



# Effect of temperature on thermo-acoustical parameters of arginine in colloidal solutions



Sadaf Naz<sup>a</sup>, Muhammad Asghar Jamal<sup>a,\*</sup>, Muhammad Kaleem Khosa<sup>a</sup>, Bushra Naseem<sup>b</sup>, Majid Muneer<sup>a</sup>

<sup>a</sup> Department of Chemistry, Government College University, Faisalabad 38040, Pakistan

<sup>b</sup> Department of Chemistry, Lahore College for Women University, Jail Road, Lahore 54000, Pakistan

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## ABSTRACT

Volumetric and acoustic studies of L arginine in water and in aqueous sodium dodecyl sulphate (SDS) solutions were carried out to understand intermolecular interactions in solutions of arginine with water and colloidal solutions containing anionic micelles. Density and ultrasonic velocity data for arginine in water and in aqueous colloidal solutions were measured over a temperature range (288.15 K–308.15 K). The experimental data have been used to calculate apparent and partial molar volume ( $\Phi_v, \Phi_v^0$ ), apparent and partial molar compressibility ( $\Phi_K, \Phi_K^0$ ), transfer volume ( $\Phi_v^t$ ), partial molar expansibility ( $\Phi_E^0$ ), acoustic impedance ( $Z$ ) and relative association ( $\tau$ ) etc. to comprehend inter and intra molecular interactions. The above mentioned parameters have been used to explore the arginine-surfactant interactions among ions of arginine and water molecules. The trends of transfer volumes have been interpreted by the cosphere overlap model. Moreover, the expansibility factor showed the structure making the behavior of arginine both in water and in aqueous SDS solutions.

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## 1. Introduction

In living organisms proteins are one of the most essential biomolecules which play a pivotal role in various bio chemical processes. The title role of proteins and their basic functions in such processes can be apprehend by their interaction with their neighboring environment [1]. Proteins have very complex structures. The direct study of proteins is difficult due to complex structures, therefore their interactions can be explored using amino acids. Amino acids are the building blocks of more complex peptides and proteins. Study of amino acids gives valuable information about solubility, stability and biological activity of proteins [2,3]. The structure of proteins is highly affected by the solvent. The solvent highly influence the structure of proteins and it may lead to some ilk of degradation in the structure of proteins. Solvent is the basic cause of alteration in its solubility, stability and biological activity of the protein.

Surfactants play a vital role in the production of many chemical products and are used to stabilize emulsions. There is a large number of applications of surfactants in industries including food, pharmaceuticals, petroleum and in oil recovery, etc. [2]. Their role as a constituent in numerous biochemical industries cannot also be neglected. At the molecular level, the interaction of the protein with surfactant have great significance [3] because they are extremely employed in biotechnological [4] and pharmaceutical [5] process. This study has great interests

of many researchers [6,7] because of technological perspective protein-surfactant interaction modulates the functional properties of proteins [8]. The change in molecular properties of globular proteins occurs due to mesh with surfactant molecules that may cause a change in binding with other molecules; i.e. they alter the functional characteristics by absorbing at the interface and they self-assemble. However, several details regarding the way of interaction of proteins with surfactant remain unanswered. Hence, it is mandatory to apprehend the nature and origin of surfactant-protein interactions quantitatively and qualitatively.

Proteins are complex biomolecules so the direct study is somewhat difficult. Therefore, to understand the native structure and thermodynamic stability of proteins, the best methodology is to study simpler model compounds like amino acids which are elementary units of proteins. Refined and unrefined aqueous solutions are used to carry out most of the researches in amino acids [9]. The inspection of molecular interactions of amino acids and peptides in water and water mixed solvents has been the area of attentiveness of a number of researchers [10].

The goal of this work is to lift the primary knowledge related to amino acid-surfactant interactions in solutions which is still unaware. Many biological reactions involve an alteration in volume and the solvation of molecules also occur [11]. The present study is the continuation of our previous work on the effect of anionic micellar medium on amino acids solutions [12]. In this paper, present study embrace measurement of density and sound velocity of arginine in water and aqueous (0.005, 0.01, 0.05) mol·kg<sup>-1</sup> sodium dodecyl sulphate (SDS) from (288.15–308.15) K are reported. From the calculated data, apparent

\* Corresponding author.

E-mail address: [m.asgharjamal@gmail.com](mailto:m.asgharjamal@gmail.com) (M.A. Jamal).

molar volume, apparent molar compressibility, partial molar volume, partial molar compressibility and their associated constants  $S_v$  and  $S_k$  along with partial molar expansibility, Hepler's constant, acoustic impedance,  $Z$ , and relative association,  $R_A$ , were calculated. The solute–solvent and the solute–solute interactions occurring in the binary (*arginine* + water) and ternary (*arginine* + different concentration of aqueous SDS) systems and the structure making/breaking tendency of the solutes in the given solvent have been discussed. We have also reported transfer of partial molar volumes,  $\phi_{v_i}^0$  of arginine from water to aqueous sodium dodecyl sulphate (SDS) solution and discussed the interactions operating in these systems.

