

Research paper

## The study of Enzyme-Water Mutualism Theory

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### ABSTRACT

A variety of experiments have shown that water can occur as a liquid of high and low density, with various physical characteristics, as the product of two kinds of hydrogen association between H<sub>2</sub>O molecules. This is essential intracellular, since solutes may favor a water type or other, creates local gradients of different waters behaviors which, due to volume restrictions, cannot be balanced by the flux but can be balanced by a shift between water shapes. It is quite probable that the developmental powers have manipulated this extraordinary water capacity, contributing to mutualism among adjacent H<sub>2</sub>O molecules and macromolecules. A consequence is a spectrum of substrate unique enzyme with macromolecular hydration, which enhances the catalysis, and hydrated by the more favorable ones of the two water configurations. Moreover, owing to selective isolation of enzyme reaction components, the variations in the water structure of low /high density purvey the pathway for protein folding; a basic requirement for enzyme functions without neglecting thermodynamics.

### Introduction

This correspondence harmonizes the latest creation of hydrated macromolecules to the unresolved issue of the function of organized water as a catalyst for its catalytic activities (Knight, 1991). A hydrogen-linked three-dimensional H<sub>2</sub>O network plays a central role in water behavior, and water as a combination of high-density compound (HDW) and low-density compound (LDW) has long been known to occur in the packed cytoplasm (Pollack, 2003). This may have an effect on natural mechanisms and human activities because the way biochemical behaviors are directed relies on the free energy of reactor hydration. The low-density water (LDW) is ice-like and low density (HDW) is more undisciplined and responsive for both polymorphs. Several investigators who used different strategies to evaluate the phenomena were motivated to determine the presence of LDW and HDW and

numerous features studied were consistent with the relationship of two molecular structures of polymorphs, LDW and HDW. A range of data confirms both the presence of water in following components: the high/low density structure (HDW and LDW) meaning that at any one moment, the LDW/HDW balance may be crucial (Knight). Usage of incredibly slow postponed illumination (Grasso et al., 2018). Research on water organizing in glycerol (exemplified by hydrogen bonding only between compounds) offers findings that correspond with LDW complexes as defined by someone else (Perakis et al., 2017). Offered proof about shows that HDW is more prone to fragile and restored hydrogen bonds, as it is energy-efficient to sever intermolecular hydrogen bonds with water molecules compared to the organized one (Maestro et al., 2016, Soper and Ricci, 2000). The LDW maximum is 3200 cm<sup>-1</sup> as IR spectroscopy is seen at HDW maximums at 3400 cm<sup>-1</sup>

<sup>1</sup>. Using a related process, spectral variations in living cells are detected arising from variations to hydration in unrepaired living matter (Minnes et al., 2017). The hydration variations are attributed to HDW and LDW shifts. This aims to act as a method for evaluating the tumor progression and the identifying of aging of tumor cells. More HDW or fewer LDW is present in cells with greater metastasis. Through neutron transmittance, Soper et al., (2016) noticed a persistent transition from LDW to HDW of water with growing heat, although Voeikov (Del Giudice et al., 2013) leveraging Quantum Electrodynamics (QED) showed that water compounds are moving to a less energy status above the compression extent and underneath the critical temperature showing not only temperature but also pressure will influence the HDW/LDW balance. In the alimentary industry the significance of pressurized improvements in water composition have also not been underestimated, as illustrated in an overview of processes for food products that communicate under pressure to conserve themselves (Guignon et al., 2016). If substances are prone to strain, collaborative results can also be proposed, with other occurrences involving water including the gel-forming mechanism. The aims of investigation: if conversion of the LDW to HDW happens in the dynamic aqueous medium including food production with high pressures or otherwise. The LDW-HDW transition into purified water was also visible in sodium caseinate solution and milk products utilizing ultrasound under tension calculations. Findings indicate that the intrinsic sol-gel transfer characteristic plays a key function in the self-regulation of the Autonomous Translational Enzyme-Water Mutualism Phenomenon in amoeba (Wiggins, 1982). The preferred pathway focuses on future improvements in the action that contribute to actin and myosin-like cytoskeleton polymerization. The cell cortex actin-myosin is intended to contract an increase of cell tension that results in cell membrane breakage in the direction of movement needed. The sol-gel transition is the product of osmotic tension and some ionic modifications induced by contraction and relaxation. Within the amoeba, proteins may be enabled to transform gel into a liquid phase, and  $Ca^{++}$  is stated to be essential for the transformation of sol-gel. An unregulated shift in the tension elsewhere in the device would arise from consecutive motion. In embryonic growth, injury recovery, and tumor metastasis, the cell navigation process is essential. Sarcomas or tumors triggered by connective tissue cells are especially ideal for amalebic agitation that results in increased metastasis (Wiggins, 1982). The method of conversion of the sol-gel, such as a gate signal and regulatory

