Ultrasonic Study of Thermophysical Characteristics of Amino acids in Aqueous 2% D-glucose Solution at Varied Temperatures

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Abstract

Thermodynamic parameters like density (ρ), viscosity (η), and ultrasonic velocity ($\cup$) have been measured for 0.01 to 0.1 molal concentration of L-alanine, L-arginine and, L-glutamine in 2% aqueous D-glucose solution at different temperature ranges from 293.15 to 313.15K. These measurements have been performed to evaluate some important parameters like adiabatic compressibility (β), molar hydration number (n_H), apparent molar volume (φ_v), partial molar volume (φ_v^o), apparent molar compressibility (φ_k), limiting apparent molar compressibility (φ_k^o), and their constant ($S_{k,}\ S_v$) and viscosity A and B coefficients of the Jones-Dole equation. These parameters have been interpreted as molecular interactions in terms of solute-consolute and solute-solvent interactions.

Keywords: Hydrophilic, Hydrophobic, volumetric studies, electrostriction effect, apparent molar volume, partial molar volume.
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Introduction

Among the most vital biomolecules in living organisms, proteins play a pivotal role in various biochemical processes. The crucial functions of proteins within these processes are best understood by examining their interactions with their immediate environment [1]. Due to their complex structures, studying proteins directly can be challenging. Therefore, their interactions are often explored by studying amino acids, which are the fundamental building blocks of more complex molecules. Investigating amino acids provides valuable insights into the solubility, stability, and biological activity of proteins [2, 3]. This is particularly important because proteins are extensively utilized in biotechnological [4] and pharmaceutical [5] processes. The interaction between proteins and surfactants is of great interest to many researchers [6, 7] due to its technological implications. This interaction can modulate the functional properties of proteins [8]. When globular proteins interact with surfactant molecules, their molecular properties can change, potentially altering their binding with other molecules. This occurs as proteins absorb at interfaces and self-assemble, leading to a change in their characteristics.

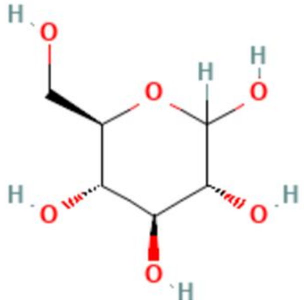

Figure 1: Chemical structures of D-Glucose.

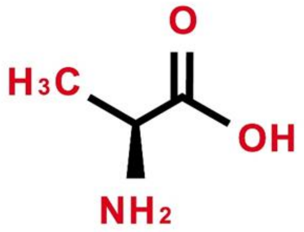

Figure 2: Chemical structures of L-alanine.

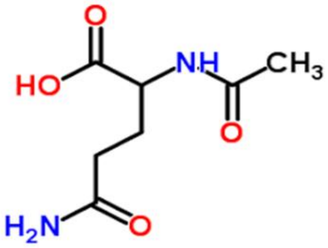

Figure 3: Chemical structures of L-arginine.

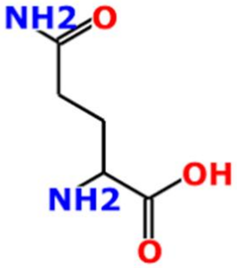

Figure 4: Chemical structures of L-glutamine.

However, several details regarding the precise mechanisms of protein-surfactant interactions remain unknown. Therefore, it is crucial to quantitatively and qualitatively understand the nature and source of these interactions. Given the complexity of proteins, studying simpler model compounds like amino acids provides the best methodology to understand the native structure and thermodynamic stability of proteins. Most research on amino acids is conducted using both refined and unrefined aqueous solutions [9]. Significant research attention has been garnered by the molecular interactions of amino acids and peptides in water and water-mixed solvents. [10]. Amino acids, as the basic components and model compounds of protein molecules, are particularly suitable for this type of research. Investigating their thermodynamic properties provides valuable information to understand the nature of biological molecules [11-13]. Studying how proteins interact with their surrounding liquid is tough because proteins are big and complicated. A good way around this is to look at simpler molecules like amino acids, which are the building blocks of proteins. See figure 1-4. By examining how the liquid interacts with different parts of amino acids – like their side chains and the main chain that links them – we can understand the crucial role these interactions play in how proteins are structured, shaped, and function in watery environments [14, 15]. This study aims to investigate the molecular interactions and their effects on water structure through physicochemical and thermodynamic studies of amino acids in mixed aqueous solutions. While significant attention has been given to the behaviour of amino acids in various salt-water mixed solvents, our study focuses on a different co-solvent system: 2% aqueous D-glucose solutions. We report the density, viscosity, and ultrasonic velocity values for 0.01 to 0.1 molar concentrations of L-alanine, L-arginine, and L-glutamine in these solutions at 293.15 K. From these experimental data, various physical and thermodynamic parameters were calculated. These include adiabatic compressibility, molar hydration number, apparent molar volume, partial molar volume, apparent molar compressibility, limiting apparent molar compressibility, and the viscosity A and B coefficients of the Jones-Dole equation. This study is examining how the presence of D-glucose and any other dissolved compounds influences the fundamental molecular attractions and repulsions within the water, and how these interactions, in turn, affect the measurable properties of the solution.

Experimental

L-arginine, L-alanine, L-glutamine, and D-fructose with AR grade with a minimum of 99.9% were used from E-Merck, Germany chemicals. They were used without further purification. The stock solutions of L-Arginine, L-alanine, and L-glutamine in 2% D-Fructose were prepared with double-distilled water (Model number SSA-DDAQ-15 All Quartz Distillation) and their concentrations were measured gravimetrically. See table 1. Before creating the solutions, the water used for experimentation was degassed and deionized using distillation. The "ternary aqueous solutions" were precisely created using highly accurate Metter Toledo balances, which measure mass to an impressive four decimal places (± 0.0001 grams). This involved carefully weighing the two concentrated "stock solutions" and water in specific ratios to achieve the desired concentration range of 0.01 to 0.1 molar. The weighing process itself was carried out using "mass burettes," which are specialized pieces of equipment designed for dispensing precise masses of liquids. In order to make a 0.01 to 0.1 molality solution, the two chemicals are taken in a clean and dry conical flask with a stopper. Necessary amounts of water and glucose were added. The necessary quantities of amino acids for a certain molality were dissolved, and a similar process has been used for other amino acids with varying molarities. Viscosity measurements were done (Ostwald Viscometer standards) for double-distilled water for the flow time. The ultrasonic interferometer was calibrated with double-distilled water for sound velocity measurement (Considering Madder's Velocity) and the error factor was found to be 0.2 m/s. The velocity was measured using an ultrasonic interferometer operated at 3 MHz, (Mittal's Interferometer Enterprises, New Delhi) with an overall precision of ±3 ms^{-1}. Adiabatic Densities were measured using a digital a densitometer (Metter Toledo). Temperatures were controlled to ± 0.002 K at intervals of $293.15 \leq T/K \leq 313.15K$. Calibration of densitometer is about ± 0.0001g/ml.

