more than other modes, and immobilization activity in the presence of magnetic field also showed enhancement. Km for immobilized α-amylase was found to be higher than that of the free enzyme, which may be due to interparticle diffusional mass transfer restrictions.

Keywords: Static Magnetic Field, A-Amylase, Enzyme Immobilization, Kinetic Parameters.

Abstract No.175

Interaction of Cu(II) Phthalocyanine and Porphyrazines with Plasmid DNA and Their Antibacterial Properties

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Multiple resistances to antibiotics are a growing public health issue that is compounded by the inability of the pharmaceutical industry to generate new strains of antibiotics to combat infections. Identification of new antibacterial agents and exploitation of new approaches for the drug-resistant bacteria is in great demand. Among the novel developed antibacterial agents, porphyrin complexes have attracted much attention. Phthalocyanines differ from porphyrins by having nitrogen atoms link the individual pyrrol units. Tetrapyridinoporphyrazines are phthalocyanine aza analogs in which four pyridine moieties formally substitute four benzene moieties in the macrocycle. The tetramethylated quaternized forms of tetrapyridinoporphyrazines (tmtppa) are tetra-positively charged and hence water soluble. In this study, the antibacterial effect of an anionic phthalocyanine Cu(PcTs) and two cationic tetrapyridinoporphyrazine including [Cu(2,3-tmtppa)]4+ and [Cu(3,4-tmtppa)]4+ complexes towards Staphylococcus aureus and Escherichia coli growth were investigated. In addition, their interaction with plasmid DNA was studied using spectroscopic and gel electrophoresis methods. The results indicated that both porphyrazines have significant antibacterial propertiesagainst the Gram negative and the Gram positive bacteria. but, Cu(PcTs) has a very weak antibacterial effect. Gel retardation assay implied that [Cu(2,3-tmtppa)]4+ (the figure is shown) and [Cu(3,4-tmtppa)]4+ degrade plasmid DNA and Cu(PcTs) causes no retardation in movement of the plasmid.Stern–Volmer dynamic quenching constant, binding constant and number of binding sites for interaction of the complexes with plasmid DNA were measured using analyzing of the fluorescence and absorption spectroscopic data. The results indicated interaction of [Cu(2,3-tmtppa)]4+and [Cu(3,4-tmtppa)]4+ with plasmid are more stronger than Cu(PcTs).

Keywords: Interaction, Phthalocyanine, Tetrapyridinoporphyrazine, Antibacterial properties.

Abstract No.176

Applying a Bi-chaperone System to Prevent Insulin Aggregation

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The aggregation of insulin is a big medical- and biotechnological challenges, therefore in this study a Bi-chaperone system consisting of alpha-crystallin (α-Crs) and beta-casein (β-CN) with different molar ratios were applied to prevent insulin aggregation spectroscopically. These two proteins are amphiphilic, each contains distinct polar and non-polar regions in their primary structures. While polar domain of α-Crs is highly electropositive, the counterpart domain in β-CN is strongly electronegative. The results of both fluorescence study and native gel electrophoresis confirmed a non-covalent interaction between α-Crs and β-CN. Consequently the synergistic chaperoning operation observed in Bi-chaperone system can be explained with the possible electrostatic interactions between its chaperone components through their polar/charged domains. Furthermore, the results of this study may provide useful information to identify potential interacting molecular partners for α-Crs chaperone.

Keywords: Alpha-crystallin, Beta-casein, Aggregation, Chaperone activity, Bi-chaperone system.

Abstract No.177

Caseoperoxidase: Novel Peroxidase-Like Nano-Artificial Enzyme

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Robust biocatalysts may be formed by encapsulating prosthetic group in hydrophobic pocket like micelles, vesicles and macrocyclic compounds that mimic the polypeptide envelope protecting the catalytic center located in the natural enzymes. Artificial enzymes could biomimetically constructed from native protein as host for prosthetic active site to simulate the catalytic functions exhibited by natural enzymes.New four-component nano-biocatalyst concluding Camel β-Casein (Cβ-Casein), SDS, heme, imidazole, coined by us "Caseoperoxidase" provided high catalytic efficiency, as peroxidase-like nano-artificial enzyme, that was 24.5% native horseradish peroxidase (HRP). Caseoperoxidase is a biomimetic of native peroxidase that incorporates the active site by protein hydrophobic inside. Camel β-casein was selected as an appropriate apo-protein for heme active site by homology modeling method. Heme docking into new obtained camel β-casein structure indicates one heme incorporates with β-casein. Docking analysis has predicted the presence of one main active site and minor sites for heme ligand to Cβ-Casein. The presence of one main electrostatic site for the active-site into β-casein protein was also confirmed by experimental method through Wyman binding potential. Further experiments also confirm the retention of caseoperoxidase structure and function as artificial enzyme.

Keywords: Caseoperoxidase, Nano-artificial Enzyme, Horseradish Peroxidase (HRP), Biomimetic, Camel β-Casein, SDS, Heme.

Abstract No.178

Study of the Interaction Between Human Serum Albumin and Co (III) –Salen Complex Using Fluorescence Spectroscopy

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Distribution, metabolism and elimination of drugs, depend on the binding of drugs to protein. The characterization of molecular interactions between protein and drugs provide important clue for designing of effective drugs for the treatment of disease.Human serum albumin (HSA) is responsible protein for binding and transporting of numerous compounds, such as hormones, fatty acids and drugs. The discovery that cobalt (III) Schiff base complexes are potent antiviral agents prompted us to initiate an investigation of Co (III) interactions with proteins and nucleic acids. Co (III) Schiff base complexes with two amines in axial positions have been used as antimicrobial agents. The interaction of the Co (III)-salen complex with DNA using fluorescence Spectroscopy has been studied.Here, the interaction of Co (III)-salen of N, N ′-dipyridoxyl (1, 4-butanediamine) Schiff-base complex with human serum albumin (HSA) in phosphate buffer solution has been investigated using fluorescence spectroscopy.The successive fixed amount of drug solution was added to HSA solution. Upon additions of ligand, fluorescence intensity of HSA decreased, so successive binding of the drug should occur close to tryptophan residue that causes quenching. Also a blue shift was observed, which indicated the fall of polarity and the increase of hydrophobicity around tryptophan residues. The Stern-Volmer quenching constant, K_{sv} = 7.7 × 10^4 M^{-1} and quenching rate constant of the biomolecule, K_q = 7.7 × 10^{12} L mol-1 s^{-1} were determined using the Sterns–Volmer equation to provide a measure of the binding affinity between ligand and HSA. Also, according to the Lineweaver-Burk equation binding constant has been calculated. The results indicated that the binding between drug and HSA are strong and the possible quenching mechanism between HSA and ligand was suggested as static quenching.

Keywords: Human Serum Albumin, Cobalt (III)-Salen, Quenching, Fluorescence Spectroscopy.

Abstract No.179

Radical Scavenging Capability of Different Phenolic Acids: Caffeic, Ferulic, P-coumaric and Sinapinic Acids

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