influences, is unknown and is still being studied. The experiments referenced here constitute a selection of the huge volume of useful study which reinforces the principle and assumption behind this essay. They also have a resource for previous research. The hydrogen-bonded  $H_2O$  clusters in two key types are considered as the liquid polymorphs in a quick exchange balance:  $H_2O$  clusters with long straight Hydrogen bonds (LDW) or categories with concise curved weaker ones (HDW). The effect is that the segmentation of any one solution is based on the volume and its electrical structure, each with numerous physical and solvent characteristics and polymorphisms. The  $Na^+$  ions section is identified to vary from  $K^+$  ions, for instance (Maestro et al., 2016). The polymorphic characteristics illustrated how easy hydrogen bonding is to be cracked in one shape or another. The former favors HDW because of its ionic format, while the latter prioritizes LDW. This is why the selected solvent defines the hydration power of the species and the alteration in hydration energy during the polymorphic transformation. The fast exchange between HDW and LDW leads to alteration of free energy (modern power) of the substitute polymorph, combined with the power of hydration of any LDW or HDW species. Instead, these changes lead to a free energy alteration. It continues that, when a solute facilitates a separation in one type of water or another, an osmotic tension gradient will occur over an connection between adjacent cellular water microdomains. This will alter the composition and characteristics of the chosen microdomain as follows: whenever the solute decomposes in HDW or LDW and the induced parameter of water activity cannot be subsided through water movement solely because of volume constraints, the balance is calculated by shifting in HDW/LDW or LDW/HDW, thus alleviating the regional activity gradient. The distinction will shift and the balance will be recovered at the same period. This is instigated by an accelerated  $H_2O$ - $H_2O$  interchange between categories that enables for a shift in the balance between the LDW and HDW dynamics. Thermodynamic expense therefore becomes an immediate component whenever the surrounding water shifts from one polymorph to another, which becomes the exterior communication for the hydration of a solute movement, where free energy of hydration in relation to hydration power costs is decreased by reaction to substitute shape of nearby water. Thus, each polymorph of  $H_2O$  molecules are less responsive than the other polymorph and hindered hydration. If these relocations occur and there are thermodynamic expenses, a protein molecule folds. If a protein is in communication with

HDW and the free energy of reagents is greater than the item's free energy (protein in solution), the reactions occur automatically. Additionally, the protein becomes unsolvable as the HDW is transferred to the LDW in a manner where  $\Delta G_w$  is wide and sufficient. As the solution and folding of the protein is assumed to be a unifying mechanism, when fewer LDW is in conjunction with the protein, adjacent HDW is increased,  $\Delta G_w$  declines, and protein solution is preferred caused by communication with the substitute polymorphic protein (HDW). Predictable effects for cyclic enzymes are the folding or cycling of macromolecular activities triggered by the solute selection for either polymorph. This theory was formulated and validated by experimental studies (Maestro et al., 2016). Thus, any shift in the solvent characteristics of water will shift deeply in the hydration of ions and macromolecules and so the intensity and indication of solvent energy would alter. There are major variations in the free energy of solvation of phosphate ester substances, promoting the likelihood of reciprocal enzyme reactions owing to a difference in the solvent energy (George et al., 1970). When the abundance of  $H_2O$  hydration varies in such a way that the free hydration energy of ADP and  $P_i$  (inorganic phosphate) surpasses the free hydration energy of ATP, the mechanism will occur automatically and ATP is formed. Wiggins has presented proof of ATP formation from ADP and inorganic phosphate in the LDW system without enzyme participation. The Wiggins findings provide support the involvement of two-phase water in a variety of biochemical processes, namely poly L-lysine production, Na-K-ATPase process, membrane traffic, mechanical characteristics and dehydration mechanisms, all focused on this principle of two distinct  $H_2O$  solvents and improvements in solvents free energies. The probability of improvements accompanying ATP attachment in the microenvironment of active phosphorylation enzyme sites may be very common. In order to work the Na-K-ATPase as well as the ATP synthesis while the pumping is inverted, the same phosphoenzyme moiety is important. The aspartic acid residue is the phosphorylated one. The aspartic acid residue of the enzyme, which is phosphorylated, are still included in ATP situations. Nevertheless, in the mechanisms of energy bonding proposed for those mechanisms, the conventional concept of thermodynamic is not traditionally observed.