A layered measuring cylinder made of steel is used to hold the liquid mixture. At the proper temperature, it has been filled using an electronically controlled constant temperature bath. The temperature is accurate to within ± 0.1.

Table 1: Specification of chemicals.

Name of chemical	Molar mass g.mol-1	Source	CAS number	Mass purity
L-Alanine	89.09	Sigma-Aldrich	56-41-7	≥ 99%
L-Arginine	174.2	Sigma-Aldrich	74-79-3	≥ 99%
L-Glutamine	146.15	Sigma-Aldrich	56-86-9	≥ 99%
D-Glucose	180.15	Sigma-Aldrich	50-99-7	≥ 99%

Theory and Calculations

Using the experimental values, following acoustical and thermodynamical parameters have been calculated using the standard relations.

Adiabatic compressibility

$$\beta = \frac{1}{U^2\rho} \qquad (1)$$

Molar hydration number has been computed using the relation.

$$n_H = \left(\frac{n_1}{n_2}\right)\left(1-\frac{\beta}{\beta_0}\right) \qquad (2)$$

Where, β and β_0 Adiabatic compressibility of solution and solvent, respectively, $n_1$and n_2 Number of moles of solvent and solute, respectively.

Apparent molar volume has been calculated using density data.

$$\varphi_v = \frac{M}{\rho} - \frac{(\rho-\rho_{0})}{m\rho\rho_0} \qquad (3)$$

Where, M is the molar mass of the solute, m is the molality of amino acid, ρ and ρ_0 are densities of solution and solvent, respectively.

Apparent molar volume, φ_v^o is also known as partial molar volume of co-solute [16]

$$\varphi_v = \varphi_v^o + S_v m \qquad (4)$$

Where, φ_v^o is the partial molar volume, S_v is the experimental slope

The apparent molar compressibility has been calculated from relation

$$\varphi_k = \frac{1000}{m\rho_0}\left(\beta\rho_0 - \rho\beta_0\right) + \left(\frac{\beta_0 M}{\rho_0}\right) \qquad (5)$$

Where, β, ρ and β_0, ρ_0 are the adiabatic compressibility and density of solution and solvent, respectively m is the molar concentration of the solute and M the molecular mass of solute. φ_k results can be shown as follows;

$$\varphi_k = \varphi_k^0 + S_k m\ {}^{1}/_{2} \qquad (6)$$

Where, φ_k^0 is the limiting apparent molar compressibility at infinite dilution. S_k is a constant and have been evaluated by least- square method.

The important of viscometric study of electrolyte solution in mixed solvent system is well established [17]. The entire viscosity data have been analysed in the light of Jones-Dole equation [18].

$$\frac{\eta}{\eta_0} = 1+\mathrm{A}m^{1/2}+\mathrm{Bm} \qquad (7)$$

Where, η and η_0 viscosities of solution and solvent, respectively, m is the molar concentration of the solute-solvent system and B are constants which are definite for a solute-solvent system. A is known as the Falkenhagen coefficient which characterises the ionic interaction and B is the Jones-Dole or viscosity B-coefficient which depends on the size of the solute and the nature of solute-solvent interactions.

Result and discussion

Analysis of Acoustical and Thermodynamic Parameters

From the experimental measurements, several acoustical parameters were calculated. These include Adiabatic compressibility (β), Hydration number (nH), Apparent molar volume (φ_v), Partial molar volume (V^0), Apparent molar compressibility (φ_k), Limiting apparent molar compressibility (φ_{k0}) and its constant (K), Viscosity B-coefficient from the Jones-Dole equation

The results of these calculations are presented in Tables 2-5 (Supplementary Material).

Table 2 presents the ultrasonic velocity (u) values, which are observed to increase as both the concentration of the dissolved substances (solutes) and the temperature rise. These measured ultrasonic velocity and density (ρ) values were subsequently used to calculate the adiabatic compressibility (βs) of the solutions. These values are calculated using a standard equation (Equation 1). Increase in the amount of solute, amino acid, and temperature results in a decrease of intermolecular free length leading to strong intermolecular forces among the solute and the solvent molecules [19]. Adiabatic compressibility (β) decreases with increasing solute concentration and temperature in all three systems studied (Table 3). This is primarily due to the electrostriction effect, where amino acid ions tightly pack surrounding solvent molecules, leading to a more rigid and less compressible structure.

Table 2: Values of density (ρ), viscosity (η) and ultrasonic velocity (U) of amino acid in 2% aqueous D-glucose solution at 293.15K-313.15k.

