CHAPTER 1

INTRODUCTION

1.1 GENERAL

Proteins are very large molecules and besides water, protein forms the largest portion of our body weight. In order to understand the role played by the biological molecules in the living organism, it is necessary to study the interactions of proteins with their surrounding environment. These interactions are mainly those between the protein molecules and ions present in biological fluids. 3.9% of body weight comes from elements present in the form of salts. They are very important for the maintenance of homeostasis (meaning well balanced organism). Since proteins are complex molecules of linked amino acids, amino acids have been quite useful as model for understanding the thermodynamic behaviour of proteins in solution. Amino acids are considered the building blocks that comprise protein. Protein cannot exist without the correct combination of amino acids. The processes of assembling amino acids to make proteins and of breaking down proteins into individual amino acids for the body’s use are continuous ones.

Amino acids are the fundamental, structural units of proteins, peptides and certain types of hormones and antibiotics participate in all the physiological processes of a living cell. These organic compounds are not components of living organisms but they affect the cellular fluid when used in the form of cosmetics or medicine (Wusteman et al 1996, Hotamisligil et al 1996). Therefore, many physical and chemical studies have been done to
elucidate interaction mechanisms between amino acids and organic compounds in cell fluids or compounds with the same functional groups, as those exists in biomolecules of living organisms (Abu-Hamdiyyah and Shehabuddin 1982). Generally, amino acids and peptides can serve as useful models in estimating the properties of proteins and such approach is widely used in recent years (Kharakoz 1997, Hackel et al 1999, Hackel et al 2000).

Amino acids possess two characteristic functional groups, the amino group NH$_2$ and the carboxylic group COOH and in aqueous solution they are zwitterions. The electrostatic field of zwitterions have a tendency to produce structural changes in the solution as it influences considerable structural arrangement of molecules of solvent. This in turn has pronounced effect on compressibility of the system. Thus compressibility and related parameters provide significant information regarding the state of affairs taking place in the solution on the background of ion-solvent interactions.

The study of some of the thermodynamic properties of proteins can be facilitated by investigating the behaviour of their constituents viz., amino acids and peptides. Some of the properties are found to be implicate in several biochemical processes such as protein hydration, aggregation, denaturation and antigen-antibody reactions (Ling 1972, Bull and Breese 1968, Franks 1979, Cassell and Christensen 1967, Hakin et al 1994 a, Simpson and Kauzmann 1953, Bendzko et al 1988, Hedwig and Hoiland 1994, Lauffer 1975).

Hydration of proteins plays an important role in the stability, dynamic, structural characteristic and fundamental activities of biomolecules. Considerable studies have been carried out to investigate hydration of proteins through volumetric and ultrasonic measurements during the last two decades. It is necessary to study both the native and denatured state of protein to understand the role of hydration in protein folding/unfolding transition.
Hydration of proteins can be investigated through volumetric and ultrasonic measurements, since these properties are sensitive to the degree and nature of hydration (Rohanker and Anwar 2002).

By denaturation one means that class of reactions which leads to changes in structure of the macromolecule with no change in molecular weight (Rice et al 1958). During the denaturation process, various structural changes occur in protein solutions. The knowledge of solute-solvent and solute-solute interactions in various solvents is prerequisite to understand the process of denaturation. The majority of protein exists in aqueous mixed solvents containing many organic substances (Ren et al 2000). They are all very important organic synthesis materials, applied in the field of medicine, pesticides and polymer chemistry.

Electrolytes have significant roles in different branches of science and engineering such as environment, chemistry and biology and hence thermodynamic and transport properties of electrolyte solutions are of interest. Thermodynamic properties are generally used to explain solute-solvent and solute-solute interactions in the solution phase.

‘Salting in’, an increase in protein solubility upon the addition of salt, appears to occur when ions bind to proteins and increase their net charge. ‘Salting out’ appears to result from interfacial effects of strongly hydrated anions near the surface of proteins. Na\(^+\) and F\(^-\) are classified as water structure makers and K\(^+\) is described as water structure breaker by Collins (2004). It is found that the radius of ions used in this study are Na\(^+\) = 0.102 pm, K\(^+\) = 0.138 pm and F\(^-\) = 0.133 pm (Marcus 1993). Sharma and Ahluwalia (1973) have observed increasing structure making order for larger cations, when the anion is either chloride or fluoride and of reverse order with bromide or iodide as anion. These results are explained by the concept of ‘water structured enforced ion-pairing’ by large cations and anions.
The effectiveness of various salts towards the destabilizing tendency of proteins is known as Hofmeister series. The ability of salt out of protein of various cations and anions follow the order:

Cations : \( \text{NH}_4^+ > \text{K}^+ > \text{Na}^+ > \text{Mg}^{++} > \text{Ca}^{++} > \text{Gdn}^+ \)

Anions : \( \text{SO}_4^{--} > \text{HPO}_4^{--} > \text{acetate} > \text{citrate} > \text{tartrate} > \text{Cl}^- > \text{NO}_3^- > \text{ClO}_3^- > \text{I}^- > \text{ClO}_4^- > \text{SCN}^- \)

It is observed (Arakawa et al 1990) that salting in agents work as good denaturants and salting out agents as good stabilizers of protein structure.

Volumetric, ultrasonic and viscometric studies of these model compounds in aqueous medium of electrolytes provide information about solute-solvent and solute-solute interactions that can be of great help in understanding the effect of these salts on biomolecules (Yan et al 1998, Castronuovo et al 1999, Kumar 1999, Rohankar and Aswar 2001).

Volumetric properties of solutes such as the partial molar volume, compressibility and expansibility, are known to be sensitive to the degree and nature of solute hydration (Saravazyan 1991). Shahidi and Farrell (1978) have reported the partial molar volumes of \( \alpha, \omega \)-amino carboxylic acids at 298.15 K. They observed an apparent decrease in the overall volume of the water caused by solute-solvent interactions associated with the independent hydration of the charged end groups. Such a contraction of water in the vicinity of charged groups due to solute-solvent interactions is called electrostriction.

The important properties like enthalpy, entropy and Gibbs energy represent the macroscopic state of system at the given temperature and pressure. It is difficult to interpret these properties in terms of molecular
phenomena. Hence higher derivatives of these properties are effectively used in terms of molecular interactions. The partial molar volumes, which are the first derivative of Gibbs energy with respect to pressure and the compressibility property, which is the second derivative of the Gibbs energy, are sensitive indicators of molecular interactions. The different molecular processes such as electrostriction, hydrophobic hydration and cosphere overlap during interactions are obtained using partial molar volumes (Gurney 1954).


