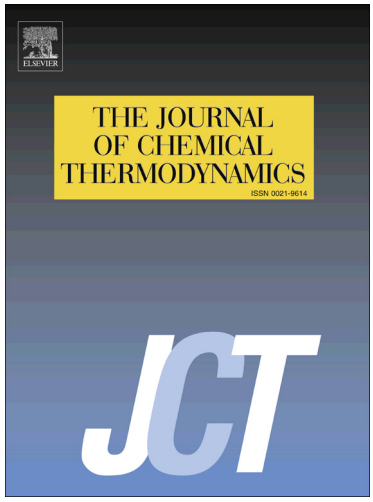

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Interaction of Methimazole / Curcumin with Human Serum Albumin: Partial Molar Volume and Partial Molar Isentropic Compressibility Studies

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ABSTRACT

Partial molar volume (V_ϕ^0) and partial molar isentropic compressibility ($\kappa_{s\phi}^0$) values of drugs methimazole and curcumin in 25 μmol·kg^{-1} human serum albumin (HSA) solution have been evaluated using density and speed of sound data. The isentropic compressibility values $\phi_{\kappa s}$ of curcumin /methimazole + HSA solutions have also been computed. The $\phi_{\kappa s}$ values decrease with an increase in the molal concentration of drugs as well as with temperature. The variations of trends $\phi_{\kappa s}$ for the studied drugs have been discussed in terms of structure breaking behavior of drugs. The values of ϕ_v^0 and ϕ_{ks}^0 have been interpreted in terms of electrostatic and hydrophobic interactions operative in the solutions.

Keywords: Human serum albumin, Methimazole, Curcumin, Isentropic compressibility, Partial molar volume, Partial molar isentropic compressibility

1. Introduction

Human serum albumin (HSA) is the most abundant soluble protein in blood plasma. HSA provides a depot for many compounds, binds some ligands in a strained orientation providing their metabolic modification, renders potential toxins harmless transporting them to disposal sites, accounts for most of the anti-oxidant capacity of human serum, and acts as a NO-carrier [1]. HSA consists of 585 amino acids that form into three structurally similar α-helical domains. These domains are characterized by a common motif of 10 α-helices. Each domain can be divided into sub-domains A and B, which contain six and four α-helical, respectively [2-3]. The domain II and III of HSA contain two primary drug binding sites, known as Sudlow's site I and site II [4]. Several additional sites were also observed [5-9]. Crystallographic structural analysis of HSA-ligand complexes can reveal the molecular details of drug