m (molal conc.)	Density (ρ) (kgm^{-1})					Viscosity (η) (NS/m2)					Velocity (U)				
						(× $10^{-4} NS/m^2$)							($^{m}/_{sec.}$)		
	293.15K	298.15K	303.15K	308.15K	313.15K	293.15K	298.15K	303.15K	308.15K	313.15K	293.15K	298.15K	303.15K	308.15K	313.15
System 1. L-alanine in 2% D-glucose solution															
0.01	1008.28	1007.4	1005.58	1003.26	1001.69	0.00106	8.58342	7.05332	6.10479	5.2045	1504	1505.5	1506.4	1507.4	1508.3
0.02	1008.49	1007.61	1005.89	1003.77	1002.21	0.00107	8.60103	7.10714	6.12099	5.22073	1510	1511.3	1512.4	1513.4	1514.5
0.03	1008.8	1008.13	1006.2	1004.39	1002.72	0.00107	8.64029	7.11220	6.13132	5.23324	1515.5	1516.4	1517.4	1518.5	1519.3
0.04	1009.1	1008.54	1006.72	1004	1002.93	0.00107	8.66756	7.16326	6.13811	5.26634	1520.3	1521.2	1522.6	1523.4	1524.5
0.05	1009.21	1008.95	1006.92	1004.8	1003.24	0.00108	8.73603	7.1776	6.17446	5.2889	1525.6	1526.4	1527.5	1528.5	1529.4
0.06	1009.62	1009.26	1007.44	1005.32	1003.55	0.00108	8.70702	7.17269	6.19602	5.29423	1530.6	1531.4	1532.5	1533.6	1534.7
0.07	1009.82	1009.67	1007.95	1005.73	1003.75	0.00108	8.72641	7.1907	6.21429	5.30021	1535.6	1536.5	1537.5	1538.6	1539.3
0.08	1010.93	1009.98	1008.57	1006.14	1004.06	0.00109	8.75287	7.19368	6.2352	5.31171	1540.4	1541.5	1542.6	1543.5	1544.3
0.09	1011.34	1001.64	1008.88	1006.25	1004.78	0.0011	8.69318	7.2146	6.25557	5.32539	1545.6	1546.3	1547.4	1548.5	1549.4
0.1	1011.85	1010.19	1009.19	1006.86	1004.57	0.0011	8.77372	7.22833	6.26593	5.33167	1550.4	1551.6	1552.3	1553.6	1554.7
System 2. L-arginine in 2% D-glucose solution															
0.01	1007.4	1005.7	1004.1	1002.5	1000.5	0.00101	8.10473	6.78946	5.82681	5.09148	1493	1497.5	1501	1505	1508
0.02	1007.8	1006.1	1004.4	1002.7	1000.7	0.00107	8.42861	7.07656	6.10269	5.16865	1501.1	1505.5	1509.5	1513.5	1517
0.03	1008.4	1006.2	1004.6	1003	1001	0.00107	8.50843	7.10805	6.13854	5.19723	1510	1515	1519	1522	1527
0.04	1009	1007.2	1005	1003.2	1001.4	0.00107	8.58172	7.16105	6.17641	5.25216	1523	1528	1533	1537	1542
0.05	1009.5	1007.7	1005.6	1003.6	1001.7	0.00107	8.63977	7.1811	6.21815	5.26603	1531	1536	1542.9	1546.8	1550.5
0.06	1010.1	1008.2	1006.2	1004	1002	0.00108	8.6678	7.21409	6.2429	5.2799	1539	1543.5	1547.5	1553.1	1556.8
0.07	1010.8	1009.4	1006.8	1004.4	1002.3	0.00109	8.69713	7.26003	6.25456	5.29625	1550	1554	1558	1562	1567
0.08	1011.5	1009.9	1007.5	1004.8	1002.6	0.00109	8.71413	7.28089	6.27802	5.33598	1558.9	1563.5	1567.8	1572.1	1576.2
0.09	1012.1	1010.4	1008	1005.2	1002.6	0.0011	8.74382	7.35638	6.30019	5.35567	1568.5	1572.6	1577.1	1582.2	1587.1
0.1	1012.8	1010.9	1008.5	1005.6	1002.9	0.0011	8.79735	7.40174	6.39191	5.40652	1577.7	1582.5	1587.5	1592.2	1597.1
System 3. L-glutamine in 2% D-glucose solution															
0.01	1006.8	1005.3	1003.8	1001.7	999.6	0.00106	8.52923	6.92773	5.77772	5.11144	1497	1501	1503	1505	1508
0.02	1007.6	1005.6	1004.1	1002	1000	0.00106	8.46547	6.88684	5.76769	5.07789	1510	1511.5	1513.6	1515.3	1517.2
0.03	1008.5	1007.1	1005.3	1002.8	1001.3	0.00106	8.44647	6.8836	5.75921	5.07097	1518.5	1520	1521.5	1522.7	1524
0.04	1008.6	1007.3	1005.6	1003.7	1001.5	0.00106	8.41652	6.85984	5.75128	5.05354	1525.3	1527	1528.7	1529.9	1531.5
0.05	1009.1	1007.5	1005.9	1003.9	1001.8	0.00104	8.38972	6.85615	5.7079	5.04522	1532.2	1533.8	1535.5	1538	1540.1
0.06	1009.8	1008.3	1006.6	1004.7	1002.8	0.00106	8.66708	7.24854	6.00344	5.27304	1541.3	1543.2	1545.1	1546.8	1549
0.07	1010.2	1008.6	1007.2	1005.2	1003.4	0.00106	8.75833	7.26148	6.22938	5.44739	1551.2	1553.2	1554.5	1556.2	1558.1
0.08	1010.7	1009.2	1007.7	1005.9	1004.1	0.00108	8.7984	7.28233	6.25996	5.45982	1520	1525	1530	1537	1540
0.09	1011.4	1009.9	1008	1006.4	1004.5	0.00111	8.87744	7.5404	6.36811	5.47925	1565.2	1567.1	1569.3	1571.1	1573.4
0.1	1011.9	1010.7	1008.9	1007.2	1005.4	0.00111	8.95905	7.55289	6.39683	5.49897	1575.2	1577.1	1578.8	1580	1581.9

Table 3: Values of adiabatic compressibility (β) and hydration number (n_H) of amino acids in 2 % aqueous D-glucose solution at temperature range (293.15K-313.15K).

