Abstract No.142

MathParam: A MATHEMATICA Package for Biomolecular Force Field Development

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Popular biomolecular force fields such as AMBER, CHARMM, OPLS and GROMOS were designed, parameterized and continuously refined for main classes of biomolecules. On the other hand many research works deal with problems in which a novel residue, ligand or organic molecule is present in the system and thus researchers seek for some new parameters that should be in agreement with the force field applied to other parts of the system. There are many alternative solutions for such problems depending on the applied force field and the accuracy of parameterization.In this work we review the current status of the MathParam package that is designed for development of biomolecular force fields to new molecules. The initial design of MathParam obeys the general protocol proposed by CHARMM developers for CHARMM General Force Field (CGenFF). Extensions for other popular force fields will be in our future work. MathParam acts as a control center for managing all tasks necessary for optimization and validation of the new set of parameters. Some of these tasks are currently performed with MOPAC2009, GAMESS, VMD and NAMD program packages. MathParam tool box provides facilities for:1) Input generation for other programs including pdb, topology and parameter files.2) Systematic extraction and analysis of data produced by other related programs.3) Extraction of available and missing parameters from CGennFF parameters.4) Random or grid-based conformational search.5) Converting different geometry specifications (Cartesian, Internal and …) to each other.6) Unique definition of atom-names and atom-types.7) Graph-based analysis of structures and numeration of bonds, angles and dihedrals.8) Providing initial guess for missing parameters by analogy or from QM calculations.9) Normal mode analysis of force constant matrices.10) Charge optimizations based on interaction with water molecules.11) Optimization of dihedral parameters based on QM energy profiles.Many other features and capabilities.

Keywords: Force Field, Parameterization, CGenFF, Molecular Mechanics.

Abstract No.143

Studies on the Interaction of Anticancer Drug Vincristine with DNA Molecule in Solution

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Vincristine belongs to the vinca alkaloid anticancer drugs and exerts its biological action by selective activity against depolymerization of mitotic microtubules. In this study we have investigated the effect of vincristine on DNA employing fluorescence spectroscopy, thermal denaturtion, and dialysis techniques. The result showed that the binding of vincristine to DNA decreases fluorescence emission intensity in a dose-dependent manner. Thermal denaturation profiles indicated that upon addition of various concentrations of vincristine to DNA solution ,Tm of DNA exhibited hypochromicity without any Tm changes. Binding of vincristine to DNA exhibits a cooperative binding pattern as illustrated by the positive slope observed in the low r regions of the binding isotherm. The curve reaches a maximum at a value of r = 0.12 and decreases in the slope is observed at higher r values. Drawing r versus Cf, clearly demonstrates that the system approaches to equilibrium or saturation. The binding of vincristine to DNA represents a binding constant of $k = 7.2 \times 10^{10}$ M^{-1} and Hill coefficient of 2. 3, confirming the positive cooperative binding of vincristine to DNA. However ΔG was -4.2 kcal mol^{-1} this confirmed that biding of vincristine to DNA is spontaneous reaction. The results suggest high affinity of vincristine to DNA providing DNA as a new target for vincristine action.

Keywords: Vincristine, DNA, Fluorescence Spectroscopy, Thermal Denaturation.

Abstract No.144

Stability Improvement of Catalase by Xylitol as a Compatible Osmolyte

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Catalase is an indispensible antioxidant enzyme in the oxidative pathway that catalyzes the disproportionation of H_2O_2 intoinnoxious