Density, apparent molar volume, and viscosity of bovine serum albumin, egg albumin, and lysozyme in aqueous RbI and CsI, and (dodecyl)(trimethyl)ammonium bromide solutions have been obtained by Singh et al (2005). The experimental data have been regressed against composition, and constants are used to elucidate the conformational changes in protein molecules. Various monovalent salts either inhibit or stimulate specific bindings of human follitropin. Andersen and Reichert (1982) have analyzed the effect of monovalent and divalent cations in follitropin binding.

One of the fascinating problems of mixed solvent systems is that of the consequences of intermolecular interactions. This is of particular significance, owing to the practical applications of mixed solvent systems for the study of various physico-chemical investigations. Ultrasonic velocity studies along with the density studies play a vital role in the investigation of intermolecular interactions in mixed solvent systems (Syal et al 1996). Due to low cost, easy operational procedure and spontaneous results, the molecular
interaction studies through ultrasonics have gained importance all over the world (Raj et al 2007). The adiabatic compressibility data show a strong correlation with hydrational behaviour of the solute, such as shape and size branching (Iqbal and Verrall 1989).

Ultrasonic velocity measurement is a reliable procedure that allows a quick and easy determination of solvent concentrations in the micelle structures that appear in oil technology, as well as a theoretical analysis to understand the solvation process (González et al 2006). Ultrasound velocity, volume and compressibility changes due to ionisation of amino and carboxyl groups in amino acids solutions. The mutual influences of the amino and carboxyl groups on the hydrational volume and compressibility have been estimated quantitatively by Chalikian et al (1992) for 12 amino acids over a wide pH range. They reported abnormal reverse sign of the compressibility change during ionization of the amino group in the amino acid skeleton and they questioned about the reliability of a previously published method of separation of the individual partial compressibilities of oppositely charged ions.

Compressibility of liquids is an essential physical characteristic reflecting intermolecular interactions and dynamic processes occurring in solution. There are three terms contributing to the overall partial compressibility of proteins in solution (i) intrinsic, from the residue-residue interaction in the globule interior, (ii) relaxational, from the structural transformations accompanied by volume changes and (iii) hydrational, from surface atomic group-water interaction. To derive the contribution from all kinds of interactions occurring in the solution, a systematic investigation of the partial compressibilities of molecules of different structure and complexity, from small to large ones, in diluted aqueous solutions is necessary. In particular, the hydrational part is the most important one and
should be quantitatively investigated. Kharakoz (1991) has reported partial adiabatic compressibilities of 21 amino acids in diluted aqueous solutions over the temperature range 15-70°C. Partial compressibilities of atomic groups have been determined as functions of temperature and interpreted in terms of hydration and intramolecular interactions between different parts of a molecule.

Ultrasonic studies in aqueous solutions of electrolytes and non-electrolytes are very useful in elucidating the nature of molecular interaction and hydration. Ultrasonic velocity studies in aqueous solutions of DNA, glycine and L-proline have been reported for various concentrations at 30°C, 40°C, 50°C and 60°C by Nambinarayanan and Rao (1989). The results have been interpreted in terms of the effect of thermal energy on the structure of DNA and structure breaking properties of the solutes.

Tikhonov et al (1995) have described a method for evaluating the thermodynamic characteristics both of pure liquids and of solutes in solutions using data derived from ultrasonic velocity measurements. The principal possibility of using ultrasound velocity lies in the fact that the velocity of ultrasound is a simple function of the adiabatic compressibility. The problem has been formulated as an initial value problem for the parabolic type differential equations in partial derivatives. The validity of the method has been demonstrated by calculation of the thermodynamic parameters for water, glycine and alanine in aqueous solutions at infinite dilution.

Viscosity and its derived parameters provide valuable information regarding the shapes and size of the molecules (Stokes and Mills 1965). The study of viscous behaviour of macromolecules in solution is important to understand the mechanism of transport processes. Viscosity B coefficients are known to provide information regarding the hydration of the solutes and their
effects on the structure of the solvent in the near environment of the solute molecules (Iqbal and Chaudhry 2009).

Thermodynamic properties such as activity coefficients for the water + biochemical systems are indispensable to design efficient separation and purification processes and drying processes in food engineering as well. These properties are also useful for studying solution chemistry and conformation of both native and denatured proteins. The number of measurements available in literature are only few in the case of L-form of amino acids (Kuramochi et al 1997).

1.2 THERMODYNAMIC STUDY OF AMINO ACIDS IN AQUEOUS SOLUTIONS

The specific interactions of water with various functional groups on the proteins as well as other solvent-related effects contribute to the formulation of the stable folded structure of proteins in solutions (Hvidt and Westh 1998). The direct study of these protein-water, protein-ion and protein-alkyl group interactions is difficult because of the complexity of these interactions in a protein macromolecule. However, one useful approach is to study these interactions with smaller constituents (amino acids) of the polymeric proteins.

The amino acids in aqueous solutions are useful model for understanding the thermodynamic behaviour of proteins, especially in determining the apolar group contributions to the biopolymers (Kauzmann 1959). The relative stability of the structure of viruses, DNA and globular proteins depend upon the molecular structure of water associated with them (Tanford 1962). In aqueous medium, amino acids exist as dipolar ions (zwitterions) at pH = 7 manifesting a unique hydration behaviour which
appears to be subtly linked to the vital biological phenomenon (Iqbal and Ahmed 1993).

Apparent molal volumes ($V_\text{m}$) of some amino acids have been obtained from precise density measurements by Wadi et al (1990) over the temperature range 288.15-308.15 K and accounted the strength of the solute-solute interactions with the corresponding values of their derivatives. Cibulka et al (2010) reported density data at different temperatures (298 to 443) K and pressures (15 to 17 and 30) MPa for dilute aqueous solutions of glycine and L-alanine and evaluated partial molar volumes at infinite dilution. They developed an equation of state for standard molar thermodynamic properties of the aqueous amino acids.

