DEVELOPMENT AND TESTING OF NEW FORCE FIELDS FOR MOLECULAR DYNAMICS SIMULATIONS

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INTRODUCTION.

Recent progress in modeling of protein folding has been achieved only after some improvements of potentials of covalent forces, taken from the standard AMBER force field; and still the force field used is not quite satisfactory to reproduce folded structures of some larger proteins, having significant, about 5A, RMS deviation between the computed and experimentally determined 3D structures. The objective of this research is to develop and test new polarizable atomic force fields (FFs) for "in-vacuum" and "in-water" non-bonded interactions based on AMBER ff99SB-ILDN force fields, improved by inclusion of new terms. FFs parameter optimization will be done using our set of molecular crystals with crystallographic data from the Cambridge Structural Database and sublimation/solvation thermodynamics characteristics from various sources.

MATERIALS AND METHODS.

At the current stage of new atomic force fields development we have to create programming package that automate various computational procedures, implementing general methodology from the previous work. We will develop and test the "in-vacuum" and "in-water" versions of force fields; then the new force fields will be used to solve reasonable tasks in protein physics.

RESULTS AND DISCUSSION.

We have used molecular crystals database and software package for computations of various characteristics of molecular crystals; performed analytical estimations for many-atom interaction and physical constraints on optimization tasks to compute FF parameters and molecular dynamics simulations of mechanical unfolding for three-helix proteins and mechanical properties of C-Cadherin.

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