c optimized geometries for the HS13L-CI are given in Å.

	MD	MAD	SD	\overline{RMSD}
GFN1-xTB	2.7	6.1	7.0	0.28
GFN2-xTB	6.7	7.4	8.2	0.27
GFN-FF	4.0	5.7	6.3	0.30
PM6	-0.3	4.5	6.1	0.29
PM7	-5.0	11.3	12.4	0.32

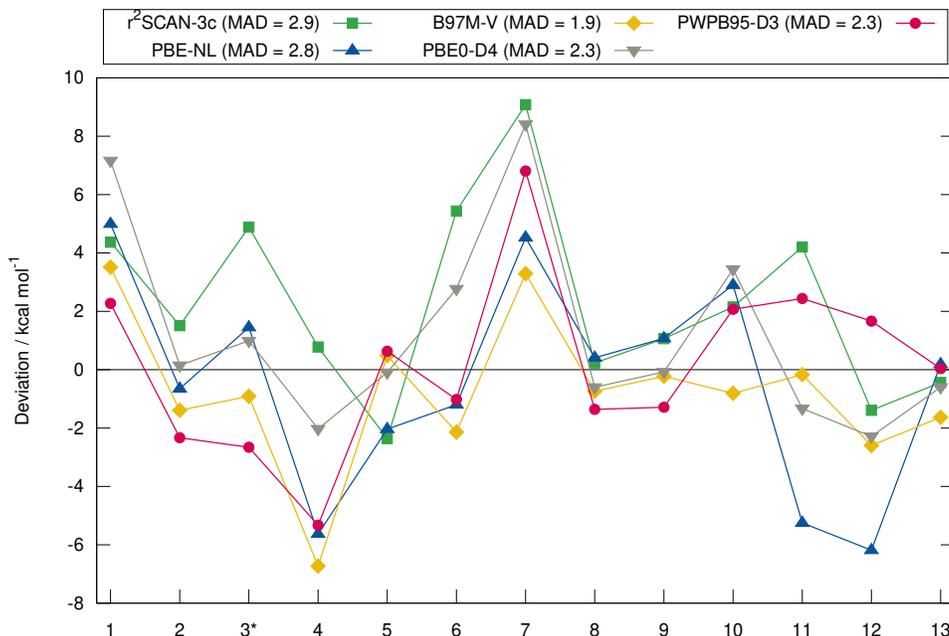


Figure S3: Deviations in kcal mol⁻¹ to the DLPNO-CCSD(T1)/CBS reference values of best-performing methods of each class for HS13L. A negative deviation indicates overbinding, a positive underbinding. For complex **3** PWPB95-D4/def2-QZVP is used as reference, as no DLPNO-CCSD(T1)/CBS reference value could be obtained for this complex indicated by the *.

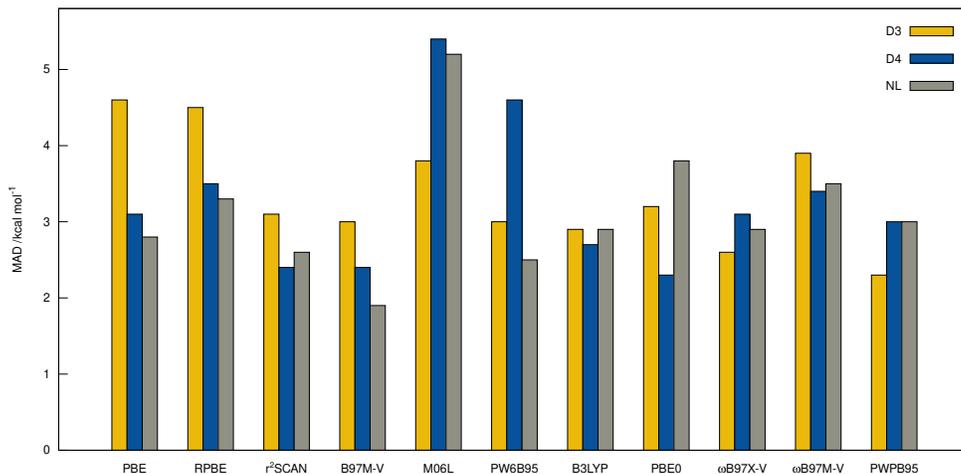


Figure S4: Mean absolute Deviations (MADs) to the DLPNO-CCSD(T1)/CBS reference values of assessed DFAs for the HS13L in combination with D3, D4, and the nonlocal VV10 dispersion correction.

References

- (S1) M. Müller, A. Hansen, S. Grimme, "ωB97X-3c: A composite range-separated hybrid DFT method with a molecule-optimized polarized valence double-ζ basis set", submitted to *J. Chem. Phys.* (2022).