The volumetric and thermochemical properties of aqueous amino acid systems have been studied by several authors. Although there is a wide selection of volumetric data as a function of temperature at ambient pressure, heat capacity data at temperatures other than 298.15K are extremely limited. Hakin et al (1997) have reported relative densities and heat capacity ratios of L-arginine, L-protine and DL-methionine in water at 288.15, 298.15, 313.15 and 328.15K. Uncertainties in apparent molar volumes and heat capacities are also calculated by the authors. Jin and Chao (1992) have reported solubility for L-serine, D-serine, DL-proline and DL-arginine in water at 25-60°C. Partial molar volumes of ten amino acids in water, have been reported from density measurements made at 35°C by Iqbal and Ahmed (1993). Furthermore, partial molar volumes of some $\alpha$-amino acids are estimated by Rao et al (1984) using empirical models and compared with experimental values. Aswar (1998 a) has obtained apparent molal volumes and apparent molal compressibilities of lysine and lysine-adenosine mixture in aqueous solution at 15, 20 and 25°C and concluded that lysine and adenosine behave as water structure breakers.
During the last two decades, considerable studies have been carried out on the partial molal volumes of amino acids in aqueous solutions. In fact, Romero and Munar (1998), Singh et al (2004), Pal and Kumar (2005a,b) and many other researchers investigated the molal volumes of amino acids. However only few have studied the compressibility of amino acids in aqueous solutions (Cabani et al 1981, Chalikian et al 1993, Kharakoz 1991) and hence the amount of available compressibility data for amino acids is much less compared with volume data, although the compressibility seems to sense the solute hydration structure at a greater distance from the solute than does the volume. Also compressibility is a powerful thermodynamic parameter for elucidating the behaviour of a solute in a solvent (Wadi and Ramasami 1997).

Chalikian et al (1993) determined the apparent molar volumes, expansibilities and adiabatic compressibilities of a homologous series of $\alpha,\omega$-aminocarboxylic acids within the temperature range 18-55°C. The temperature dependence of both the density and the coefficient of adiabatic compressibility are evaluated and interpreted in terms of hydrophobically and electrostatically perturbed solvent domains in the hydration shells of the aliphatic and charged atomic groups.

Apparent molal compressibility and adiabatic compressibility of aqueous glycine, glycolamide, $\alpha$-alanine, $\beta$-alanine and lactamide are determined at 25°C by Gucker et al (1950). The apparent molal volumes and adiabatic compressibilities of 15 amino acids in water are reported by Millero et al (1978) at 25°C from precise density and sound measurements and discussed the data in terms of hydration effect.

Ultrasonic velocities of acetamide, dimethyl urea and $\beta$-alanine in aqueous solutions at different concentrations in the temperature range of about 60°C to 80°C are presented by Muralikrishna et al (1979). The
temperature corresponding to velocity maximum (TVM) at different concentrations have been evaluated and the results are discussed in the light of the structure breaking property of these substances in water.

Several workers have reported viscosity data on amino acids in aqueous and in mixed solvents (Mason et al 1952, Sandhu and Kashyap 1986, Pal and Kumar 2004, Belibagli and Agranci 1990).

The first derivative of viscosity B coefficient over temperature (dB/dT) provides the information regarding the structure making / breaking ability of the solute (Jenkins and Marcus 1995, Sharma and Ahluwalia 1973). Sandhu and Singh (1988) observed positive dB/dT values for L-proline and L-hydroxyproline implying structure breaking property. Alanine is considered as kosmotrope (structure maker) due to its negative dB/dT values in pure water (Dey et al 1980). Awasthi and Rastogi (1980) have reported positive dB/dT values for DL-aspartic acid and DL-glutamic acid and classified these amino acids as chaotrope (structure breaker).

1.3 THERMODYNAMIC STUDY OF ELECTROLYTES IN AQUEOUS / NON AQUEOUS / MIXED SOLVENTS

Mixed aqueous solvents are used extensively in chemistry and other fields to control factors like stability, reactivity and solubility of system (Wadi and Ramasami 1997, Banipal and Sehgal 1995). The importance of solvent effects on the nature of solute solvent and hydrophobic interactions and the conformation properties of proteins and related biomolecules has been extensively examined in aqueous, nonaqueous and mixed solvent.

Liquid water has been known to posses distinctive structural features which are roughly describable by the statement that it remains a certain degree of similarity or analogy to ice. The amount of this ‘ice-
likeness’ may be altered by changes in temperature and pressure and also by the presence of ionic solutes (Frank and Wen 1957).

Ali and Nain (1994) have estimated thermodynamic parameters of sodium chloride in aqueous dimethylformamide solutions and interpreted the results in terms of ion – solvent interactions. The apparent molar volumes and viscosities of lithium chloride, sodium chloride, and potassium chloride, have been determined in a 40 mass % tetrahydrofuran + water mixture at 303, 308, 313, and 318 K by Roy et al (2001). The data are related to ion-solvent, ion-ion interactions and structure making / breaking capacities of the electrolytes.

Roy et al (2004) have calculated the apparent molar volumes, compressibilities and viscosity B coefficients of several nitrate compounds in water at the temperatures (303, 308, 313, 318, and 323) K and the results are used to account ion-solvent, ion-ion interactions and electrostriction of the solvent molecules around the metal ions.

Apparent molar volumes, expansibilities, and isentropic compressibilities of sodium bromide, sodium perchlorate, sodium tetraphenylborate, and tetraphenylphosphonium bromide in methanol at the temperatures ranging from 283.15 to 313.15 K have been reported by Wawer et al (2008). Division into the ionic contributions has been proposed on the basis of the reference electrolyte method and they suggested the existence of the high-volume intermediate shell with an enhanced structure in these systems.

Qiblawey and Abu-Jdayil (2010) have reported the viscosities and densities of ternary systems of MgCl$_2$–NaCl–water in the range of (298.15 to 318.15) K at 5 K intervals and up to 6 mol·kg$^{-1}$. The experimental viscosity data have been satisfactorily correlated as a function of concentration using the extended Jones–Dole equation. The optimized parameters show that the
presence of MgCl$_2$ had a prevailing effect on the viscosity of the ternary solutions rather than NaCl.

Apparent molar volumes, limiting partial molar volume, and relative viscosity have been obtained by Samanta and Ray (2010) from the density and viscosity data of urea in aqueous glucose solutions measured at $T = (298.15, 303.15, 308.15,$ and $313.15) \text{ K}$ and the result shows that the solute acts as water structure breaker and possess weak solute–solvent interaction. Savaroglu and Ozdemir (2008) have reported apparent molar volumes, isentropic compressibilities and apparent molar isentropic compressibilities of water + fructose + glycerol at different temperatures and the results are discussed in the light of solute–solvent and solute–solute interactions.

Apparent molar volumes for MgSO$_4$, CuSO$_4$, Na$_2$SO$_4$, NaCl, MgCl$_2$, and CuCl$_2$ and viscosity B-coefficients for MgSO$_4$/CuSO$_4$ in sucrose + water solutions are determined from density and viscosity measurements at 298.15 K by Zhuo et al (2008). The results show that the values of standard transfer volumes, viscosity B-coefficients, and free energy of activation per mole of the solute are positive and increase usually with increasing sucrose content.

