TABLE IX. ____
Summary of Hydrogen-Bonding Comparisons to Scaled HF/6-31G* Data[a]

	Interaction Energy, kcal/mol			X ··· Z Distance, Å		X-H···Z
Force Field	rms Dev.	Avg. Dev.	Max. Dev.	rms Dev.	Avg. Dev.	rms Dev.
MMFF94	0.77	-0.25	2.52	0.09	0.02	14.6°
MMFF94s	0.76	-0.24	2.52	0.10	0.03	18.1°
CFF95	2.33	1.10	6.53	0.33	0.21	27.0°
CVFF	4.36	2.24	16.39	0.41	0.23	26.1°
MSI CHARMm	3.03	0.60	13.54	0.30	0.08	34.0°
CHARMM 22	1.11	0.00	3.04	0.12	0.05	15.0°
OPLS*	2.00	-0.49	6.61	0.21	0.02	22.9°
AMBER*	1.60	0.08	6.06	0.19	0.04	26.9°
MM2*	3.86	1.92	7.53	0.26	0.06	39.5°
MM3*	3.81	2.12	13.31	0.50	0.22	34.0°

[a] Each of the force fields handles all 66 hydrogen-bonded dimers except for: (i) CVFF, for which the Cerius^2 implementation could not perform the atom typing for imidazole; (ii) MM3*, which lacks parameters for 12 of the dimers, and (iii) CHARMM 22, which even with extensions made locally (see manuscript) lacked parameters for about half the systems.