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Structural Characteristics of Serum Albumin and Its Pharmaceutical Application

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Human serum albumin (HSA) is a monomeric non-glycosylated polypeptide of about 65 kDa and comprises 585 amino acid residues. Its basic structure is mainly α-helix and composed of three homologous domains (I-III) connected by flexible hinge region that forms a heart-shaped structure in water solution. HSA is the most abundant plasma protein. It binds a great variety of endogenous and exogenous substances and has been shown to possess antioxidant and some enzymatic activities. Its biodegradability, nontoxicity and nonimmunogenecity make it an attractive macromolecule for drug delivery system carrier. Recent work using recombinant mutants and X-ray crystallography has provided much new information concerning the structural and functional properties of HSA.

The speaker initiated research on drug-plasma protein binding to investigate factors that govern the binding specificity of HSA after his appointment as a professor in biopharmaceutics in 1983. In this lecture, a topology analysis of drug binding sites on HSA using various methods including spectroscopy, QSAR, photoaffinity labeling and site directed mutagenesis will be presented. He will also discuss the clinical significance of drug-drug interactions at the protein binding level, specially the benefits of protein binding displacement. Moreover, the molecular design of albumin with a prolonged half-life using current DNA recombinant techniques will be presented. In addition,the utility of albumin-containing dialysate for extracorporeal removal of endogenous toxins and in the treatment of drug overdoses will be introduced. Finally, he will discuss new developments in studies of albumin, “an old protein but with new functions”.