Abstract No.167

Spectroscopic Studies of the Interaction Between new Designed Palladiumcomplex(II) with Human Hemoglobin

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Hemoglobin (Hb) is one- of the most important and effective of blood proteins. In the present study, the intraction oftwo new synthesized Pd complexes(bipyridine ethyldithiocarbamat palladium ((IInitratandbipyridine buthyldithiocarbamat palladium ((IInitrat) with human Hb, as a model protein, was investiyated by different spectroscopic methods of UV-visible, fluorescence and circular dichroism (CD) at different temperatures of 25, 37, 42 and 47 0C.UV-Visible resultsshowed that adding of Pd complexes tothe Hb solution increase the absorbtion of the protein in 280 nm. Intrinsic fluorescence studies represented that Pd complexes have ability to quench the fluorescence intensity of Hb via the static quenching mechanism. Also, in the presence of different concentrations of Pd complexes, the maximum emission wavelengh of Hb shifted to a higher wavelengh (red shift), which indicates that the hydrophobicity of Trp environment decreased. Also, the number of binding sites of Pd complexes on the protein and their binding affinities were investigatedusingquenchingmechanism.
Results showedthatthebindingsite may be inthe near of tryptophan residue. Far UV-CD data showed that Pd complexes can change the regular secondary structure content of Hb via decreasing of α-helix content atdifferent temperatures of25, 37, 42 and 47 0C.From above results, it can be concluded that our new designed Pd complexes can change the secondary and tertiary structure of Hb at different temperatures.

Keywords: Hemoglobin, Pd Complexes, Fluorescence, Circular Dichroism.

Abstract No.168

Study of Enzymatic Activity in Static Magnetic Field for Immobilized and free Trypsin Onto Silica Gel

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We immobilized trypsin onto silica gel particles and investigated the effects of a static magnetic field (13 mT) on the enzymatic activity, at 40°C.We found that the activity of the enzyme molecules immobilized on to silica gel particles incressed in the static magnetic field. Although the power magnetic field was weak, the significant results were observed. The effects of magnetic field on the free enzymes activity were also investigated.The results showed that free enzymes activity increased in the presence of magnetic the field similar to immobilized enzyme. Kinetic analysis carried out for both free and immobilized enzyme. Thermal and storage stabilities were found to be incress with immobilization. The estimated Michaelis constants (Km) and (Vmax) for the free and immobilized trypsin were calculated. Empolyment of immobilization lead to an increase and a decrease in Km and Vmax, respectively. Therefor enzyme activity upon immobilization method was lower than that of in free form. In addition, optimum pH shifted to basic region in immobilized form.The value of optimum pH for free enzyme was 7 while for immobilized enzyme was 7.5.

Keywords: Static Magnetic Field, Trypsin, Enzyme, Immobilization, Activity.

Abstract No.169

Study of ROS Production Manner during Hemoglobin Fructation and Its Relation to Heme Degradation

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Some probable mechanisms have been demonstrated for the source of Reactive Oxygen Species (ROS) during protein's glycation reactions in the presence of glucose. In this state, glucose autoxidation, ketoamine and oxidative AGEs formation have been introduced as major sources. On the other hand there were some evidences for heme degradation during hemoglobin glycation that demonstrated on ROS corporation for heme degradation. Two questions are proposed from these research lines: 1- Whether fructose can produce ROS alone or not. 2- The existence of the relationship between ROS production and heme

degradation process. Knowing the answer of these questions made us to investigate the probable ROS accumulation by chemiluminescence method and detecting heme degradation products by fluorescence spectroscopy (ex: 321 nm and ex: 460 nm) at the same time intervals. Our results (obtained from in vitro diabetic conditions at 37 °C and pH 7.4) demonstrated on noticeable accumulation of ROS in the fructose solution even at the beginning of its solution. The amounts of detected ROS in the presence of proteins were less than fructose solution by an increasing pattern in the first week of incubation. On the other hand, after passing the increasing phase of accumulated ROS, heme degradation products started to accumulate. Little by little amounts of heme degradation arises and made a plateau where detected ROS was at the plateau line too. Such studies indicate that diabetic patients should pay more attentions to use enough antioxidant agents in their diets.

Keywords: Hemoglobin, ROS, Glycation, Heme Degradation, Diabetes.

Abstract No.170

The Role of Bir1 in Caspase Inhibition

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Apoptosis is a controlled process of cellular destruction through which a group of proteases named caspases (Cysteinyl aspartate-specific proteases) are activated. The activity of these enzymes is brought under control through Inhibitor of Apoptosis Proteins (IAPs). Each IAP protein contains at least one BIR (Baculoviral IAP Repeat) domain, which contains ~70 amino acids folded around a zinc atom. The BIR domains alone or in combination with other domains of IAPs are responsible for directly and specifically inhibiting the caspases. The different BIR domains exhibit distinct functions. The second BIR domain (BIR2) inhibits the activity of caspase-3 and -7 whereas the third BIR domain (BIR3) targets the caspase-9. Previous studies failed to demonstrate any role for the BIR1 domain of IAPs in inhibition of executioner caspases. Therefore in this study, recombinant proteins containing BIR1 were produced to investigation their effect on caspase-7. Enzyme kinetics assays showed that BIR1 domain is essential for caspase inhibition by cIAP1 protein whereas in the case of XIAP, presence of BIR1 causes concentration dependent caspase-7 inhibition by this IAP.

Keywords: Apoptosis, IAP, BIR1, Inhibition Mechanism, Caspase-7.

Abstract No.171

In Silico Modeling of Receptor Binding Mode for two Novel Peptides Developed as EGFR Antagonists

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Epidermal growth factor receptor (EGFR) is one of the most common targets for developing anticancer drugs. It is a cell-surface receptor which plays a key role in many of human epithelial cancers. Recently we identified two novel peptides (P1 and P2) for EGFR. From drug discovery and design point of view introducing short peptides which could inhibit the protein-protein interaction is of great importance.Our aim in the current investigation was to study their mode of interactions to the receptor using computational methods. Computational approaches have become increasingly important in drug design processes. Modern computational approaches such as structure-based drug design have efficiently speeded up the drug discovery process based on some proven theoretical bases at different levels of approximation which can provide useful tools for studying the structural and dynamics behavior of biomolecules. Furthermore, such computational methods can be used to predict the possible interactions in ligand-receptor complexes and to get an estimate of binding free energies for the complexes.In order to predict the mode of interactions of the peptides initially, P1 and P2 were docked onto the active site of the receptor using GOLD program and interactions in the complex of ligand- receptor were analyzed using Ligplot program. Then the docked peptides were subjected to different MD simulation with the time lengths ranging from 0.4 to 6 ns using AMBER program and then the binding free energy were evaluated by applying the MM-PBSA/GBSA methods. The result of this study can be used in identifiying pharmacophore responsible for molecular interaction which can be useful in drug design processes.

Keywords: EGFR, Binding free energy, Amber, Docking, MMPBSA/GBSA.
