Abstract No.97

Binding Parameters in HSA Interaction with Antitumor Pd(II) Phenanthroline Derivative Complex

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The serum albumin proteins are among the most highly studied and applied in biochemistry and ligand binding to albumin has been studied for over 50 years. A number of studies have focused on the interaction of Palladium (II) complexes having fewer side effects against cancer with protein. It is important that structural change of proteins must be considered as a side effect of anticancer drug. We know the thermodynamic method is suitable for evaluating the magnitude of structural change of a protein, due to the binding of a ligand. Thus a new Palladium (II) complex of formula [Pd(phen)(TIP)](NO3)2, where phen is 1,10-phenanthroline and TIP is phenanthroline derivative has been synthesized and characterized by spectroscopic methods (see Figure 1). The interaction of HAS with Pd(II) complex was studied by isothermal titration UV-visible spectroscopy in Tris-HCl buffer solution containing 10 mM sodium chloride (pH=7.4) at 300 and 310K and binding parameters were found. Also, this compound can denature the HSA and the concentration of this complex in the midpoint of transition is decreased by increasing temperature. Using denaturation HSA, thermodynamic parameters such as conformational stability, molar enthalpy and entropy of HSA denaturation by complex were calculated.

Keywords: HSA Denaturation, Phenanthroline Derivative, Binding Parameter, Pd(II) Complex.

Abstract No.98

Fluorescence Spectroscopic Studies Of The Interaction Between A New Designed Pd (II) Complex With Human Hemoglobin

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Hemoglobin (Hb) is one of the most effective proteins in the blood that carries oxygen from the lungs to the tissues. Hb can also binds to different ligands such as drugs. In this study, we have investigated the interaction of a new synthesized anti-cancer compound (1, 10-phenanthroline butyl dithiocarbamato palladium (II) nitrate) with hemoglobin at two different temperatures of 25 and 37°C by fluorescence spectroscopic method.Intrinsic fluorescence data represented that in the presence of Pd (II) complex, the fluorescence intensity of Hb decreases. This result showed the Pd (II) complex is able to quench the intrinsic fluorescence of Hb. Also, binding and thermodynamic parameters of this interaction were calculated by fluorescence quenching methods. The binding constant (K) and the number of binding (n) were 0.02 μM and 1.1 at 25 and 37 °C, respectively. The values of DH° and DS° are 8.309 kJ/mol and 8.314 J/(mol K), respectively, which indicate that the hydrophobic interaction has a major role in this binding.The results obtained from this study suggested that interaction of this complex with Hb may be important to improved understanding of side effects of new synthesized drugs on their carriers.

Keywords: Hemoglobin, Pd (II) Complex, Fluorescence, Hydrophobic Interaction.

Abstract No.99

Preparation and Evaluation of Nisin-Loaded PLA-PEG-PLA Nanoparticles and Antimicrobial Effect on The Growth of Bacillus Cereus

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This Study was to assay the antimicrobial effect of nisin-loaded PLA-PEG-PLA nanoparticles as protein delivery vehicle. Among the potent antimicrobial agents, nisin has been found to be very efficacious against many Gram-positive spoilage, pathogenic bacteria and spore-forming bacteria such as bacillus cereus. The encapsulation of nisin

can increase antimicrobial properties of nisin and were more effective than free nisin. Methods: The nisin-loaded PLA-PEG-PLA nanoparticles were prepared using colloidal dispersion of the copolymers in the presence of nisin. After the preparation of the nisin-loaded PLA-PEG-PLA nanoparticles, their physicochemical properties such as size distribution of the formulations were studied using DLS instrument. Entrapment efficiency of the nisin-loaded nanoparticles were examined to assess the application potential of these formulations. For measuring the antibacterial activity of the nisin-loaded PLA-PEG-PLA nanoparticles, MIC methods were employed. Results: entrapment efficiency of nisin inside of the nanoparticles was about 90%. size distribution of them was 50 nm(Figure). In agar diffusion assay, an antibacterial activity (inhibition zone diameter, at 440 IU/mL) about 2 times higher than that of free nisin was observed for the nisin-loaded PLA-PEG-PLA nanoparticles. Conclusion: Our studies achieved successful formulation of nisin-loaded PLA-PEG-PLA nanoparticles, thus indicating that nanoparticle-based formulation of nisin has high potential as an antimicrobial peptide for clinical and foods application.

Keywords: Nisin, PLA-PEG-PLA nanoparticles, Bucillus Cereus, Antimicrobial Activity.

Abstract No.100

Structural Analysis of New Designed Antiangiogenic Endostatin Peptides Based on Structural Dynamics Properties and Docking Energy Landscapes

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Endostatin is a proteolytic fragment of collagen XVIII that potently inhibits angiogenesis and tumor growth. The mechanism by which endostatin exerts its antiangiogenic effect is still incompletely understood. It has been shown that some N-terminal fragments from mouse and human endostatin exhibited antitumoral activity analogous to the full-length endostatin. It has been shown that Zn++-binding is required for thermal and thermodynamic stability and also antitumor and antimigration of these endostatin peptides.In this study to understand the function mechanism of these peptides, new variant active endostatin peptides containing disulfide bond that able or unable to coordinate zinc ion on structure were designed and synthesised. The results from structural dynamics studies showed that in the presence of disulfide bond with or without Zn++, C-terminal structural dynamic properties and rigidity of the Zn++ coordinating loop of endostatin peptide are changed drastically. Our docking simulations also showed notable changes in interaction energy between new peptides and integrin αV‧3 receptor. Our findings suggest that a fine zinc dependent structure play a critical role in efficient inhibition activity of endostatin peptide.

Keywords: Antiangiogenic, Endostatin Peptide, Structural Dynamics, Docking Energy.

Abstract No.101

Designing and Producing of a Cloning Construct for Odorranain-HP

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Amphibian skin glands are rich resources for antimicrobial peptides that are parts of the armament that insects have developed to fight off pathogens.Insect AMPs are typically cationic and often made of less than 100 amino acid residues. Although their structures are diverse, most of the AMPs can be assigned to a limited number of families. The most common structures are represented by peptides assuming a α-helical conformation in organic solutions or disulfide-stabilized β-sheets with or without α-helical domains present.An antimicrobial peptide named odorranain-HP was identified from skin secretions of the diskless odorous frog, Odorrana grahami. It is composed of 23 amino acids with an amino acid sequence of GLLRASSVWGRKYYVDLAGCAKA.This peptide showed antimicrobial activities against tested microorganisms. Interestingly,odorranain-HP could exert antimicrobial capability against Helicobacter pylori, along with its antimicrobial activities similar to odorranain-W1. In order to design souitable primers for synthesis of peptide by overlapping extension polymerase chain reaction,we replace serine instead of methionine that has minimal effect on the bioactive structure of the peptide. Since,presence of methionin in the first of the peptide had spread effect on the structure and function of the pepetide.The PCR product digested with desired restriction enzymes ,and then inserted into Pcold I vector that digested with the same enzymes.

Keywords: Odorranain-HP, Antimicrobial Peptide, Overlapping Extension Polymerase Chain Reaction.
