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

water and molecular oxygen. It has one of the highest turnover numbers known ($4\times107\ s^{-1}$). Catalase has numerous industrial and medical applications. It is widely used in the food industry in order to remove the excess hydrogen peroxide from the milk and in the food wrappers to retard oxidation, it is also used in the contact lenses and in the textile manufacturing to ensure that the final product is peroxide free. In industry, it is highly desirable to increase the rate of enzymatic reaction via controlled increase in the temperature. In this report, xylitol as a compatible osmolyte increases the thermal stability of bovine liver catalase through destabilization of the denatured state. The increase in the thermal stability is augmented, in comparison to the native, by an increase in the activity at the room temperature. This increase in enzymatic activity is further enhanced by the intrinsic rate increase caused by temperature which might be of particular interest in industrial applications.

Keywords: Catalase, Xylitol, Compatible osmolyte, Functional stability, Thermal stability.

Abstract No.145

Investigation on Stability and Immobilization of Enzyme-Conjugated Models Based on Different Composition of Chitosan

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The objective of this paper replies to this question that if new chitosan carriers in film and microsphere form could be suitable support to immobilize an enzyme model.The study was conducted in two different stages. In the first stage, suitable carriers were preparated and then its physicochemical effects were investigated. In the second phase, the enzyme immobilization was studied. Briefly, some sample of the carriers in film (FG6) and microsphere (MG6) form were placed in test tubes containing solution of RNAase at pH 7.2. Finally samples were influenced on mixture of RNA and DNA present in agarose gel and rubbed in electrophoresis. To qualitatively evaluate whether RNAs were immoblized the supports, each of four samples were analyzed by native agarose gel electrophoresis stained with RNA. The results acquired from the RNAs immoblization were represented. Qualitative study on the enzyme immobilization in incubated films and microsphers was investigated.The results reflect that visually detectable amounts of RNA are sufficiently stable in the samples a, b, c and d. Similar amounts of stained RNA were observed in the samples of a and b respectively, in 4 and 25 °C. Although in the sample of d has reduced level of RNA. Therefore, the samples c and d depicted changed electrophoretic mobilities, including enzymatic degradation of trapped RNA at the bottom of the sample in 25 °C. It implies that RNAas immobilization was not appropriate as a result of inadequate stabilty. Regarding to obtained results, this investigation has obviously suggested that enzyme immobilization characteristics of chitosan were dependent on the physical form as film or microsphere.

Keywords: Physicochemical Properties, Enzyme Emmoblization, Conjugated Compound.

Abstract No.146

Kinetically Study on Mezalazine Conjugated Biomacromolecules as Bioactive Model and its Application in Enzyme Delivery

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The objective of this paper reply to this question that if an enzyme could release potentially from the prepared biomacromolecules. So prior to evaluate the release pattern of an enzyme from the films or microspheres of a biomacromolecule, it is important to study release kinetics of a bioactive molecules from the carrier (Mezalazine). In brief the following stages were carried out as order, preparation of cross-linked chitosan films and microspheres, conjugation of drug model on films and microspheres, study of in vitro release kinetics of drug-conjugatedcarriers. From these experimental data, it appears that biomacromolecules films and microspheres have shown better controlled release of mezalazine in FG18M5, MG18M5 and especially in MG12M5since their release pattern are near to zero order kinetics. By