m (molal conc.)	Adiabatic compressibility β ($\times 10^{-10}\ m^2N^{-1}$)					Hydration number (n_H)				
	293.15K	298.15K	303.15K	308.15K	313.15K	293.15K	298.15K	303.15K	308.15K	313.15K
System 1. L-alanine in 2 % D-glucose solution										
0.01	4.38453	4.38362	4.38231	4.38161	4.38125	0.53044	0.59486	0.57079	0.48962	0.52485
0.02	4.34885	4.34516	4.34462	4.34369	4.34213	2.51041	2.58884	2.60533	2.48019	2.59749
0.03	4.30602	4.30376	4.30234	4.30185	4.30049	5.78334	5.81416	5.74754	5.67662	5.71684
0.04	4.26753	4.26484	4.26369	4.26179	4.26017	10.03096	10.1087	10.24167	9.69102	10.09049
0.05	4.21733	4.21396	4.21240	4.21198	4.21141	15.61444	15.78139	15.68273	15.37178	15.53961
0.06	4.17784	4.17693	4.17449	4.17333	4.17072	22.34603	22.49195	22.4802	22.17564	22.40058
0.07	4.13952	4.13523	4.13492	4.13317	4.13263	30.12519	30.49523	30.46068	30.04591	29.86675
0.08	4.09881	4.09678	4.09665	4.09385	4.09216	39.42654	39.48163	39.73732	38.94609	38.76178
0.09	4.00913	4.00543	4.00457	4.00345	4.00274	49.80391	49.82501	49.67621	48.83508	49.18717
0.1	3.94668	3.94007	3.92456	3.91265	3.89911	60.98889	60.56832	60.78474	60.31976	60.23671
System 2. L-arginine in 2 % D-glucose solution										
0.01	4.45326	4.43402	4.4204	4.40395	4.39522	0.33296	0.62559	0.80063	1.1542	1.32792
0.02	4.40359	4.38528	4.36945	4.35376	4.34235	0.68156	1.06853	1.61043	2.17217	2.53823
0.03	4.34924	4.33003	4.31411	4.30398	4.28438	0.67958	1.87221	2.84782	2.83015	3.76229
0.04	4.27277	4.25243	4.23399	4.21954	4.19975	2.34313	3.67635	4.93213	6.04235	7.19263
0.05	4.22613	4.20617	4.17733	4.16458	4.15259	1.96851	3.63044	6.10278	6.52781	7.94557
0.06	4.17983	4.16332	4.15006	4.12921	4.11781	2.82256	3.98418	6.41851	6.83998	8.19164
0.07	4.11786	4.10237	4.09187	4.08067	4.06316	2.4199	4.48663	6.6392	7.27416	8.8114
0.08	4.06816	4.05066	4.03807	4.0268	4.01467	2.61906	4.90434	7.41354	7.32497	8.90775
0.09	4.01613	4.00194	3.9886	3.97397	3.95971	3.02054	5.10385	7.98317	9.43883	11.84975
0.1	3.96668	3.95007	3.93456	3.92265	3.90911	3.98626	7.12658	9.75476	11.58139	14.14858
System 3. L-glutamine in 2 % D-glucose solution.										
0.01	4.43214	4.41512	4.40996	4.40747	4.39917	0.75547	1.00109	1.00432	1.07319	1.23652
0.02	4.35269	4.3527	4.34711	4.34645	4.34425	4.71476	4.52324	4.54965	4.61291	4.69407
0.03	4.30026	4.29774	4.29695	4.29688	4.29677	10.23288	10.10182	9.85486	9.67157	9.71428
0.04	4.26158	4.25758	4.2553	4.25467	4.25411	16.77968	16.72751	16.52213	16.48326	16.43183
0.05	4.22119	4.21908	4.21644	4.21111	4.20844	25.0403	24.78954	24.57348	25.23451	25.45047
0.06	4.1686	4.16453	4.16131	4.16002	4.15607	36.37527	36.31861	36.13717	36.39853	36.85358
0.07	4.11393	4.10985	4.10868	4.10787	4.10521	50.13952	50.0827	49.58994	49.82621	50.17554
0.08	4.28243	4.26072	4.23922	4.02821	4.19935	63.15905	63.90813	63.6001	60.74817	62.1481
0.09	4.03587	4.03207	4.02835	4.00552	4.02135	78.67913	78.57098	78.41651	79.08475	79.8089
0.1	3.98282	3.97795	3.97647	3.97613	3.97469	98.12454	98.23248	97.62108	97.65479	98.11181

Table 4: The values of apparent molar volume (φ_v) and apparent molar compressibility (φ_k) of amino acid in 2 % aqueous D-glucose solution at temperature range 293.15K-313.15K.

m (molar conc.)	Apparent molar volume φ_v ($\times 10^{-3} m^3 mol^{-1}$)					Apparent molar compressibility $-\varphi_k$ ($10^{-7} m^2 N^{-1}$)				
	293.15K	298.15K	303.15K	308.15K	313.15K	293.15K	298.15K	303.15K	308.15K	313.15K
System 1. L-alanine in 2 % D-glucose solution										
0.01	88.17	88.18	88.36	88.65	88.74	3.4002	3.02882	3.79636	3.06496	3.41208
0.02	88.24	88.28	88.44	88.65	88.77	3.52994	3.78314	3.76821	3.49078	3.72631
0.03	88.23	88.26	88.44	88.61	88.75	3.49294	3.64483	3.55496	3.47923	3.54721
0.04	88.22	88.24	88.41	88.68	88.75	3.36462	3.50157	3.51443	3.21804	3.44154
0.05	88.22	88.22	88.41	88.6	88.73	3.30531	3.45464	3.39486	3.28453	3.3558
0.06	88.19	88.2	88.36	88.56	88.71	3.27575	3.38532	3.36561	3.28309	3.33073
0.07	88.18	88.17	88.32	88.53	88.7	3.22481	3.3517	3.3392	3.25633	3.24013
0.08	88.07	88.15	88.27	88.49	88.68	3.26639	3.30532	3.33417	3.22588	3.20808
0.09	88.04	88.98	88.24	88.49	88.61	3.25318	3.23533	3.27971	3.17669	3.2249
0.1	87.99	88.14	88.22	88.43	88.64	3.2268	3.20264	3.23889	3.18244	3.16667
System 2. L-arginine in 2 % aqueous D-glucose solution										
0.01	172.82	173.12	173.4	173.69	174.04	2.08254	3.47561	4.30987	6.02625	6.86231
0.02	172.78	173.08	173.38	173.68	174.03	1.14271	1.59267	2.22222	2.87558	3.31298
0.03	172.68	173.08	173.36	173.64	173.98	0.653173	1.20758	1.72471	1.73413	2.49589
0.04	172.58	172.9	173.29	173.61	173.92	0.64615	1.15158	1.65533	1.95891	2.31551
0.05	172.5	172.81	173.18	173.54	173.87	0.631981	0.927952	1.3458	1.38511	1.46608
0.06	172.4	172.73	173.08	173.47	173.81	0.490780	0.761163	0.54467	0.780968	0.952051
0.07	172.28	172.51	172.97	173.4	173.76	0.484174	0.689634	0.541073	0.744075	0.942929
0.08	172.16	172.43	172.85	173.33	173.71	0.443573	0.54732	0.527112	0.602518	0.74461
0.09	172.06	172.35	172.77	173.26	173.70	0.420013	0.530652	0.496349	0.576003	0.680231
0.1	171.94	172.26	172.68	173.19	173.66	0.419141	0.526274	0338542	0.5665327	0.649131
System 3. L-glutamine in 2 % aqueous D-glucose solution										
0.01	145.12	145.33	145.54	145.9	146.22	3.92887	5.18781	5.22052	5.31841	6.06517
0.02	144.99	145.3	145.51	145.84	146.14	2.64356	3.11219	3.27349	3.28687	3.31642
0.03	144.85	145.04	145.31	145.71	145.91	2.30044	2.41402	2.39822	2.41786	2.51962
0.04	144.85	145.03	145.28	145.56	145.89	1.21320	1.23367	1.28683	1.29424	1.318923
0.05	144.78	145.01	145.24	145.54	145.85	0.697248	0.752946	0.789194	0.81984	0.825758
0.06	144.68	144.89	145.14	145.42	145.69	0.315581	0.348101	0.355017	0.36211	0.370114
0.07	144.62	144.85	145.05	145.34	145.60	0.305178	0.535835	0.424464	0.42611	0.437167
0.08	144.55	144.76	144.98	145.24	145.50	0.227534	0.311379	0.390703	0.46924	0.487552
0.09	144.45	144.66	144.94	145.17	145.44	0.169593	0.173658	0.194815	0.256904	0.280357
0.1	144.38	144.54	144.8	145.05	145.31	0.132218	0.169626	0.175463	0.184075	0.192797

