COMPARATIVE ASSESSMENT OF THE EFFICIENCY AND ACCURACY OF THE KIRKWOOD-BUFF FORCE FIELD IN PROTEIN MOLECULAR DYNAMICS SIMULATIONS: AN IN-SILICO INVESTIGATION

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This research compares the accuracy and efficiency of the Kirkwood-Buff force field (KBFF), a less common force field in applications, with the widely used CHARMM36 force field. The study focuses on the stability variations of human uracil DNA glycosylase (hUNG) enzyme in its wild form and when complexed with toxic metal ions Cd(II), Pb(II), and Ni(II). Four systems were considered, including the free enzyme and the enzyme complexed with each mentioned toxic ion. Utilizing the CavityPlus server, the binding pockets for the metal ions were identified, and molecular dynamics simulations were conducted for 100 ns with repetition using both KBFF and CHARMM36 force fields. The enzyme stability in each system was analyzed using root mean square deviation and radius of gyration methods. Results revealed that irrespective of the force field, Cd(II), Ni(II), and Pb(II) ions consistently stabilized the hUNG enzyme compared to the free enzyme. These findings highlight the efficiency of both force fields in capturing the stabilizing interactions between toxic metal ions and the enzyme, showcasing the reliability of KBFF in biomolecular simulations. Consequently, this study suggests that KBFF can be considered an efficient and accurate force field for investigating the dynamics of biomolecular systems.

Keywords*: Kirkwood-Buff force field, CHARMM36, CavityPlus server, MD simulations*

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