Interplay between peptide bond geometry and local conformation: molecular dynamics analyses

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Several statistical and quantum chemical investigations performed in the last two decades have unveiled a strong correlation between protein backbone geometry (bond angles, dihedral angles and pyramidalization) and the local conformation (Berkholz et al. 2012; Berkholz et al. 2009; Esposito et al. 2005; Esposito et al. 2000; Esposito et al. 2013; Improta et al. 2011; Karplus 1996). This finding has important implication for protein structure prediction, determination, refinement and validation. Predictive protein modeling has shown an improved convergence when these effects are considered. Therefore, force fields currently available for modeling and molecular dynamics should be able to reproduce these geometric properties. We have recently shown that quantum mechanics calculations on small peptide systems are able to reproduce the dependence of the bond distances/angles on the conformation and the interplay between the peptide bond distortions from planarity and ψ dihedral angle thus demonstrating that the peptide bond geometry of proteins is essentially ruled by local effects (Improta et al. 2015). We here evaluated the ability of several commonly used force fields to reproduce subtle structural details related to the peptide bond. Our results indicate that these force fields are unable to accurately reproduce the experimental/statistical trends.

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