VeraChem's Optimized Dreiding Parameters
Comparison with GAFF/AM1-BCC

The original Dreiding bonded energy terms (J. Phys. Chem. 94, 8897-8909, 1990)) are broadly applicable and appear to be reasonably accurate. However, they were found to yield incorrect conformational preferences of some common functional groups, such as esters. In addition, the van der Waals parameters are quite different from those of well-optimized force-fields like AMBER and CHARMM, and Dreiding does not provide for partial charges.

VeraChem has built on original Dreiding by adjusting key bonded parameters, tuning van der Waals parameters to more "CHARMM-like" values, and coupling the bonded terms with VeraChem's accurate partial charges. The resulting energy model, Dreiding-v

- Has a standard, efficient functional form
- Can be applied to a wider range of molecules than GAFF
- Produces ligand conformations as good as or better than GAFF, based upon crystal conformations.

Dreiding-v is assessed here based upon its ability to generate ligand conformations similar to their crystallographic conformations in protein-ligand complexes. VeraChem's conformational search program Vconf were used to generate 100 energy-minima for 259 ligands from the CDCC set (`http://www.ccdc.cam.ac.uk/products/life_sciences/validate/`) of ligands for which protein-ligand structures are available. Three energy models were tested: Dreiding-v with charges from Vcharge; GAFF with charges from Vcharge; and GAFF with AM1-BCC charges. The following table shows that VeraChem's parameters yield results at least as good as GAFF.

		Lowest Energy Conformations		**Lowest RMSD Conformations**	
Force Field	**Partial Charges**	**<RMSD>**	**N_{best}**	**<RMSD>**	**N_{best}**
Dreiding-v	VC/2004	1.70	112	0.85	121
GAFF	VC/2004	1.71	84	0.94	49
GAFF	AM1-BCC	1.71	71	0.86	99

<RMSD>: root-mean square deviation in Angstroms of the lowest-energy (columns 3,4) or lowest RMSD (columns 5,6) conformation relative to the crystallographic bound conformation of the ligand. **N_{best}**: Number of lowest-energy (left) or lowest-RMSD (right) conformations generated with this energy model that were most similar to the crystal conformation of the ligands. (In the event of a tie, the ligand is counted toward the value of N_{best} of both energy models.)