



ELSEVIER

Available online at www.sciencedirect.com

SCIENCE @ DIRECT®

C. R. Geoscience 337 (2005) 173–179



COMPTES RENDUS

GEOSCIENCE

<http://france.elsevier.com/direct/CRAS2A/>

External geophysics, Climate and Environment

Hydrophilic–hydrophobic interplay: from model systems to living systems

Marie-Claire Bellissent-Funel

Laboratoire Léon Brillouin (CEA-CNRS), CEA Saclay, 91191 Gif-sur-Yvette, France

Received 29 December 2003; accepted after revision 17 October 2004

Available online 8 December 2004

Written on invitation of the Editorial Board

Abstract

Water is a unique liquid, many of whose properties are critical for the continued support of life. In living systems, essential water-related phenomena occur in restricted geometries in cells, and at active sites of proteins and membranes or at their surface. The stability of biological systems is controlled by the subtle hydrophilic–hydrophobic interplay. It is well known that hydration water plays a prominent role in the relationship between structure, dynamics, and biological function. Various examples of systems developing either hydrophilic or hydrophobic interactions, or both, are presented. The static and transport properties of what is defined as confined or interfacial water are compared with those of bulk water. Finally, it is shown that there is some strong evidence that structural and dynamic properties of water close to a hydrophilic surface, at room temperature, are similar to that of bulk supercooled water. **To cite this article:** *M.-C. Bellissent-Funel, C. R. Geoscience 337 (2005).*

© 2004 Académie des sciences. Published by Elsevier SAS. All rights reserved.

Résumé

Interactions hydrophiles–hydrophobes : des systèmes modèles aux systèmes vivants. L'eau est un liquide unique, dont les propriétés sont cruciales pour les processus de la vie. Dans les systèmes vivants, les phénomènes essentiels ont lieu, en géométrie confinée, dans les cellules vivantes, et à proximité des sites actifs des protéines et des membranes ou à leur surface. La stabilité des systèmes biologiques est contrôlée par le jeu subtil entre les interactions hydrophiles et les interactions hydrophobes. Il est admis que l'eau d'hydratation joue un rôle prédominant dans la relation entre la structure, la dynamique et la fonction des systèmes biologiques. Dans cet article, nous présentons des exemples variés de systèmes qui sont le siège d'interactions hydrophiles ou hydrophobes ou des deux types d'interactions. Les propriétés statiques et de transport de l'eau confinée ou de l'eau interfaciale sont comparées à celles de l'eau en grand volume. Enfin, nous montrons que les propriétés structurales et dynamiques de l'eau, à température ambiante et au voisinage d'une surface hydrophile, sont comparables à celles de l'eau surfondue. **Pour citer cet article :** *M.-C. Bellissent-Funel, C. R. Geoscience 337 (2005).*

© 2004 Académie des sciences. Published by Elsevier SAS. All rights reserved.

E-mail address: mcbel@llb.saclay.cea.fr (M.-C. Bellissent-Funel).

1631-0713/\$ – see front matter © 2004 Académie des sciences. Published by Elsevier SAS. All rights reserved.
doi:10.1016/j.crte.2004.10.011

Keywords: Hydrophilic interaction; Hydrophobic interaction; Porous glass; Aqueous solutions; Biological systems; Structure; Dynamics; Confined water; Hydration water; Supercooled water; Glass transition; Neutron scattering

Mots-clés : Interaction hydrophile ; Interaction hydrophobe ; Verre poreux ; Solutions aqueuses ; Systèmes biologiques ; Structure ; Dynamique ; Eau confinée ; Eau d'hydratation ; Eau surfondue ; Transition vitreuse ; Diffusion de neutrons

1. Introduction

Water is the most abundant fluid on earth and the major constituent of organisms (70% of total weight in most cases). The understanding of hydrophilic and hydrophobic effects is of prime importance. These effects are related to the solvent properties of water and to the fact that some compounds are more or less soluble in water. The solvent abilities of water arise primarily from two properties: its tendency to form hydrogen bonds (very short characteristic lifetime, between 10^{-13} and 10^{-12} s) and its dipolar character [3]. The high dielectric constant ($\epsilon \sim 80$), already alluded to, results from its dipolar character.

