

A Consistent AMBER Parameter Set for Zwitterionic Amino Acid Residues

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Isolated amino acids play an important role in biochemistry e.g., as neurotransmitter transporters, transcriptional regulators, or disease-mediators. They are therefore an interesting object of study. Molecular dynamics (MD) simulations can provide detailed insights into the dynamics of these species, especially in their biological environment.

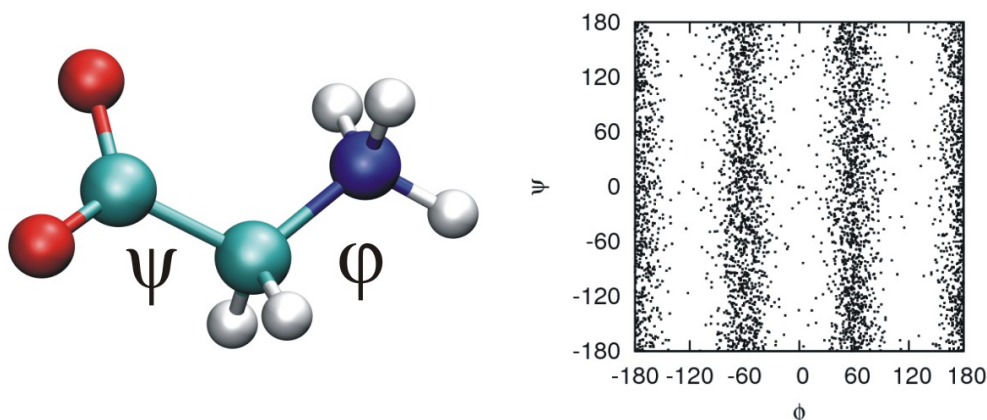
Unfortunately, most standard force field packages lack predefined parameter libraries for isolated amino acids in their zwitterionic form. Although several MD studies have used ad-hoc parameterizations for single amino acids, a consistent force-field parameter set for these molecules is still missing.

Here, we present such a parameter library derived from and compatible with the widely used parm99SB set from the AMBER program package.[1] The parameter derivation for all 20 proteinogenic amino acids transparently followed established procedures. For the sake of completeness, histidine was treated in three different protonation states.

For comparison, MD simulations of all amino acids in four different forms were performed: zwitterionic, N-terminally capped with acetyl, C-terminally capped with N-methyl, and capped at both termini. Simulation results show similarities between the different forms. A subset of five zwitterionic amino acids (E, F, G, L, R) was simulated in its respective protein environment, where proteins and ligands generally retained their initial structure.

Additionally, a set of eight isolated zwitterionic amino acids (A, C, I, K, L, M, R, T, R) was simulated in an aqueous solvent and their orientations were utilized as a pseudo-random number generator.

The new parameter set is freely available [2] and will thus facilitate future atomistic simulations of these species.



[1] A. H. C. Horn, *J. Mol. Model.*, **2014**, *20*, 2478.

[2] R. Bryce, *AMBER Parameter Database*, www.pharmacy.manchester.ac.uk/bryce/amber