Abstract No.282

Spectroscopic Studies of Human Serum Albumin Upon Interaction with An Anti-Tumor Pd(II) Complex

Maryam Saeidifar[1], *Hassan Mansouri-Torshizi*[2], *Adeleh Divsalar*[3], *Ali.Akbar Saboury*[4]

1. Nanotechnology and Advanced Materials Department, Materials and Energy Research Center, Karaj, IR
2. Department of Chemistry, University of Sistan and Baluchestan, Zahedan, IR
3. Department of Biological Sciences, Tarbiat Moallem University, Tehran, IR
4. Institute of Biochemistry and Biophysics, University of Tehran, IR

(E-mail: m.saidifar@gmail.com)

Protein is an important chemical substance in our life and one of the main targets of all medicines in organism. Serum albumin, the most abundant protein in the circulatory system, is one of the most extensively studied proteins because it can interact with many endogenous and exogenous substances [1]. Binding of drugs to plasma protein is an important pharmacological parameter, since it frequently affects the distribution and elimination of a drug as well as the duration and intensity of its physiological action. The studies on this aspect can provide information of the structural features that determine the therapeutic effectivity of drugs, and have been an interesting research field in life science, chemistry, biochemistry and clinical medicine [2]. Therefore, in this investigations, we present our results on the interaction studies of HSA with an antitumoral water-soluble palladium(II) complex, which possesses dithiocarbamate and 1,10-phenanthroline ligands because of modulating activity and toxicity of platinum based drugs. The binding properties of this complex to Human serum albumin were studied using absorption spectroscopy and Circular dichroism techniques under physiological condition at 300 K and 310 K.Spectroscopic data would be used to quantify binding parameters, number of binding site and the binding constants of Pd(II) complex to HSA and thermodynamic parameters, , molar Gibbs free energy of binding, , molar enthalpy of binding and, molar entropy of binding. In addition, the experimental result indicated that this complex interacted with HSA. In general, we can assert that promising results obtained for the antitumor agent presented in this work make it possible candidates for the treatment of cancer and encourage us to design new complexes, which have better antitumor activity and helpful in the development of their potential biological, pharmaceutical and physiological implications in the future.

Keywords: HSA, Pd(II) complex, Thermodynamic Parameters, Circular Dichroism, Dithiocarbamate.

Abstract No.283

4D-QSAR and Docking Study on the Pan Class I Phosphoinositide-3-Kinase (PI3K) Inhibitors: A Comparison to CoMFA Modeling

Reihaneh Safavi, *Jahan B. Ghasemi**

Chemistry Department, Faculty of Sciences, K. N. Toosi University of Technology, Tehran, IR

(E-mail: reihaneh.safavi@gmail.com)

At least one Holy Grail for many academic researchers and pharmaceutical research divisions alike has been to identify therapeutically useful selective PI3K inhibitors. The class I PI3Ks is currently investigated and attracted as a promising target toward anticancer therapies. A 4D-QSAR has been carried out on a series (42 compounds) of PI3Ks inhibitors. This approach makes use of the molecular dynamics (MD) trajectories and topology information retrieved from the GROMACS package. This new methodology is based on the generation of a conformational ensemble profile, CEP, for each compound instead of only one conformation, followed by the calculation intermolecular interaction energies at each grid point considering probes and all aligned conformations resulting from MD simulations. These interaction energies are independent variables or descriptors employed in a QSAR analysis. We developed the method by using docked multiple reference compounds as bioactive conformations in alignment step for building several regression models. The comparison of the proposed methodology to comparative molecular field analysis (CoMFA) formalism was performed. This methodology explores jointly the main features of CoMFA and 4D-QSAR models. Leave-N-out cross-validation (LNO), Y-randomization and application domain analysis (AD) of the obtained model were performed in order to confirm the robustness of the model in addition to analysis of the independent test set. Statistical parameters of the best 4D-QSAR model are (R2 = 0.941, q2LOO = 0.691, R2Pred = 0.751). Docking study was applied to investigate the major interactions in protein-ligand complex with CDOCKER algorithm. Visualization of the descriptors of the best model helps us to interpret the model from the chemical point of view, supporting the applicability of this new approach in rational drug design. Excellent statistical parameters and the suitable predictive ability of the results explain that this model can

help to rational design of novel PI3Ks inhibitors with preferred activities.