2. Hydrophilic interactions

2.1. Hydrogen-bond formers

Any molecules that carry groups capable of forming hydrogen bonds can do so with water; such groups will tend to make these molecules hydrophilic. Water readily dissolves hydroxyl compounds, amines, sulphhydryl compounds, esters, ketones, and a wide variety of other organic compounds.

In the presence of a solid substratum, water may also form bonds. This is the case, for instance, of glasses where silanol groups Si–O–H are present at the interface water–silica. Let us mention porous materials [2], such as Vycor glass, silica gels, and zeolites.

2.2. Ionic compounds

Water is also an excellent solvent for ionic compounds. The explanation lies in the dipolar nature of the water molecules. Dipoles interact with ions such that cations and anions in aqueous solutions are surrounded with hydration shells. Careful neutron scattering experiments allowed us to determine the characteristics of the hydration shell around many ions,

that is to say the distance between the ion and the water molecule, the tilt angle and the hydration number [16]. Around a cation, the water molecule is oriented with the oxygen close to the cation corresponding to a minimisation of the energy between the ion and the water dipole. Instead, around an anion, the hydrogen atoms are close to the ion. The hydration number, i.e. the number of water molecules inside the first hydration shell, and the lifetime of this shell depend on the nature of the solute and on its concentration. Layer-like clays minerals [32,36] have been the objects of many studies.

3. Hydrophobic interactions

The dipolar nature of the water molecule also contributes to dissolve non-ionic, but apolar molecules. Substances like hydrocarbon that are non-polar and non-ionic and cannot form hydrogen bonds show only limited solubility in water. Such hydrophobic molecules do not form hydration shells, as hydrophilic substances do. Instead, the regular water lattice forms 'cages' of ice-like clathrate structure about non-polar molecules, probably with some geometry close to that of polyhedra such as icosahedra [20].

4. Hydrophilic/hydrophobic interactions

Amphipathic molecules simultaneously exhibit both hydrophilic and hydrophobic properties. They have a head group that is strongly hydrophilic, coupled to a hydrophobic tail, usually a hydrocarbon. When one attempts to dissolve them in water, amphipathic substances form peculiar structures. Possible structures are a monolayer on the water surface, a micelle, and a bilayer vesicle, with water both inside and out. Examples of other structures that impose spatial restrictions on water molecules include polymer gels and micro-emulsions. In these cases, since the hydrophobic effect

is the primary cause for the self-organisation of these structures, obviously the configuration of water molecules near the hydrophilic–hydrophobic interfaces is of considerable relevance [23].

An important field of interest of the subtle hydrophilic–hydrophobic interplay is that of associated water-soluble polymers. There is a novel type of polymers, namely telechelic polymers, where the hydrophilic chain is end-capped by hydrophobic short blocks. Their unique properties in aqueous systems make them very useful materials as rheology modifiers, suspension stabilisers, and drug carriers in pharmaceutical applications [40].

5. Structure and dynamics of confined water

In many technologically important situations, water is not in its bulk form, but instead attached to some substrates or filling small cavities. Common examples are: water in porous media, such as rocks or sandstones, and water in biological material as in the interior of cells or attached to surfaces of biological macromolecules and membranes. This is what we define here as the ‘confined’ or the ‘interfacial water’.

The structure and dynamics of water are modified by the presence of surfaces, by a change of hydrogen bonding, but also by modification of the molecular motion that depends on the distance of water molecules from the surface. Therefore, a detailed description of these properties must take into account the nature of the substrate and its affinity to form bonds with water molecules, and also the number of water layers or hydration shells. How are the water properties modified when water is in contact with hydrophilic or hydrophobic interfaces? Or both? How does the intracellular water behave? In this section, we give some examples of model systems developing either hydrophilic or hydrophobic interactions, or both, with water. In the following, the structural and dynamic properties of confined water relative to various systems are presented.