Table 5: Values of partial molar volume (φ_v^0) and limiting apparent molar volume (φ_k^0) and their constant S_v and S_k and A and B coefficients of Jones-Dole equation of amino acids in aqueous 2 % D-glucose solution at temperature range (293.15K-313.15K.).

		Partial Molar volume	Constant	Limiting Apparent Molar volume	Constant	Coefficient of Jones-Dole equation	
Amino acid	Temperature	φ_v^0 ($\times 10^{-3} m^3 mol^{-1}$)	S_v ($\times 10^{-4} m^3 mol^{-1}$)	φ_k^0 ($\times 10^{-7} m^2 mol^{-1}$)	S_k($\times 10^{-7} N^{-1} m^{-1} mol^{-1}$)	A	B
L-alanine	293.15K	88.32	-5.0251	-3.62665	1.30253	0.02754	0.16323
	298.15K	88.41	-8.80657	-4.52302	4.95672	0.0506	0.13273
	303.15K	88.59	-9.37145	-4.06357	2.69238	0.03823	0.10764
	308.15K	88.81	-9.72316	-3.36672	4.4738	0.03927	0.13842
	313.15K	88.85	-5.56011	-3.81655	2.00817	0.00913	0.14034
L-arginine	293.15K	173.37	-4.23031	-2.20416	6.511	0.02649	0.1671
	298.15K	173.71	-4.30949	-3.63526	11.1767	0.00933	0.2059
	303.15K	173.91	-.3.6166	-4.80342	15.0383	0.01754	0.2163
	308.15K	173.99	-2.31756	-6.39696	20.7184	0.02547	0.2267
	313.15K	174.28	-1.92723	-7.37898	23.7838	- 0.010	0.21002
L-glutamine	293.15K	145.47	-3.37553	-6.11663	22.44754	0.07903	- 0.19671
	298.15K	145.73	-3.52675	-6.74233	24.7501	0.09461	- 0.21166
	303.15K	145.94	-3.71223	-6.81516	25.0222	0.0139	0.1093
	308.15K	146.37	-3.98205	-6.49825	23.9377	- 0.053	0.36222
	313.15K	146.69	-4.16241	-6.91171	25.5139	0.01087	0.11573

A decrease in the value of β (Adiabatic Compressibility) indicates that the solution has become less compressible. This suggests that the molecules within the solution are interacting more strongly, making the overall structure more rigid [19]. Specifically, this reduction in compressibility implies an increase in Ionic-hydrophilic interactions and Hydrophilic-hydrophilic interactions.

The decrease in β with increasing temperature suggests a thermal breakdown of the structured water clusters around the zwitterionic groups (–NH^{3+}and –COO^{-}) of the amino acids and the hydrophilic –OH groups of D-glucose. This breakdown may lead to less aggregation of water molecules, but the overall effect is a reduction in compressibility due to enhanced interactions. L-arginine shows a larger magnitude of adiabatic compressibility values compared to the other two amino acids. The zwitterionic groups on the amino acid molecules allow for very strong electrostatic interactions with the polar water molecules. Water molecules, being polar, have partial positive and partial negative ends, and they can effectively surround and interact with both the positively and negatively charged parts of the zwitterionic amino acid. This strong interaction contributes to the solubility and specific behaviour of amino acids in aqueous solutions.

Solvation and Hydration

The interaction between the solute and water molecules is known as hydration.

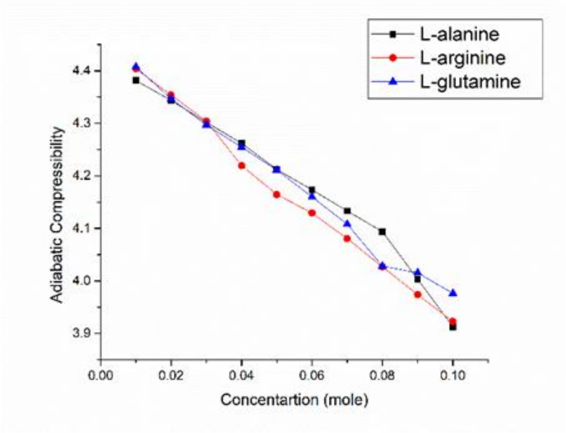

Figure 5: Plot between Adiabatic compressibility and concentration at 308 K.