Keywords: 4D-QSAR, CoMFA, CDOCKER, Molecular Dynamic Simulation, Phosphoinositide-3-Kinase (PI3K) Inhibitors.

Abstract No.284

Hydrophilicity of Ionic Liquids Plays Important Role on Choline Oxidase Electron Transferring

Hedayatollah Ghourchian, Parvaneh Rahimi*

Laboratory of Microanalysis, Institute of Biochemistry and Biophysics, University of Tehran, Tehran, IR
(E-mail: hadi@ibb.ut.ac.ir)

Room-temperature ionic liquids (RTILs) and their related nano-composites attracted considerable attention because of their desirable properties and potential applications in biomolecular immobilization, biocatalysis, electrochemical biosensors and bioreactors. In the present report, six different nano-composites contaning the same amine functionalized multi-walled carbon nanotubes (NH2-MWCNTs) but different room temperature ionic liquids (RTILs) were prepared. Then, the efficiency of these nano-composits as supporting materials for studying the electrochemistry and electrocatalysis of choline oxidase (ChOx) as a model enzyme were compared. The corresponding cyclic voltammetric and amperometric data showed that the electrocatalytic activity and the electroanalytical performance of immobilized ChOx depend on the degree of hydrophilicity of RTILs used in the applied nano-composite. The higher stability (180 days), more enzyme loading (6.56 M cm^{-2}), lower detection limit (3.85 µM) and wider linear range (0.005-0.8 mM) were obtained for the most hydrophilic RTIL (1-allyl-3-methylimidazolium bromide).

Keywords: Nanocomposite, Choline Oxidase, Electron Transfer, Functionalized Carbon Nanotubes, Ionic-Liquid, Choline.

Abstract No.285

Chemical Modification of Antibody Using Gold Nanoparticles Bearing Luminol

Soheila Sabouri [1], Hedayatollah Ghourchian [2]*

1. Institute of Biochemistry and Biophysics, University of Tehran, IR
2. Laboratory of Microanalysis, Institute of Biophysics and Biochemistry, University of Tehran, IR
(E-mail: hadi@ibb.ut.ac.ir)

Gold nanoparticles (GNPs) are very attractive labels due to their special physical and chemical properties such as ease of synthesis, simplicity of conjugation and excellent biocompatibility. Because of these advantages they can be used as the carrier for a large number of markers and bio-catalysts. In the present work, at first luminol was attached to GNPs then the modified GNPs were chemically bound to antibody as a secondary antibody (Ab2-GNPs). The characteristics of chemically modified antibody were investigated by three methods including: UV-Vis spectroscopy, chemiluminescence emission and ELISA (Enzyme linked immuno-sorbance assay). The native antibody showed a UV-Vis absorbance at 521 nm wavelength. But after chemical modification it has a broad peak along with 10 nm red shift compared to GNP. In second method, Ab2-GNPs were added to Ab1-Ag (primary antibody (Ab1) bonded to antigen (Ag)), after washing, chemiluminescence emission was recorded in 425 nm. High chemiluminescence emission shows antibody preserves its function in conjugation with GNP-Luminol. Preservation of antibody function has been proved by ELISA method too. This bio-composite proposed for diagnostic and medical usage, due to its praiseworthy detection limit of antigen in this immuno-sensors (14 pg/ml).

Keywords: Gold Nanoparticles, Chemiluminescence, Immuno Sensor, Antibody Function, Antigen Detection.

Abstract No.286

Fine Structural Analysis of Human Serum Albumin

Mostafa Rezaei-Tavirani [1], Roya Tadayon, Minoo Shahani [2]*

1. Shahid Beheshti University of Medical Sciences, Tehran, IR
2. Department of Base Science, Science and Research Branch, Islamic Azad University, Tehran, IR
(E-mail: tavirany@yahoo.com)

Human serum albumin is the most abounding protein in human blood plasma. It plays essential roles such as maintaining pH level and osmotic pressure in blood. This protein possesses a particular adequacy to bind to a great number of various endogenous and exogenous compounds. This article outlines different features of HAS and its multifunction eligibility. These studies can be obtained by pH metery, ligand binding, UV spectroscopy, fluorescence spectroscopy and CD techniques. The results compared and discussed based on data