5.1. Water in hydrophilic systems

Water in porous materials such as Vycor glass, silica gel, and zeolites has been actively under investigation because of its relevance in catalytic and sep-

aration processes. In particular, the structure of water near layer-like clay minerals [32,36] condensed on hydroxylated oxide surface [22], confined in various types of porous silica [3] has been studied by neutron and/or X-ray diffraction. Water molecules adsorbed on ionic surfaces have been investigated by FT-IR, quasi-elastic neutron scattering and dielectric relaxation techniques [35]. Water in cement (hydrated tricalcium silicate) has been the subject of several studies by quasi-elastic neutron scattering [17].

The structure of water in Vycor has been investigated as a function of the hydration level and temperature. We present here some of our results for two levels of hydration: for full hydration (0.25 g water/g dry Vycor) and 25% [5]. The latter one corresponds roughly to monolayer coverage.

Results for two levels of hydration of Vycor demonstrate that the fully hydrated case is almost identical to the bulk water and the partially hydrated case is of little difference. It seems that the confinement of the water favours the nucleation of cubic ice that appears superimposed on the spectrum of liquid water and whose proportion can be deduced from the intensity of the (111) Bragg peak. The proportion of cubic ice increases with decreasing temperature. In fact, at -100°C , the spectrum of confined water looks similar to that of cubic ice (Fig. 1). This is in sharp contrast to bulk water that always nucleates into hexagonal ice. In Fig. 2, we show a spectrum that gives a clear evidence that liquid water is present below the Bragg peaks at -18°C , obtained by subtraction of the weighted spectrum of the same sample cooled down to -100°C .

Results relative to a 25% hydrated Vycor glass corresponding to a monolayer of water molecules indicate that, at room temperature, interfacial water has a structure similar to that of bulk supercooled water at a temperature of about 0°C , which corresponds to a shift of about 30 K [3]. Therefore, the structure of interfacial water is characterized by an increase of the long-range correlations, which corresponds to the building of the H-bond network, as it appears in low-density amorphous ice [4]. There is no evidence of ice formation when the sample is cooled from room temperature down to -196°C (liquid nitrogen temperature). Nevertheless, despite the fact that interfacial water and LDA show the same position of the first sharp diffraction peak (FSDP), their structures are not strictly identical. Such structural differences could be related

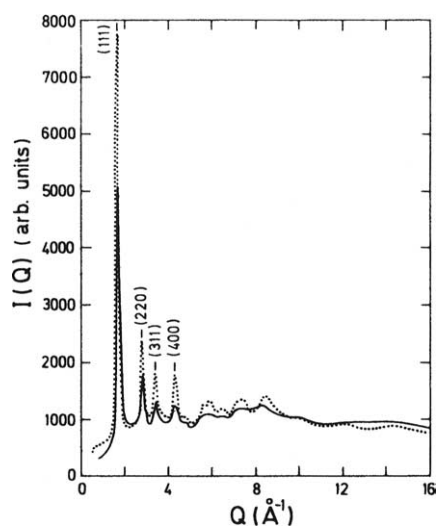


Fig. 1. Spectrum of cubic ice (-198°C) (dotted line) compared with that of confined D_2O at -100°C from fully hydrated Vycor (full line).

Fig. 1. Comparaison entre le spectre de la glace cubique (-198°C) (traits pointillés) et celui de l'eau (D_2O), à -100°C , confinée dans le Vycor, à hydratation totale (trait plein).