## 2. Experimental

### 2.1. Chemicals

L-Arginine and SDS (sodium dodecylsulphate) were purchased from Merck, Germany. According to supplier specification as shown in Table 1 the purity exceeded 99%. For purification recrystallization was done using ethanol–water mixture. These chemicals were dried in vacuum over  $P_2O_5$  at room temperature for about two days. All the solutions were prepared in molal concentration. The 0.005, 0.01 and 0.05 molal solutions of SDS in water were prepared and used as a solvent to prepare 0.05–1.05 mol·kg<sup>-1</sup> solution of arginine using doubly distilled, deionized and degassed water. The weighing was done using an electronic digital balance (Sartorius CP224S, model SAR CP224S, USA) with an accuracy of  $\pm 0.1$  mg. The solutions were prepared with great care and stored in special airtight bottles to stop atmospheric moisture and CO<sub>2</sub>.

### 2.2. Methods

DSA 5000 M was used to measure density ( $\rho$ ) and sound velocity ( $u$ ) of investigated solutions. It holds a highly precise vibrating tube and an ultrasound speed measuring device. The instrument has a built-in thermostat to maintain the temperature. The precision and repeatability of DSA 5000 M for temperature is 0.01 °C and 0.001 °C and for the density is  $5 \times 10^{-6}$  g cm<sup>-3</sup> and  $1 \times 10^{-6}$  g cm<sup>-3</sup> respectively. The sample density is determined by measuring the oscillation frequency of a completely filled U-shaped sample tube. The sample is placed between two piezoelectric ultrasound transducers. One transducer discharge sound waves through the sample-filled cavity (frequency around 3 MHz) and the other waves are received by the second transducer [13]. So, by dividing the noted distance between transmitter and receiver with the help of propagation time the sound velocity is obtained up to 0.5 m·s<sup>-1</sup> accuracy and 0.1 m·s<sup>-1</sup> repeatability.

Density and sound velocity data of solutions (*arginine* + SDS) were prepared in molal concentration. The 0.005, 0.01 and 0.05 molal solutions of SDS in water were prepared and used as a solvent to prepare 0.05–1.05 mol·kg<sup>-1</sup> solution of *arginine* using doubly distilled, deionized and degassed water. An electronic digital balance (Sartorius CP224S, model SAR CP224S, USA) was used for weighing with an

accuracy of  $\pm 0.1$  mg. The solutions were formulated with great caution and kept in special airtight bottles to stop atmospheric moisture and CO<sub>2</sub>.

## 3. Results and discussion

### 3.1. Apparent and partial molar volume

The distinction between the volume of solution and the volume of solvent (pure) is regarded as apparent molar volume ( $\phi_v$ ) of a solute. This parameter is calculated using the following general relationship [14]:

$$\phi_v = \frac{1000(\rho_s - \rho)}{m\rho\rho_s} + \frac{[M]}{\rho} \quad (1)$$

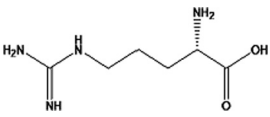
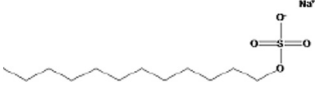
$M$  is the molar mass of the solute (*arginine*),  $\rho$  is the density of the solution,  $\rho_s$  is the density of solvent;  $m$  is the molality of the arginine solutions in water and aqueous SDS micellar solutions. The  $\phi_v$  value is the actual measurements of the molecular size of the hydrated solute molecules in solution which create a gap among themselves and the adjacent solvent molecules [15]. Using the measured density of arginine in water and aqueous SDS solutions at different temperatures, apparent molar volume was calculated and the obtained data has been presented in Table 2. Apparent molar volume is actually the measure of the packing order of amino acid molecules with solvent molecules like the interaction of *arginine* with water and micellar surfactant solutions. The apparent molar volume values are valuable because they form the base for apprehending molecular interactions. Graphical representation of the variation of  $\phi_v$  with molality ( $m$ ) of arginine solutions in water and aqueous SDS has been shown in Figs. 1–4.

The apparent molar volume  $\phi_v$ , increases with increasing both temperatures of the solutions and concentration of arginine at different temperatures. The values of  $\phi_v$ , which are positive and show an increase by increasing the temperature in case of water while decreases by increasing the amount of the co-solute (SDS) from 0.005–0.05 mol·kg<sup>-1</sup>. The densely hydrated molecules have less apparent molar volumes than those which are not heavily hydrated. This is the cause of greater interaction with water and SDS molecules and hence greater electrostrictive forces and the collapse of SDS and water structure around them as shown in Figs. 1–4.

A low apparent molar volume (Table 2) explores better packing features, hence better interaction with SDS and water. Generally, following types of interactions in the ternary system of surfactant, water and amino acid may be assumed:

- Ion–ion interactions among  $SO_4^{2-}$  group of SDS and the  $NH_3^+$  group of amino acids or may be among the  $Na^+$  ion of SDS and the  $COO^-$  group of amino acids.
- Ion–hydrophilic interactions among the hydrophilic area of surfactant (SDS) and the ions of amino acids.

**Table 1**  
Specifications of chemicals used in the present study.

Chemical names	Source	CAS No.	Chemical structures
L-Arginine	Merck (Germany)	74-79-3	
Sodium dodecylsulphate (SDS)	Merck (Germany)	151-21-3	

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