Rather just, the chemical combining in between one response (A) and another mechanism (B) demands that an item of mechanism (A) must be a substrate of mechanism (B). As a result, combined with this, the principle of biochemical power

transduction has continued to be trouble in bioenergetics.

The totally free power, in this case, is considered the matching of that generated by the Na-K-ATPase as well as somehow connected to the mechanism of the Na-K-pump. Here likewise there has actually been no appropriate molecular mechanism recorded for a really combined process in the classic feeling, although the link in between both occasions is never ever contested. The energy combining based on the Wiggins (Wiggins and Knight, 1979), need to come about, not by a purported power transduction however by the environmental (HDW/LDW) change induced by the phosphorylation of the aspartic acid residue. Incorporating-classical thermodynamic Principles, and also has actually elegantly demonstrated how energetic transportation of ions can be described by a change in adjacent water at a cell membrane layer when ion transportation occurs. Moreover the addition of ATP to the suspension of actomyosin shows a transition in light dispersal and other parameters, which have arisen before all the ATP have been hydrolyzed with the Ca-ATPase of the contractile protein (Wiggins and Knight, 1979). More than half century ago, it was suggested that muscular contraction and relaxation will rely on a crash, a regulation of the water phase by actomyosin, which indicates an adjacent association between water and the macromolecule (Szent Györgyi, 1957). In the history, swelling of mitochondria has been substantial and has been associated with oxidative phosphorylation. Investigations reveal that, as it was calculated using lasing techniques, what had historically been perceived as swelling in several experiments could not be reconciled with adjustments in real mitochondrial scale (Knight et al., 1981). With these studies the shifts in the light dispersion only may be attributed to a shift in the potassium ionophore balance of the LDW/HDW. In non-breathing mitochondria immersed in  $K^+$  -free environment, valinomycin (val) stimulates ATP synthesis (Cockrell et al., 1966). The alternative explanation here is that, unless an existing anti-anion extends beyond the matrix, the Val- $K^+$  species participates in a hyperpolarization in the binding membrane and this dissemination is restricted by the accumulation of external positive charge. This rise in optimization and hyperpolarization is predicted to create a topological shift in the connection surface, an improvement in the development of LDW and ATP. The theory is that due to a crucial rise in LDW/HDW intrinsically correlated to the F1-ATPase ATP is randomly created. The shifting balance between HDW and LDW is triggering not only the shifts in free hydration energies but also the restoration of the