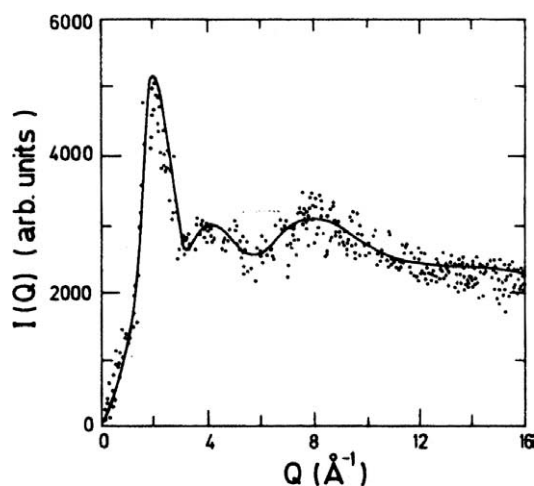


Fig. 2. Spectrum of confined D_2O at -18°C from fully hydrated Vycor after subtraction of Bragg peaks. There is 23% liquid water [5].

Fig. 2. Spectre de l'eau (D_2O) à -18°C , confinée dans le Vycor, à hydratation totale, après soustraction des pics de Bragg. Il y a 23% d'eau liquide [5].

to a topologically distorted hydrogen-bond network, as already invoked in the case of other interfacial water systems.

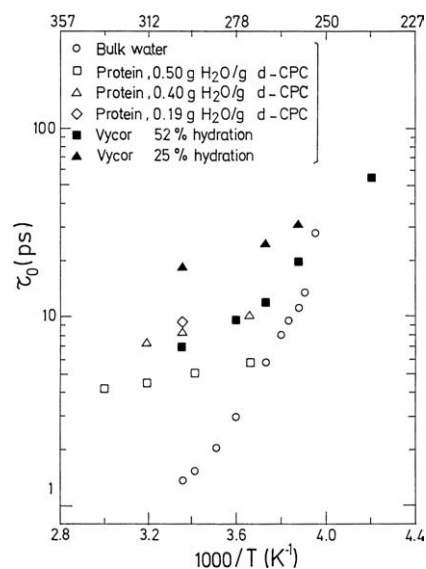


Fig. 3. Arrhenius plot of the residence time τ_0 for different levels of hydration: water at the surface of H_2O -hydrated d-CPC protein (empty symbols); water contained in hydrated Vycor (solid symbols); as compared with bulk water (empty circles) [8,37].

Fig. 3. Représentation d'Arrhénius du temps de résidence τ_0 pour différents taux d'hydratation : eau à la surface d'une protéine deutériée (d-CPC) (symboles vides); eau contenue dans du Vycor hydraté (symboles pleins); comparaison avec l'eau volumique (cercles vides) [8,37].

Fig. 3 gives the Arrhenius plots of τ_0 for hydration water at the surface of a protein [8] as compared with those of water in Vycor at different levels of hydration [8] and bulk water [37].

The residence times τ_0 of confined water from 25% hydrated Vycor and from hydrated proteins are always longer than the residence time of bulk water, at the same temperature. They increase rapidly as either the temperature or the level of hydration decreases. For example, for the 25% hydrated Vycor sample, $\tau_0 = 25$ ps at -15°C .

The hydrogen-bond lifetimes τ_1 for confined water are close to that of bulk water [37]. They have an Arrhenius temperature dependence (Fig. 4), while the residence time τ_0 does not exhibit such a behaviour (Fig. 3).

Fig. 3 gives the evolution of the residence time for confined water as compared with bulk water, and Fig. 4 that of hydrogen-bond lifetime.

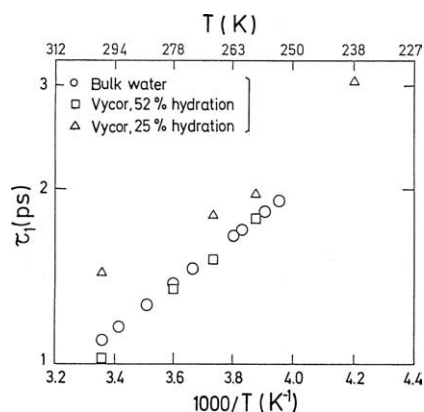


Fig. 4. Arrhenius plot of the hindered rotations characteristic time, τ_1 . This time can be associated with the hydrogen-bond lifetime [8, 37].