Roy et al (2010) have calculated apparent molar volumes and viscosity B-coefficients for D-glucose, D-mannose, and D-sucrose in (0.001, 0.003, and 0.005) mol·kg$^{-1}$ aqueous cetrimonium bromide (N-cetyl-N, N, N-trimethyl ammonium bromide) (C$_{19}$H$_{42}$BrN) solutions from solution density, and viscosity, measurements at (298.15, 308.15, and 318.15) K as a function of the concentration of carbohydrates. The data on limiting apparent molar volume viscosity A and B coefficients are related in terms of solute–solute and solute–solvent interactions in the mixed solutions.
Viscosity and density of MgCl$_2$, NH$_4$Cl, CuCl$_2$, and AlCl$_3$ in methanol and in water have been measured at the temperatures (303.15, 308.15 and 313.15) K and atmospheric pressure by Huque et al (2006). Apparent specific volume, B-coefficient of Jones–Dole equation, activation enthalpy and entropy are calculated. From the results, structure intensifying and destroying properties of electrolytes are discussed.

The densities of tetraalkylammonium perchlorates and ammonium perchlorate solutions in N, N - dimethylacetamide, dimethyl sulfoxide, and triethylphosphate have been reported (Krakowiak et al 2001) over the whole composition range at T = 298.15 K. From these densities, apparent and limiting partial molar volumes of the electrolytes and ions have been evaluated and discussed in terms of interactions of solute-solvent interactions.

Densities at T = (293.15, 298.15, 303.15, 313.15, 323.15 and 333.15) K and sound velocities at T = 298.15 K of tetraphenylphosphonium bromide, sodium tetraphenylborate, sodium bromide, and sodium perchlorate in dimethylsulfoxide have been measured by Warmińska and Grzybkowski (2010) over the composition range from (0 to 0.3) mol · kg$^{-1}$. The results have been discussed in terms of employing tetraphenylphosphonium tetraphenylborate as a reference electrolyte in splitting the limiting apparent molar volumes and apparent molar isentropic compressibilities into ionic contributions.

1.4 THERMODYNAMIC STUDY OF AMINO ACIDS IN AQUEOUS ELECTROLYTES / NON AQUEOUS / MIXED SOLUTIONS

In biological fluids of living organisms there are specified quantity of ions, especially sodium, potassium and chloride ions, which are indispensible for the metabolic process of living organisms to proceed. The property of electrolytes known as structure-maker or structure breaker has been widely
used to understand the effect of electrolytes on the structure and function of both proteins and nucleic acids (Makhatadze and Privalov 1992, Kauzmann et al 1962, Sharp and Honig 1995, Kumar 1995).

In physiological media such as blood, membrane, cellular fluids etc. the dipolar character of amino acids in presence of ions such as Na+, K+, Mg2+, Cl- etc. dissolved in body water has an important bearing on their biological functions. Therefore, knowledge of water-amino acids interaction and the effect of inorganic ions on such interactions are necessary to understand several biological processes occurring in living organisms (Moision and Armentrout 2002).

Study of the interactions of ions and biomolecules provide important information about physiological systems and can be used in the separation and purification processes for biomaterials. Salt-induced electrostatic forces are known to play a role in modifying the protein structure by affecting the properties like solubility, denaturation and activity of enzymes. Remarkable experimental work has been reported on thermodynamics of amino acids in aqueous alkali metal salts (Badarayani and Kumar 2002, Shen et al 2000, Basumallick et al 1986, Sote et al 1998).

The interactions of a set of six amino acids in aqueous alkali-chloride have been studied by Ogawa et al (1984b) at 25°C. The limiting values $V_\phi^0$, $K_\psi^0$ and the extended Jones-Dole viscosity B and D coefficients are calculated by a linear extrapolation using the least squares method. The result has been discussed in terms of the dehydration effect of the electrolytes upon the amino acids.

Apparent molal volumes, apparent molal adiabatic compressibilities and hydration numbers of glycine, DL-alanine, and DL-α-amino-n-butyric acid are determined at 298.15K in water and in aqueous LiCl, KCl, CsCl, KBr and
KI solutions by Basumallick et al (1986). Changes in salt concentration appear to prominently affect transfer functions but not those due to the variation of cationic or anionic size.

Wadi and Goyal (1992b) have reported densities and viscosities as functions of electrolyte concentration (1, 3 and 5M) and amino acid (upto 0.5 mol·kg$^{-1}$) concentrations for water + potassium thiocyanate + amino acid (seven) systems at 288.15, 298.15 and 308.15K. Free energies of activation have been obtained by application of the transition-state theory to the B coefficient data. The result showed that the flow process is accompanied by zwitterions-solvent and zwitterion-ion (potassium thiocyanate) bond breaking in addition to ion solvent and solvent-solvent bond making.

Partial molal volume, partial molal adiabatic compressibility and their variations with temperature are reported by Wadi and Ramasami (1997) for glycine and DL-alanine from water to aqueous sodium sulfate at 288.15, 298.15 and 308.15K. The data are interpreted in terms of the hydration of the hydrophobic and hydrophilic parts of the amino acids.

Tabhane et al (1999) have measured ultrasonic velocities, densities and viscosities in the aqueous solution of L-cysteine and L-tyrosine with NaOH at different molar concentrations at 303.15K. The variation of ultrasonic velocity and other related thermoacoustical parameters with molar concentration have been found nonlinear. This nonlinearity confirms the presence of solute-solvent, ion-ion, dipole-dipole, ion-solvent interactions. They observed molecular interaction, complex formation and hydrogen bond formation are responsible for the heteromolecular interaction in liquid mixture.

Yan et al (2001) reported the densities and viscosities of aqueous solutions of α-amino acids (glycine, DL-alanine, DL- amino-n-butyric acid,
DL-valine and DL-leucine) with sodium butyrate as a function of concentrations of amino acid and electrolyte at 298.15K. These data are used to calculate several thermodynamic parameters and the results are discussed in terms of interaction between amino acids with sodium butyrate.

Rohankar and Aswar (2001, 2002) calculated apparent molar volume and apparent molar compressibility of glycine in aqueous nickel sulphate and aqueous vanadyl sulphate solutions at 298.15, 303.15 and 308.15K. They have also determined the limiting apparent molar volume of transfer ($\Delta V^0_{i,j}$) for different values of salt concentrations. It is reported in both cases the $\Delta V^0_{i,j}$ values are negative for 0.1 and 0.05M salts and positive for 0.01M salts. The negative volume transfer is due to the increased electrostriction of the solvent by glycine.