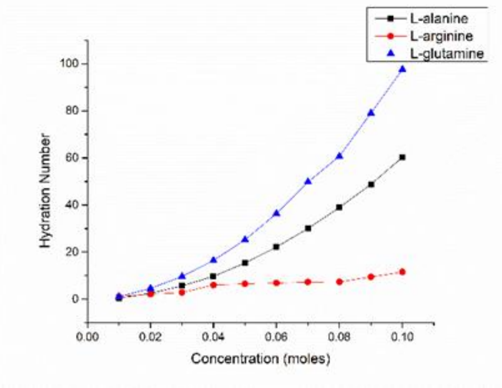

Figure 6: Plot between Hydration Number and concentration at 308 K.

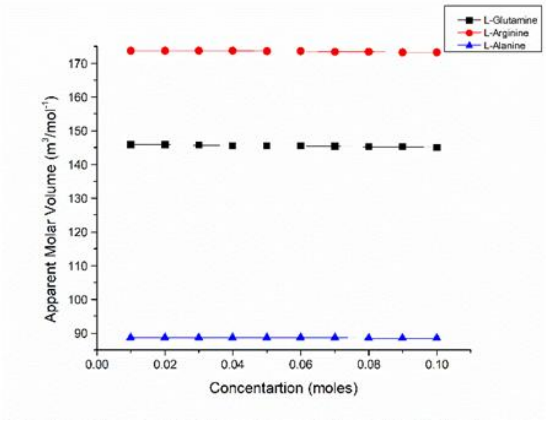

Figure 7: Plot between Apparent Molar Volume and concentration at 308 K.

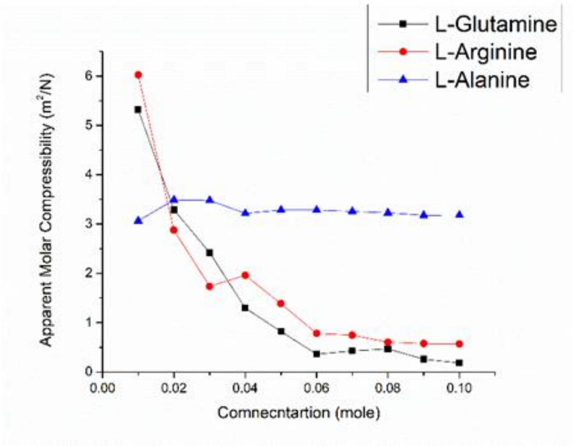

Figure 8: Plot between Apparent Molar Compressibility and concentration at 308 K.

The hydration number values are positive across all systems, which indicates significant solvation of the solutes. This offers further proof of the structural role of solutes and highlights the significant dipolar interactions occurring between amino acids and water molecules. Since the solution is less compressible than the pure solvent, the solutes gain mobility and have a higher probability of interacting with solvent molecules, thereby enhancing solute-solvent interactions. The study also observed that hydration values increase with the concentration of amino acids. This implies that an increase in the number of amino acid molecules enhances the interactions between solute and solvent, resulting in a decrease in electrostriction. This indicates that D-glucose may have a dehydrating impact on the amino acids, potentially by vying for water molecules present in the solution. For all three amino acids, the hydration number increases as the concentration increases [20]. This suggests that more water molecules are associated with each solute molecule at higher concentrations.

Relative Hydration Efficiency: At any given concentration, the order of hydration number is: L-glutamine > L-alanine > L-arginine.

Structural Influence: The differences in hydration numbers likely reflect variations in the molecular structure and the number and type of hydrophilic groups present in each amino acid. L-glutamine, with its amide side chain, can form more hydrogen bonds with water, resulting in higher hydration numbers. L-alanine, with a smaller, less polar side chain, interacts less with water than L-glutamine but more than L-arginine in this context. L-arginine, despite being a basic amino acid, shows the lowest hydration numbers, possibly due to its side chain's specific interaction dynamics with water.

Nonlinear Increase: The increase in hydration number with concentration is nonlinear for L-glutamine and L-alanine, suggesting cooperative or concentration-dependent hydration effects. For L-arginine, the increase is much less pronounced, indicating a weaker or more limited hydration response.

The following observations were made regarding the apparent molar volume (φ_v) and apparent molar compressibility (φ_k) of amino acids in 2% aqueous D-glucose solution, as presented in Table 4.

The apparent molar volume (φ_v) of a solute is defined as the difference in the volume of the solution after the addition of one mole of solute, compared to the volume of the pure solvent. This measurement is important as it reflects the intensity of the interface between the solute and solvent in the solution. [21-23].

For L-alanine, L-arginine, and L-glutamine, their apparent molar volumes (φ_v) were observed to vary linearly with their molar concentrations. See figure 7.

- **Positive Values**: The consistently positive values φ_v indicate strong solute-solvent interactions.
- **Temperature Dependence**: At higher temperatures, φ_v values rise, indicating a stronger attraction between the solute and the solvent, which results in increased solute-solvent interactions.
- **Concentration and Solute-Co-solute Interactions**: While φ_v values remain positive across the entire range of molality and temperature studied, they decrease as the amino acid concentration increases, even as they rise with temperature. This suggests the presence of solute-co-solute interactions that are influenced by temperature (Table 3), possibly due to enhanced solvation at higher temperatures.

The apparent molar volume φ_v values in the present ternary systems are observed to change linearly with the molar concentration of L-alanine, L-arginine, and L-glutamine.

Strong evidence for the presence of deep solute-solvent interactions is provided by the consistently high values of φ_v across the whole temperature and molality range (Table 4). Strong ion-ion interactions can be indicated by a drop in φ_v, even though it is usually positive. On the other hand, a rise in φ_v temperature indicates that the solute has a stronger affinity for the solvent at higher temperatures, which improves solute-solvent interactions [24]. This behaviour could be explained by an intensified solvation phenomenon, especially at high temperatures.

The higher φ_v values for L-arginine suggest it forms a more stable and organized structure within the solutions compared to the other two amino acids, indicating a stronger molecular association.

Apparent Molar Compressibility (φ_k)

Apparent molar compressibility (φ_k) is a key thermodynamic property, derived from ultrasonic velocity and density measurements, used to analyse solute-solvent interactions in solutions. Its behavior offers crucial information about how molecules are arranged and packed together, hydration effects, and intermolecular forces. See figure 8.

