

Protein force field meeting

Chapin E. Cavender

Open Force Field Initiative

September 9, 2021

Assessing OpenFF force fields on tetrapeptide torsion profiles

- ▶ Dave Cerutti's [TorsionDrive datasets](#) on Ace-X-Y-Z-Nme
 - ▶ Central residues Y are Ala, Arg, Ash, Asn, Asp, Cys, Glh, Gln, Glu, Gly, Hid, & Hie
 - ▶ Flanking residues X & Z are Ala, Gly, Ser, & Val
 - ▶ Dihedrals scanned are phi, psi, chi1, chi2, & omega
- ▶ Test GAFF 2.11 and OpenFF 1.2.0, 1.3.1, & 2.0.0 with [AM1-BCC charges](#)
- ▶ Output is RMSE (magnitude) and normalized RMSE (shape), adapted from Simon Boothroyd

Computing MM torsion profiles

- ▶ Reference profiles are QM energies **offset** to the minimum QM energy

$$x_{\min} = \underset{x}{\operatorname{argmin}} U_{\text{QM}}(x)$$

$$E_{\text{QM}}(x) = U_{\text{QM}}(x) - U_{\text{QM}}(x_{\min})$$

- ▶ MM energies are evaluated after **local minimization** $F(x)$ with torsion atoms frozen and are offset to the MM energy of the coordinates with the minimum QM energy

$$E_{\text{MM}}(x) = U_{\text{MM}}(F(x)) - U_{\text{MM}}(F(x_{\min}))$$

Comparing MM torsion profiles to QM reference

- ▶ MM energies are shifted to **optimally superimpose** the MM and QM profiles

$$E_{MM} = E_{MM} + \langle E_{QM} - E_{MM} \rangle$$

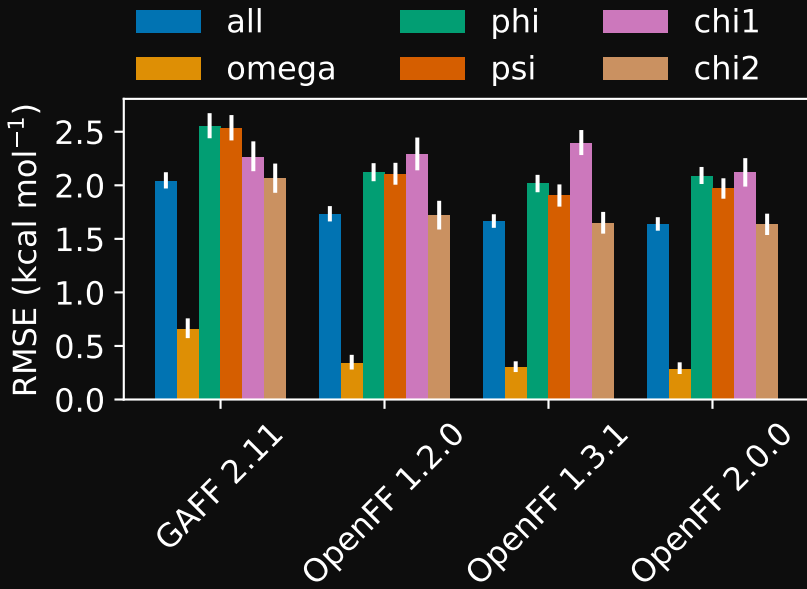
- ▶ **Magnitude** is represented by RMSE