Wang et al (2005) have determined the enthalpies of dilution of glycine, L-alanine and L-serine in aqueous potassium chloride solutions of various molalities. It is found that pairwise enthalpic interaction coefficients of glycine and L-serine are all negative and become less negative with increasing of the molalities of potassium chloride, while pairwise enthalpic interaction coefficients of L-alanine are positive on which the influence of potassium chloride is not obvious. The results have been interpreted from the point of view of solute–solute interactions involved by solvent effects.

Riyazuddeen and Khan (2008, 2009) have carried out isentropic compressibility and viscosity studies of L-alanine, L-proline, L-valine, L-leucine in aqueous KCl/KNO$_3$ solutions at 298.15, 303.15, 308.15, 313.15, 318.15 and 323.15 K. The trends in the behaviour of compressibility and viscosity parameters with changes in the concentration of amino acids/zwiterions as well as in temperature have been discussed in terms of zwitterions–ions, zwitterions–water dipoles, ions–ions, ions–water dipoles intermolecular/interionic interactions operative in the systems.
From densities and ultrasonic speeds, compressibility ($\beta_s$), acoustic impedance ($Z$) hydration number ($n_H$) apparent molar volume ($V_{\phi}$), apparent molar compressibility ($K_\phi$) partial molar volume ($V_{\phi}^o$) and partial molar compressibility ($K_\phi^o$) at infinite dilution are calculated by Ali et al (2003) for glycine + NaCl + water and glycine + MgCl$_2$ + water ternary systems at 303.15 K. The result shows that dipole-dipole and ion-solvent interactions are strong in glycine-aqueous NaCl and MgCl$_2$ solutions.

Venkatesu et al (2007) have presented the data on density of glycine, diglycine, triglycine, tetruglycine and cyclic glycyglycine in aqueous and in aqueous electrolyte solutions of potassium chloride, potassium bromide and potassium acetate at $T = 298.15$ K under atmospheric pressure. The density increments resulting from the addition of the different model compounds of amino acids and the ionic salts have been investigated.

Ultrasonic velocities, densities and viscosities of L-phenylalanine, L-leucine, L-glutamic acid, and L-proline + 2 mol·L$^{-1}$ aqueous NaCl and 2 mol·L$^{-1}$ aqueous NaNO$_3$ solutions have been measured for several molal concentrations of amino acids at different temperatures from $T = (298.15$ to $328.15)$ K by Riyazuddeen and Afrin (2010a, 2010b). The trends of variation of compressibility and viscosity with the variation in molal concentration of amino acids as well as with temperature have been discussed in terms of various interactions operative in solutions.

Denaturating agents affect the structural changes in the proteins (Arumugam et al 1995). Urea is one of the most widely used denaturants. It is efficient at relatively high concentration. Even at high concentration many proteins are not completely unfolded. The variation in velocity in urea gelatine shows minimum change beyond 4M concentration. It was also shown that the free length and adiabatic compressibility were changed minimum with the increase in concentration.

Ogawa et al (1984 a) have determined apparent molal volumes and apparent molal adiabatic compressibilities for glycine, L-alanine, \( \beta \)-alanine, \( \alpha \)-aminoisobutyric acid, L-valine, L-serine and L-threonine in water and in urea-water mixtures at 25°C. It has been reported that the magnitudes of the transfer functions increase continuously with urea concentration. The same trend was observed by Enea and Jolicoeur (1982) for the transfer functions of the heat capacities and volumes of three amino acids (Gly, Ala and Ser) and several oligopeptides in urea-water systems.

Viscometric and volumetric studies of some transition metal chlorides in aqueous glycine solution have been reported by Mishra and Gautam (2001). They conclude all the electrolytes behave as structure makers. Densities and viscosities of L-proline and L-glutamine in aqueous metal electrolytes solutions of Cu (II) nitrate and Ni (II) chloride have been determined at 308.15 K by Akhtar (2007) and the results are discussed in terms of the dehydration effect of the electrolyte upon the amino acids.

Metal ions like Na (I), K (I), Ca (II) and Mg (II) are present in the body in trace concentrations. Nucleotides and nucleic acids generally occur as complex coordinated with metal ions. These complexes are of importance for the biological action of nucleotides, nucleic acids, co-enzymes and nucleoside and triphosphates. Aswar (1998 b) has carried out ultrasonic, volumetric,
refractive index and ultraviolet studies of lysine, lysine-adenosine in aqueous solutions in the presence of Mg (II) ion at 298K. It has been reported that the hydrogen bonding interactions increases between the lysine molecules and adenosine due to strong solute - solvent interaction.

Apparent molar volumes and viscosity B-coefficients of some saccharides in aqueous glycine and in aqueous L-alanine solutions have been reported at 298.15 K. by Zhuo et al (2006) and the results are discussed in terms of the structural interaction model and the stereo structure of monosaccharide molecules.

Pal and Kumar (2005b) have calculated several thermodynamical parameters from density and viscosity data of glycine in aqueous sucrose solutions ranging from 5 to 25 mass% of sucrose at 288.15, 298.15 and 308.15K and discussed the nature of interactions present in these systems. Zhao et al (2005) have determined the standard-state partial molar volume, hydration number and viscosity B-coefficients of arginine in (glucose + water), (sucrose + water) and (L-ascorbic acid + water) mixed solvents at T = 298.15 K. The results indicate that the hydration number of arginine decreases owing to the interaction of sugar or L-ascorbic acid and the zwitterionic groups.

Banipal et al (2002) have reported partial molar volumes and volumes of transfer at infinite dilution of glycine, DL-alanine DL- amino-n-butyric acid and L-leucine in using density measurements in aqueous 1, 2 propanadiol and using viscosity data, B coefficients are calculated at 298.15K. Results showed that in the case of glycine and DL-alanine, the ion-dipolar interactions are dominating while hydrophobic-hydrophobic and hydrophilic - hydrophobic interactions are predominant in other cases.

Ali et al (2007 a) have measured the densities and viscosities for binary mixtures of 0.01 M aqueous tetramethylammonium bromide (TMAB)
and tetraethylammonium bromide (TEAB) and ternary mixtures of glycine, DL-alanine and DL-valine (0.01 to 0.05 M) in 0.01 M-aqueous tetra-n-alkylammonium bromides at T = (298.15, 303.15, 308.15, and 313.15) K. Using densities and viscosities, they have determined various thermodynamical parameters and interpreted the results in terms of structural influence of the quaternary ammonium salts upon solvent.

Nain and Chand (2009) have analysed the volumetric, ultrasonic, and viscometric behaviour of glycine, DL-alanine, and L-valine in aqueous 1, 4-butanediol solutions at different temperatures. It has been observed that there exist strong solute–solvent interactions in these systems, which increase with rise in temperature.