ATPase. In comparison, as binding mitochondria in hypertonic KCl are immersed, decreasing light dispersion reinforces the opinion that depolarization of the binding membrane by internal propagation of K<sup>+</sup> transforms the matrix LDW to HDW, disassociates mitochondria and inhibits the ATP production (Knight V. Unpublished results). The opinion expressed here confirms the Wiggins template is focused on these emphasized trials (Wiggins, 1990). As long ago as 1957, it was suggested that the biological roles comprise of the creation and removal of water systems, of all sections and parcels of biological equipment involve the electronic stimulation (Wiggins, 1990). The aforementioned studies confirm those statements and the examiner's opinion. There is strong view that an aquatic molecular combination was formed at one stage in youngest development, and that macromolecules were possibly not well recognized as a consequence of endergonic process. In the basic earth settings, ATP or a polyphosphate substrate might have been participating in energy-driven mechanisms, which unsurprisingly synthesized molecules that played a key role during macromolecular development. It is anticipated, coinciding with the macromolecular development of the soluble enzymes, that the production of unique substrate binding sites could have been enhanced when integrating close water groups, gaining from molecular metallization between the enzyme and one type of water or another. The biological tissue is dynamic and the fundamental character of this neighboring H<sub>2</sub>O is difficult to understand (Cho et al., 1997). The physics and chemical abnormalities of H<sub>2</sub>O have shown that differential attachment near the surface is more significant, indicating that HDW is best connected to certain interfaces and LDW is more properly linked to other portions. The first waters identified by DROST Hansen as neighbor water have been changed by their vicinity to the membrane and subsequently examined by someone else, like Zheng JM (Zheng et al., 2006). Wiggins has further clarified the dynamics of surface water associations (Maestro et al., 2016). There is an effort to include a function and/or explanation in enzymatic operation for this neighboring LDW and HDW. Although enzymes perform a multitude of mechanism and the energy pool given by two-stage water allows for improvements in hydration energy supporting the reversing of exergonic processes in particular conditions without the involvement of enzymes, the possibility that the precision and performance of the changes are combined and intrinsic in the enzyme-water interaction is not excluded. The earliest solved enzymes probably would have folded and given a break or a similar structure with a complex chemical

composition which not only defined its uniqueness but also the existence of its surrounding water. The specific macromolecule comprised of amino acid units have the advantage to have an optimum hydration for one form of H<sub>2</sub>O or another. This will serve to increase the precision of the substrate (Maestro et al., 2016). The performance of the catalytic mechanism therefore positively is affected. The mechanism for releasing the substance, redistribution of HDW, LDW and enzyme molecule recycling are given by the two water types (Perakis et al., 2017). It has been argued that the water molecules surrounding the soluble macromolecules may adopt various crystalline shapes, based on the atomic groups' polar or non-polar existence. In this situation, as the bonding of H<sub>2</sub>O-H<sub>2</sub>O varies, multiple polar groups in the enzyme are revealed and are finding dynamic hydration, with topological alternatives, folding or unfolding before the favorable energy equilibrium. It is heavily discussed what governs the folding of proteins. Water effectively engages and communicates with organic compounds at nano-scales and according to Frauenfelder et al., (2008) incorporation of myoglobin has demonstrated that the hydration membrane composition defines the physiological activity of the protein and also regulates contact with other proteins and precursors. Fruen archive revealed that the compound's conformational movement is lorded by hydration membranes. Thus, there are two water solvents (HDW and LDW) in the cellular micro environments where one can be transformed into the next if an osmotic gradient is present. This extraordinary water ability is dependent on the hydrogen attachment of H<sub>2</sub>O molecules and the intrinsic universal energy cannot be manipulated by evolutionary pressures. The effect is the diversity of solved enzyme macromolecules with a particular capacity to respond to the high performance (Frauenfelder et al., 2009). It can be better recognized and described as molecular collectivism, a apparent and allergic tendency across the whole of the live earth and also the enzyme reactions co-exist throughout the soluble process, with one water structure (HDW) or the other (LDW), promoting the particular catalytic mechanism. The interactive processing of the Na-K pump between H<sub>2</sub>O and ATPase is a fundamental illustration of molecular collectivism formed by Wiggins PM (Knight, 1991). An advanced system is essential for the cell's protection (Szent Györgyi, 1957).

## Conclusion

Relevant enzyme functions are given for chosen hydrated macromolecules. The development of the principal protein composition dictating the

specificity of the ligand site and which is fitted with the described hydration may well account for changes of macromolecular length and folding elements. Soluble enzymes will have an improved role since the key molecular structure of the enzyme is compatible with the favored water form. The (H<sub>2</sub>O)<sub>x</sub>-enzyme interaction strengthens the catalytic reaction, and the products of this mechanism contributes to a transition in HDW/LDW formulation if the enzyme folds with water-filled fractures. This transition in water balance produces the energy reservoir transition ( $\Delta G_w$ ), a requirement to enzyme processing for the folding or unfolding of organic compounds. This theory focused on the collectivism between enzymes and water is a very potential option for the concept of substrates. The exact geometric fitting of hydrogen bond donors is assumed to work in the contrary load of substrates and/or dipole. This mechanism is theoretically capable of being converted into an enzyme-changing chemical reactor: an organization of poor coupling with no molecular or thermodynamic description of this point.

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