$$\text{RMSE} = \sqrt{\frac{1}{N} \sum (E_{QM} - E_{MM})^2}$$

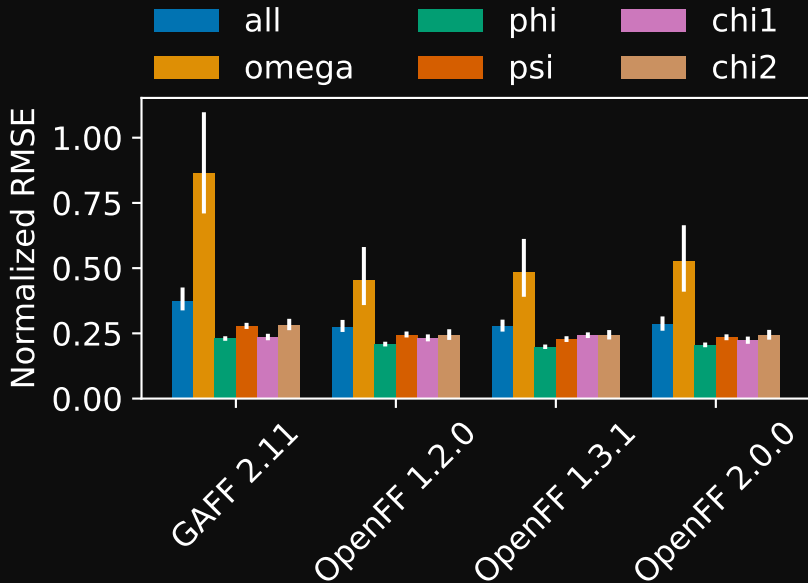
- ▶ **Shape** is represented by normalized RMSE

$$\text{NRMSE} = \sqrt{\frac{1}{N} \sum \left(\frac{E_{QM}}{\max(E_{QM}) - \min(E_{QM})} - \frac{E_{MM}}{\max(E_{MM}) - \min(E_{MM})} \right)^2}$$

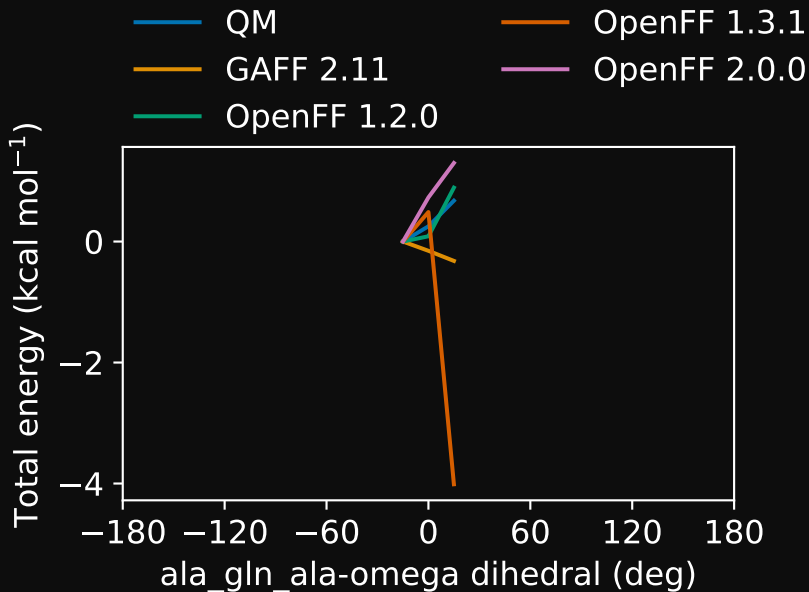
OpenFF force fields have lower RMSE than GAFF for dihedrals except chi1



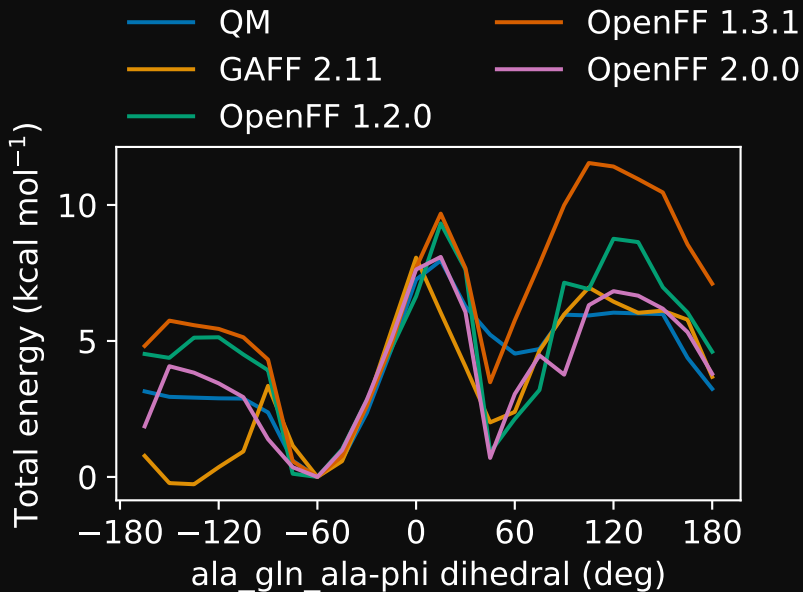
All FFs fail to describe shape of omega profile