Sinha et al (2007) have reported apparent molar volumes and viscosity B-coefficients of glycine, L-alanine, and L-valine in 0.05, 0.10, and 0.15 mol·dm$^{-3}$ aqueous tetramethylammonium iodide solutions at 298.15 K from density and viscosity measurements. It has been found that the partial molar volume and viscosity B-coefficient varies linearly with the number of carbon atoms in the alkyl chain of the amino acids which are related to ion–dipolar, hydrophobic–hydrophobic, and hydrophilic–hydrophobic group interactions.

It is evident from literature that similar studies of amino acids on mixed solvents have been reported by many other researchers (Shekaari and Jebali 2010, Palecz and Nadolna 2006, Harutyunyan et al 2010, Singh et al 2010 and Liu et al 2010).

1.5 **OBJECTIVE OF THE PRESENT THESIS**

Volumetric, ultrasonic and viscometric studies of amino acids in aqueous solutions of electrolytes and nonelectrolytes provide useful tool in understanding the physico-chemical properties of the interacting components.
The molecular interactions are generally weak and hence spectroscopic probe has major difficulties in monitoring molecular interactions. Therefore in order to understand the effects of ionic species on amino acids, the thermodynamic, volumetric, compressibility and transport properties of ions-amino acids are investigated (Jayabalakrishnan 2009).

On going through literature it is observed that no report of amino acids has been found in the presence of sodium/potassium fluoride and sodium/potassium carbonate at the studied temperatures except a report on volumetric properties of glycylglycine in aqueous sodium fluoride solutions. Sodium fluoride is colourless crystalline salt and is used in the treatment of tooth decay. Potassium fluoride on the other hand, is used in the excretion of urea to maintain proper health (Waddell 1884). Sodium carbonate is used in tooth paste, where it acts as a foaming agent, an abrasive and to temporally increase mouth pH. Potassium carbonate is sometimes used as a buffering agent in the production of mead or wine. DMSO has been chosen because of its wide range of applicability as a solvent (Bernazzani et al 2006) in synthetic chemistry (carbohydrates, dyes, resins, polymers), in biological processes and in pharmacy and medicine (dermatology, immunology, microbiology). It easily penetrates biological membranes, facilitates chemical transport into biological tissues and it is well known for its cryoprotective effects on biological systems (Syamala et al 2006).

This thesis highlights the effect of temperature on various thermodynamical and transport properties of four homologous amino acids in aqueous sodium/potassium fluoride solutions at different concentrations. Furthermore, the effects of sodium/potassium fluoride in aqueous DMSO solution have been analysed. In addition to this, interaction studies of glycine in aqueous sodium/potassium carbonates at different temperatures have also been reported.
This thesis deals with the estimation of thermodynamic parameters like apparent molal volumes ($V_\phi$), partial molal volumes ($V_{\phi}^0$), Hepler coefficient ($\partial^2 V_\phi^0 / \partial T^2$), transfer volumes ($\Delta V_\phi^0$) and hydration number ($n_H$) using density data. Similarly, apparent molal compressibility ($K_\phi$), partial molal compressibility ($K_{\phi}^0$), transfer compressibility ($\Delta K_{\phi}$) and hydration number ($n_H$) have been calculated using ultrasonic speed data. Viscosity B-coefficients of Jones-Dole equation, transfer B-coefficient ($\Delta B$), variation of B with temperature ($dB/dT$), free energy of activation per mole of solvent ($\Delta \mu_1^0$) and solute ($\Delta \mu_2^0$) are estimated from viscosity data. Pair and triplet interaction coefficients $V_{AB}$, $K_{AB}$ and $\eta_{AB}$ and $V_{ABB}$, $K_{ABB}$, and $\eta_{ABB}$ respectively have also been calculated from transfer parameters. The linear correlation of $V_{\phi}$, $\Delta V_{\phi}$, $K_{\phi}$, $\Delta K_{\phi}$, and B for the homologous series of amino acids have been used to calculate the contribution of charged end groups ($NH_3^+$, $COO^-$), methylene group (CH$_2$) and other alkyl chain of the amino acids. These parameters have been interpreted in terms of solute-solute and solute – solvent interactions and structure making / breaking ability of solutes in the given solution.

1.6 THEORETICAL EXPRESSIONS FOR EVALUATING THERMODYNAMIC AND TRANSPORT PROPERTIES

1.6.1 Apparent Molal Volume ($V_\phi$)

The apparent molal volumes ($V_\phi$) are calculated from the measured densities ($\rho$) using the following equation (1.1):

$$V_\phi = (M / \rho) - 1000 (\rho - \rho_0) / m \rho \rho_0$$  \hspace{1cm} (1.1)

where $M$ is the molar mass of amino acid, $m$ is the molality of amino acid and $\rho$ and $\rho_0$ are the densities of the solution and solvent respectively.
1.6.2 Uncertainty Values (δρ, δu and δη)

Uncertainty values associated with the experimentally measured parameters such as density (δρ), ultrasonic speed (δu) and viscosity (δη) are evaluated based on “Evaluation of measurement data – Guide to the expression of uncertainty in measurement” JCGM 100:2008.

1.6.3 Error Values in Apparent Molal Volume (δVφ)

The error values in apparent molal volumes (δVφ) have been calculated using the equation (1.2) (Hedwig 1988, Yan et al 1999)

\[ δVφ = - (\frac{M +1000}{m}) \frac{δρ}{δρ^2} \] (1.2)

where δρ is the uncertainty in densities of the solution.

1.6.4 Partial Molal Volume (Vφ₀)

The partial molal volume (Vφ₀) are obtained using the following equation (1.3) (Banipal and Singh 2003)

\[ Vφ = Vφ₀ + S_v m \] (1.3)

where S_v is the experimental slope.

1.6.5 Group Contribution Values of Vφ₀/ ΔVφ₀/ Kφ₀/ ΔKφ₀ and B

A linear regression analysis of the Yφ₀ values as a function of the number of carbon atoms in alkyl chain of the amino acids n_c at various solution concentrations is determined using (Mishra and Ahluwalia 1984, Natarajan et al 1990, Rajagopal and Jayabalakrishnan 2010c)

\[ Yφ₀ = Yφ₀ (NH₃⁺, COO⁻) + n_c Yφ₀ (CH₂) \] (1.4)
which gives $Y_{ij}^0 (\text{NH}_3^+, \text{COO}^-)$, the zwitterionic end groups and $Y_{ij}^0 (\text{CH}_2)$, the methylene group contributions. Here $Y_{ij}^0$ stands for $V_{ij}^0 / \Delta V_{ij}^0 / K_{ij}^0 / \Delta K_{ij}^0$ and $B$.