The φ_k values are consistently negative across the complete range of amino acid concentrations and temperatures studied. Negative values clarify that solvent molecules surrounding the solute have a lesser compressibility than those in the bulk. These negative values unequivocally indicate strong solute–solvent interactions, including hydrophilic and ionic interactions within the systems. The observed behaviour of φ_k consistently demonstrates a strengthening of these interactions. It is a well-established principle that substances (solutes) that cause electrostriction will reduce the compressibility of a solution. Electrostriction refers to the compression of a solvent (like water) around charged particles due to their strong electric fields. This effect is clearly demonstrated by the negative compressibility values observed for amino acids when dissolved in aqueous D-glucose solutions. Negative values of compressibility clear the overall constriction in solution due to the range of electrostriction or hydrophobic hydration. [25-27]. In essence, negative φ_k values imply strong electrostrictive solvation, where ions effectively compress the solvent structure.

Partial Molar Volume at Infinite Dilution (φ_v^0) and Interaction Parameters

The partial molar volume at infinite dilution (φ_v^0) represents the limiting value of the apparent molar volume as the solute concentration approaches infinite dilution. This parameter is critical for understanding solute-co-solute interactions. The slope (S_v) obtained from the concentration dependence of φ_v^0 indicates the nature of solute-solute interactions, while the intercept, φ_v^0, directly reflects the strength of solute-co-solute interactions at infinite dilution, in the absence of solute-solute interactions.

The viscosity values consistently increase with both the molar concentration of amino acids and with increasing temperature, suggesting an enhancement of solute-solvent interactions that follows the order: arginine > glutamine > alanine. Therefore, the positive values strongly indicate the existence of robust solute-solvent interactions within this system.

Further, electrostriction reduces with the increase in φ_v^0 with a rise in amino acid concentration. This process loosens the grip of water molecules on the ends of the amino acids' zwitterions. As a result, some water molecules are released into the main body of the solution, causing an expansion in overall volume. Additionally, the φ_v^0 values for L-alanine, L-arginine, and L-glutamine in 2% aqueous D-glucose solution across the temperature range of 293.15 K to 313.15 K indicate a discernible increase in solute-solute interactions. Notably, the φ_v^0 values for L-arginine in 2% aqueous D-glucose solution within this temperature range are consistently greater than those for the other two amino acids. This effect might be happening because L-arginine has a longer alkyl chain. This longer chain could make it interact less favourably with the surrounding solvent, which is an aqueous solution of D-glucose. Generally, negative values suggest that the solute-solute interactions are weaker compared to the solute-co-solute interactions. The parameters S_v and φ_k^0 provide comprehensive information regarding solute-solvent and solute-solute interactions, respectively. The values are depicted in Table 4.

As the temperature rises, φ_k^0 values tend to become more negative. This indicates a reduction in electrostriction, meaning the water molecules are less tightly bound around the solutes. Consequently, some water molecules are released into the main body of the solution, making the overall medium more compressible. The relatively small β_s values across all the systems studied suggest that solute-solute interactions are very weak. However, as the concentration increases, the magnitude of different types of interactions also increases. This leads to less negative β_s values for all amino acids in all cases.

Furthermore, it's noted that dehydration of amino acids occurs due to strong interactions between the polar groups of amino acids and water molecules. This process, as explained in reference [28], ultimately reduces the electrostriction of the solvent around the amino acid.

Apparent Molar Compressibility measurements are particularly valuable because they can detect subtle molecular interactions and structural changes in the solvent that may not be readily apparent from other macroscopic properties, such as partial molar volume alone. A lower or decreasing compressibility typically signifies increased molecular association, enhanced electrostriction, or the formation of a more ordered hydration shell, where water molecules are more tightly bound and less compressible around the solute. Conversely, an increasing compressibility can suggest a disruption of the inherent water structure or the formation of less compact aggregates. When solutes cause electrostriction-the compaction of water molecules due to strong electrostatic forces-the solvent becomes less compressible, leading to a decrease in φ_k. Conversely, if solutes disrupt the water's hydrogen bond network, it can lead to a more "open" and thus more compressible structure, increasing φ_k. Stability in the values of L-alanine indicates, a simple structure and consistent hydration number.

Generally, the types of interaction occurring between amino acids and aqueous D-glucose are-

Hydrophilic-Hydrophilic, Hydrophilic-Ionic, Hydrophilic-Hydrophobic, Hydrophobic-Hydrophobic Interactions.

The Falkenhagen (A) and Jones-Dole (B) coefficients provide insight into the nature of solute interactions in solution. The A coefficient reflects solute–solute interactions, while the B coefficient accounts for the size, shape, charge, and structural effects. Table 4 shows that the A coefficient values-both positive and negative-for all amino acids across the entire temperature range in aqueous D-glucose solution indicate the presence of solute–solute interactions. Similarly, the B coefficient values, which are also either positive or negative for all amino acids over the entire temperature range, point to the presence of weak solute–solute and dominant ion–solvent interactions. Specifically, the positive B values for *L-alanine* and *L-arginine* suggest stronger ion–solvent interactions, indicating that these amino acids act as structure makers in solution.

Furthermore, the B coefficient increases with rising concentration of amino acids and temperature, implying that solute–solvent interactions become more prominent compared to other amino acid interactions. This enhancement suggests that increasing the amino acid concentration in aqueous glucose solution contributes to reinforcing the structure of the solvent.

However, a decrease in B values with rising temperature indicates that hydration effects are temperature dependent, weakening at higher temperatures.

Conclusion

The present study systematically elucidates the thermo physical and molecular interaction behaviour of L-alanine, L-arginine, and L-glutamine in 2% aqueous D-glucose solution at varying temperatures (293.15–313.15 K) and concentrations (0.01–0.1 mol kg⁻¹), employing precise ultrasonic, densimetric, and viscometric measurements. Analysis of the derived acoustic and volumetric parameters-such as adiabatic compressibility, apparent and partial molar volumes, and their limiting values-demonstrates a predominance of solute–solvent interactions over solute-solute interactions for all three amino acids. The consistently positive apparent molar volume values (φ_v) for all systems, increasing with temperature, signify intensified solvation and stronger amino acid-glucose-water interactions at elevated temperatures. Apparent molar compressibility (φ_k)), and its decreasing tendency with concentration and increasing temperature, further indicate the formation of more structured hydration shells and enhanced electrostriction around amino acid moieties.