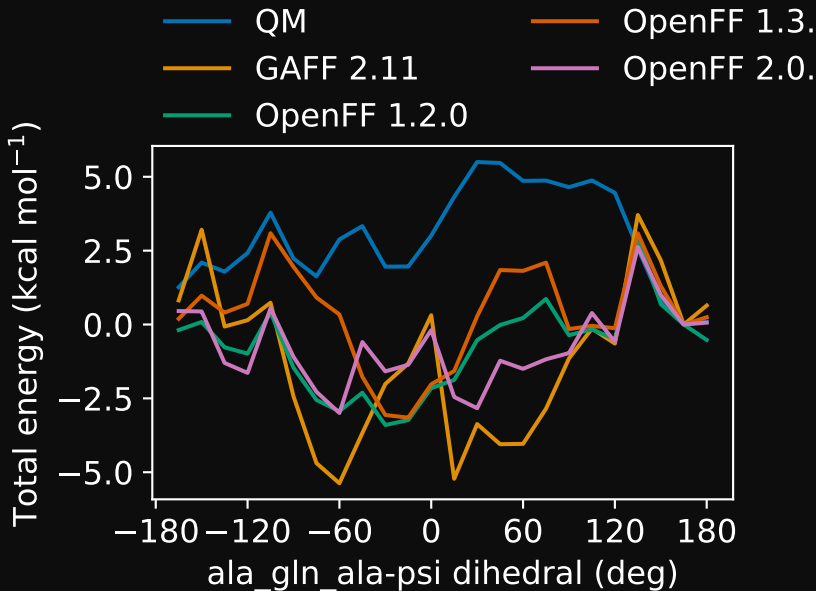
Ace-Ala-Gln-Ala-Nme omega



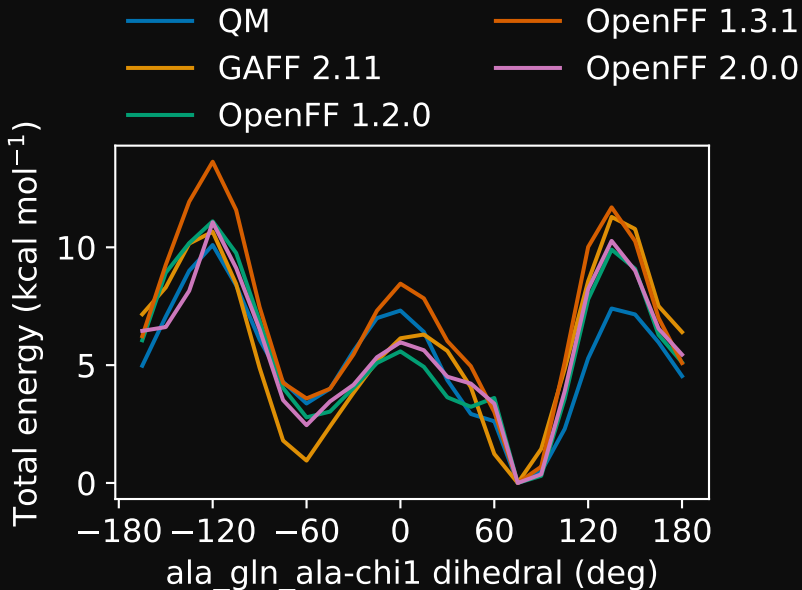
Ace-Ala-Gln-Ala-Nme phi



Ace-Ala-Gln-Ala-Nme psi



Ace-Ala-Gln-Ala-Nme chi1



Ace-Ala-Gln-Ala-Nme chi2