The contribution from the alkyl chain of homologous series of $\alpha$-amino acids may be evaluated using equation (1.7) by incorporating the following assumptions proposed by Hakin et al (1994b, 1995).

\[
Y_{ij}^0 (\text{CH}_3) = 1.5 Y_{ij}^0 (\text{CH}_2) \quad (1.5)
\]
\[
Y_{ij}^0 (\text{CH}) = 0.5 Y_{ij}^0 (\text{CH}_2) \quad (1.6)
\]
\[
Y_{ij}^0 (\text{NH}_3^+, \text{COO}^-) / Y_{ij}^0 (\text{R}) = Y_{ij}^0 (\text{NH}_3^+, \text{COO}^-) / Y_{ij}^0 (\text{R}) \quad (\text{in aqueous cosolute}) - Y_{ij}^0 (\text{NH}_3^+, \text{COO}^-) / Y_{ij}^0 (\text{R})(\text{in water}) \quad (1.7)
\]

where $R = \text{CH}_2$- for (glycine), $\text{CH}_3\text{CH}$- for (alanine), $\text{CH}_2\text{CH}_3\text{CHCH}$- for (valine) and $\text{CH}_3\text{CH}_3\text{CHCH}_2\text{CH}$- for (leucine).

1.6.6 Transfer Parameters ($\Delta V_{ij}^0 / \Delta K_{ij}^0$ and $\Delta B$)

The transfer partial molal volumes $\Delta V_{ij}^0$, transfer partial molal compressibilities $\Delta K_{ij}^0$ and transfer $B$ coefficient $\Delta B$ of amino acids from water to solution are calculated using equation

\[
\Delta Y_{ij}^0 = Y_{ij}^0 (\text{in aqueous solution}) - Y_{ij}^0 (\text{in water}) \quad (1.8)
\]

where $\Delta Y_{ij}^0$ denotes $\Delta V_{ij}^0 / \Delta K_{ij}^0$ or $\Delta B$.

1.6.7 Hydration Number ($n_H$) from Volumetric Data

The standard partial molal volumes of amino acids are used to determine the number of water molecules $n_H$, hydrated to the amino acid by using the following equations (Franks et al 1970, Millero et al 1978, Pal and Kumar 2005c)
\[ V_{\phi}^0 = V_{\phi}^0 \text{(int)} + V_{\phi}^0 \text{(elect)} \]  

(1.9)

where \( V_{\phi}^0 \text{(int)} \) is the intrinsic partial molal volume of the amino acids and \( V_{\phi}^0 \text{(elect)} \) is the electrostriction partial molar volume due to the hydration of the amino acids. The \( V_{\phi}^0 \text{(int)} \) is made up of two terms, the van der Waals volume and the volume due to packing effects. As suggested by Millero et al (1978), the values of \( V_{\phi}^0 \text{(int)} \) for the amino acids can be calculated from crystal molar volume using the following equation:

\[ V_{\phi}^0 \text{(int)} = (0.7/0.634) V_{\phi}^0 \text{(cryst)} \]  

(1.10)

where 0.7 is the packing density for molecules in the organic crystal and 0.634 is the packing density for random packing spheres. The crystal molar volume can be estimated by equation:

\[ V_{\phi}^0 \text{(cryst)} = M/ \rho \text{(cryst)} \]  

(1.11)

where \( \rho \text{(cryst)} \) is the crystal density of the amino acid. Since crystal density has a very small change with temperature, the \( \rho \text{(cryst)} \) value at 298.15 K (Berlin and Pallansch 1968) is used for all other reported temperatures, as reported by Lin et al (2006). \( V_{\phi}^0 \text{(elect)} \) can be estimated from the experimentally measured \( V_{\phi}^0 \) values by the equation:

\[ V_{\phi}^0 \text{(elect)} = V_{\phi}^0 - V_{\phi}^0 \text{(int)} \]  

(1.12)

The number of water molecules \( n_H \) hydrated to the amino acid are estimated by (Millero et al 1974)

\[ n_H = V_{\phi}^0 \text{(elect)} / (V_{OE}^0 - V_{OB}^0) \]  

(1.13)

where \( V_{OE}^0 \) is the molar volume of the electrostricted water and \( V_{OB}^0 \) is the molar volume of bulk water (Hoyau and Ohanessian 1997). Following the
procedure used by Wang et al (1999), it is found that \((V^\circ_E \! - \! V^\circ_B) \cong - 4 \text{ cm}^3\text{mol} \) at 
\(T = 308.15 \text{ K}\). This value of \((V^\circ_E \! - \! V^\circ_B)\) has been retained at the studied 
temperatures, as suggested by Lark et al (2006).

1.6.8 Pair and Triplet Interaction Coefficients \((V_{AB} / K_{AB} / \eta_{AB} \text{ and } V_{ABB} / K_{ABB} / \eta_{ABB})\)

Kozak et al (1968) have proposed a theory based on McMillan-Mayer (1945) theory of solutions that permit the formal separation of effects due to interactions between pairs of solute molecules and those due to interactions involving three or more solute molecules. This approach has further been discussed by Friedman and Krishnan (1973a) and Frank and Evans (1945) in order to include the solute – cosolute interactions in the solvation sphere and used by various workers (Chalikian et al 1993, Banipal et al 2000, Mishra and Ahluwalia 1981, Lark and Bala 1989), to study the interactions of the amino acids and cosolutes in aqueous medium. According to this treatment, a thermodynamic transfer function at infinite dilution \(\Delta Y_{\psi}^0\) \((\Delta Y_{\psi}^0 \text{ denotes } \Delta V_{\psi}^0 / \Delta K_{\psi}^0 \text{ or } \Delta B)\) can be expressed as

\[
\Delta Y_{\psi}^0 = 2Y_{AB} m_B + 3Y_{ABB} m_B^2 + ---- \quad (1.14)
\]

where \(Y_{AB} (Y_{AB} \text{ denotes } V_{AB} / K_{AB} \text{ or } \eta_{AB})\) and \(Y_{ABB} (Y_{ABB} \text{ denotes } V_{ABB} / K_{ABB} \text{ or } \eta_{ABB})\) are respectively the pair and triplet interaction coefficients corresponding to a particular thermodynamic property \((\Delta V_{\psi}^0 / \Delta K_{\psi}^0 \text{ or } \Delta B)\) and \(m_B\) is the molality of the cosolute.