Viscosity data, interpreted using the Jones-Dole equation, yield positive B-coefficients for all amino acids, following the order arginine > glutamine > alanine, underscoring robust structure-making propensities and strong hydrophilic interactions. The moderate decrease in the B-coefficient with temperature rise signals temperature-dependent weakening of hydration effects. The hydration number calculations and observed trends in thermodynamic parameters converge to suggest that the amino acids, especially L-arginine, act as effective structure-makers in the glucose–water solvent matrix, promoting compact and ordered intermolecular associations.

The combined analysis affirms that the investigated ternary systems exhibit pronounced, temperature-enhanced, solute–solvent interactions driven by the amphoteric and hydrophilic nature of the amino acids. These findings are of broad physicochemical and biochemical relevance in understanding the behaviour of amino acids and proteins in carbohydrate-rich, aqueous biological environments, with implications for protein stability, pharmaceutical formulations, and food chemistry.

In summary, ultrasonic, densimetric, and viscometric studies collectively substantiate the efficient structuring role of amino acids in aqueous D-glucose systems. This work provides a robust physicochemical foundation for further probing of bio molecular interactions in complex biological and industrial systems.

References

1. T. Gaudin, P. Rotureau, I. Pezron, G. Fayet, Comput. Theor. Chem., 1101 (2017), 20-29.
2. B. Lu, M. Vayssade, Y. Miao, V. Chagnault, E. Grand, A. Wadouachi, D. Postel, A. Drelich, C. Egles, I. Pezron, Colloids Surf. B: Biointerfaces, 145 (2016), 79-86.
3. K. Thalberg, B. Lindman, in: E. D. Goddard, K. P. Ananthapadmanabhan (Eds.), *"Interactions of Surfactants with Polymers and Proteins"*, CRC Press, Bocca Raton, FL, 1993.
4. C. E. Forney, C. E. Glatz, Biotechnol. Prog. 11 (1995), 260-264.
5. S. K. Singh, A. Kundu, N. Kishore, J. Chem. Thermodyn. 36 (2004), 7-16.
6. T. Cserháti, Environ. Health Perspect. 103 (1995) 358.
7. S. Chauhan, J. Jyoti, G. Kumar, J. Mol. Liq., 159 (2011), 196-200.
8. Z. Yan, X. Wang, R. Xing, J. Wang, J. Chem. Eng. Data, 54 (2009), 1787-1792.
9. R. Curtis, J. Prausnitz, H. Blanch, Biotechnol. Bioeng., 57 (1998), 11–21.
10. M. Singh, M. Pandey, R. K. Yadav, H. Verma, J. Mol. Liq., 135 (2007), 42–45.
11. Gekko, K. J. Biochem. 1981, 90, 1633-1641.
12. Gekko, K. J. Biochem. 1981, 90, 1633-1652.
13. Palecz, B., Piekarski, H. J. Solution chem. 1997, 26, 621-629.
14. S. A. Lippard, J. M. Berg, *"Principles of Bioinorganic Chemistry"*, University Science. Books, Mill Valley, CA, 1994.
15. Z. Yan, X. Wang, R. Xing, J. Wang, J. Chem. Eng. Data, 54 (2009), 1787-1792.
16. Bhat, R. and J. C. Abluwalia, 1985. *"Partial molar heat capacities and volumes of transfer of some amino acids and peptides from water to aqueous sodium chloride solutions at 298.15 K"*, J. Phys. Chem, 89: 1099-1105.
17. Chauhan, M. S., K. Sharma and G. Kumar, 2002. *"Transport studies of ion-solvent interactions in acetonitrile-rich regions of benzene and ethanol"*, Ind. J. Chem, 40; 481-483.
18. Jones, G. and M. Dole. 1929. *"The viscosity of aqueous solutions of strong electrolytes with special reference to barium chloride"*, J. Am. Chem. Soc., 51; 2950-2964.
19. Chauhan, S., Singh, K., Kumar, K., Neelakantan, S. C., Kumar, G.: *"Drug-amino acid interactions in aqueous medium: volumetric, compressibility, and viscometric studies"*, J. Chem. Eng. Data, 61, 788-796 (2016).
20. A. Buranwoski, J. Glinski, *"Hydration Numbers of Nonelectrolytes from Acoustic Methods"*, Chem. Rev. 2012, 112, 4, 2059–2081.
21. D. Brahman, B. Sinha, *"Partial molar volumes and viscosity B-coefficients of N, N'-ethylene bis (salicylideneiminato) cobalt (II) in binary mixtures of 1,4-dioxane+methanol at T= (298.15, 303.15, 308.15, and 313.15) K"*, J. Chem. Eng. Data 56 (2011) 3073–3082.
22. J. Krakowiak, *"Apparent molar volumes and compressibilities of tetrabutyl-ammonium bromide in organic solvents"*, J. Chem. Thermodyn. 43 (2011) 882–894.
23. D. Brahman, B. Sinha, *"Partial molar volumes and viscosity B-coefficients for N, N/-ethylene bis(salicylideneiminato)-diaquochromium(III) chloride in methanolic solutions of 1-butyl-2,3 dimethylimidazolium tetrafluoroborate at T=*

(298.15, 308.15, and 318.15) K", J. Chem. Thermodyn, 68 (2014) 260–269.

24. H. Kumar, I. Behal, M. Singla, J. Chem. Thermodyn, 95 (2016) 1-14.
25. A. K. Nain, M. Lather, J. Chem. Thermodyn., 2016, 102, 22 38, doi: 10.1016/j.jct.2016.06.030.
26. M. A. Jamal, B. Naseem, S. Naaz, I. Arif, M. Saeed, S. Atiq, *"Thermo-acoustic properties of maltose in aqueous amino acids system"*, Journal of Molecular Liquids, 309, 112932 (2020).
27. Mohd. R. and E. Verrall, *"Apparent molar volume and adiabatic compressibility studies of aqueous solutions of some drug compounds at 25°C",* Can. J. Chem. 67, 727 (1989).
28. Prakash S., F. M. Ichhaporia and J. D. Panday, 1964, *"Standard study of complex Barium citrate by Ultrasonic waves"*, J. Phys., Chem. USA 58:3078.