1.6.9 Variation of Partial Molal Volume with Temperature

According to Hepler’s criteria, when \(\partial V_{\psi}^0 / \partial T > 0\) and \(\partial^2 V_{\psi}^0 / \partial T^2 < 0\) the solute has the hydrophilic character while \(\partial V_{\psi}^0 / \partial T < 0\) and \(\partial^2 V_{\psi}^0 / \partial T^2 > 0\) the solute has hydrophobic character. In order to evaluate the structure
making / breaking properties of solute, the variation of partial molal volume \( V_{ij}^0 \) with temperature \( T \) can be expressed using the quadratic equation (Pal and Kumar 2004)

\[
V_{ij}^0 = a + bT + cT^2
\]  

(1.15)

The coefficients \( a, b \) and \( c \) are constants.

1.6.10  Apparent Molal Compressibility (\( K_{ij} \))

The apparent molal compressibilities (\( K_{ij} \)) are calculated from density and compressibility data using the following equation (Wadi and Ramasami 1997):

\[
K_{ij} = \frac{M \beta_s}{\rho - 1000 (\beta_0 \rho - \beta_s \rho_0)/ m \rho \rho_0}
\]  

(1.16)

where \( \beta_s \) and \( \beta_0 \) are the coefficients of adiabatic compressibility (Given \( \beta = 1/(\rho u^2) \) Chalikian et al 1994) of the solution and solvent respectively.

1.6.11  Partial Molal Compressibility (\( K_{ij}^0 \))

The partial molal compressibility (\( K_{ij}^0 \)) of solutions are obtained using the Masson’s equation (Iqbal and Verrall 1987)

\[
K_{ij} = K_{ij}^0 + S_k \ m
\]  

(1.17)

where \( S_k \) is the experimental slope. The values of \( K_{ij}^0 \) are obtained from the linear plots of \( K_{ij} \) vs \( m \) by the method of least squares.

1.6.12  Hydration Number (\( n_H \)) from Compressibility Data

The hydration number (\( n_H \)) of amino acids in aqueous sodium fluoride solutions are calculated using compressibility data by the following method proposed by Millero et al (1978)
\[ n_H = -K^0_{\phi}(\text{elect}) / V^0_B K^0_B \]  

where \( K^0_B \) is the compressibility of bulk water. The value of \( V^0_B K^0_B \) is taken as \( 8.1 \times 10^{-6} \text{ m}^3 \cdot \text{mol}^{-1} \cdot \text{GPa} \) (Pal and Kumar 2005c). The electrostriction partial molar compressibility \( K^0_{\phi}(\text{elect}) \) can be estimated from the value of \( K^0_{\phi} \).

\[ K^0_{\phi}(\text{elect}) = K^0_{\phi} - K^0_{\phi}(\text{int}) \]  

where \( K^0_{\phi}(\text{int}) \) is less than \( 5 \times 10^{-6} \text{ m}^3 \cdot \text{mol}^{-1} \cdot \text{GPa}^{-1} \) for ionic crystal and many organic solutes in water Millero et al (1978). So one can assume \( K^0_{\phi}(\text{int}) \approx 0. \) Therefore equation (1.19) becomes

\[ K^0_{\phi}(\text{elect}) = K^0_{\phi} \]  

Hence using the calculated values of partial molal compressibility \( (K^0_{\phi}) \) the values of hydration number are calculated.

1.6.13 Relative Viscosity \( (\eta_r) \)

The relative viscosities \( \eta_r \) of solutions are calculated using the equation (1.21)

\[ \eta_r = \eta / \eta_0 \]  

where \( \eta \) and \( \eta_0 \) are the viscosities of the solution and solvent respectively.

1.6.14 Viscosity B Coefficient

The variation of relative viscosity \( \eta_r \) of the solution can be analysed by Jones – Dole equation (1929)

\[ \eta_r = 1 + A \times c^{1/2} + B \times c \]
where \( c \) is the molar concentration, \( A \) is the Falkenhagen coefficient and \( B \) is the Jones – Dole viscosity coefficient.

However, in amino acids + salt + water mixture, as suggested by many authors (Yan et al 2002, Wang et al 2004, Banipal et al 2006 b), the modified form of Jones – Dole equation is used.

\[
\eta_r = 1 + B \times c \tag{1.23}
\]

1.6.15 Partial Molal Volume of the Solvent (\( \overline{V}_i^0 \))

The partial molal volume of the solvent is the mean volume of the solvent given by the following equation (Ali et al 2006):

\[
\overline{V}_i^0 = \left( \sum x_i m_i / \rho \right) \tag{1.24}
\]

where the terms \( x_i \) and \( m_i \) denote the mole fractions and molecular weights of water (1) and solute (2) and \( \rho \) is the density of the solvent mixture.

1.6.16 Relation Between Free Energy of Activation and Viscosity \( B \) Coefficient

Free energy of activation of viscous flow (\( \Delta \mu_2^{0\ast} \)) is an useful parameter to assess the complexity of liquid structure. The viscosity \( B \) coefficients are related to the free energy of activation per mole of the solvent (\( \Delta \mu_1^{0\ast} \)) and solute (\( \Delta \mu_2^{0\ast} \)) as suggested by Feakins et al (1993) and Eyring et al (1941) by the following equation:

\[
B = (\overline{V}_1^0 - \overline{V}_2^0) / 1000 + \overline{V}_1^0 / 1000RT \Delta \mu_2^{0\ast} - \Delta \mu_1^{0\ast} \tag{1.25}
\]
1.6.17 Free Energy of Activation per Mole of the Solvent ($\Delta \mu_1^{0*}$)

The free energy of activation per mole of the solvent ($\Delta \mu_1^{0*}$) is calculated by the following relation:

$$\Delta \mu_1^{0*} = RT \ln\left(\frac{\eta_0 \bar{V}_1^0}{hN}\right)$$

(1.26)

where $h$ is the Planck’s constant, $N$ is the Avogadro’s number, $\eta_0$ is the viscosity of the solvent and $R$ is the gas constant.

1.6.18 Free Energy of Activation per Mole of the Solute ($\Delta \mu_2^{0*}$)

The free energy of activation per mole of the solute ($\Delta \mu_2^{0*}$) is calculated using the equation (1.27)

$$\Delta \mu_2^{0*} = \Delta \mu_1^{0*} + \frac{RT}{\bar{V}_2^0} [1000 B - (\bar{V}_1^0 - \bar{V}_2^0)]$$

(1.27)

where $\bar{V}_2^0 = V^0_\phi$ is the partial molar volume at infinite dilution of the solute.