Fig. 4. Représentation d'Arrhénius du temps caractéristique des rotations gênées, τ_1 . Ce temps peut être associé au temps de vie de la liaison hydrogène [8,37].

5.2. Water in hydrophobic systems

Among hydrophobic model systems, one experimental investigation of particular interest concerns the structure of water contained in a carbon powder [7]. The structure of water has been determined both by X-ray and neutron diffraction, as functions of hydration levels, from room temperature down to 77 K. In agreement with previous work [5,6,14,38], this study gave support to the existence of a region near the interface where the properties of water are markedly different from those of the bulk liquid. A crude determination from the specific area indicates that, for a hydration equal to 50%, the thickness does not exceed 5 Å. This value must be compared with the computer simulations data [27], which indicate that structural modifications do not extend beyond 10 Å from the solid surface.

When partially hydrated, samples are cooled down to 77 K, no crystallisation peak is detected by differential thermal analysis. X-ray and neutron scattering show that an amorphous form of water is obtained. Its structure is different from those of low- and high-density amorphous ices already known [4]. This phenomenon looks similar in both hydrophilic and hydrophobic model systems.

5.3. Water in hydrophilic/hydrophobic systems [32]

The water/dimethyl-sulphoxide (DMSO) mixture is a model system to study the structure and dynamics of water under simultaneous hydrophilic/hydrophobic hydration.

The local quasi-tetrahedral structure of pure water has been found to be largely preserved in the presence of DMSO (X-ray and neutron diffraction). However, there is a transfer of hydrogen bonds from water to DMSO, in agreement with a greater hydrogen-bond affinity for water/DMSO than for water/water. Water HH pair-correlation functions of pure water and at the eutectic composition have been determined: the local coordination number is maintained [33].

The dynamic behaviour of water in dimethyl-sulphoxide solutions has been studied [9]. There is evidence of some slowing down of the translational diffusive motion of water. At the opposite, the effect on hydrogen bonding is not significant. A similar behaviour has been observed in water/trehalose [21] and water/pyridine solutions [1].

5.4. Water confined in biological systems

In the field of biology, the effects of hydration on equilibrium protein structure and dynamics are fundamental to the relationship between structure and biological function [11,24,28,31,34].

The assessment of perturbation of liquid water structure and dynamics by hydrophilic and hydrophobic molecular surfaces is fundamental to the quantitative understanding of the stability and enzymatic activity of globular proteins and functions of membranes.

The surface exposed by macromolecules to their aqueous environment consists mainly of hydrophilic domains that attract water dipoles [26,29]. However, superficial apolar domains also induce the perturbation of structure of water in contact with them, generally into a clathrate-like form. According to Wiggins and MacClement [39], significant amounts of water are retained in a highly 'structured form' inside hydrophobic pockets. The same authors defined this water, as 'structured water', this water being commonly designated as interfacial or (vicinal) water [15]. Because this form of water generally is difficult to extract, it is also called 'bound water'. The properties of this water have been described extensively [6,15,25,38,39]. This

distinction in terms of two classes of water, bound water and free water, has been often used.

Hydrophilic–hydrophobic interactions control the equilibrium of biological systems. It is worth noting that, in the presence of biological macromolecules, such as peptides, enzymes, proteins, DNA, all these behaviours can be found depending on the more or less hydrophilic or hydrophobic nature of each site or residue. Bonds, in particular, play a major role in the structure of these macromolecules.

The dynamics of water molecules on the surface of a protein [8] is slowed down. A similar behaviour is observed for water confined in a porous hydrophilic model system [8] (see Figs. 3 and 4).

Why is it so important to understand the effects of water on the shapes of biological molecules and/or that of biological molecules on water? On a practical level, understanding the relationship between structure, dynamics, and function of biological molecules in water may one day help researchers design new drugs that act by blocking or enhancing various biochemical pathways.

In cells, because of the considerable macromolecular crowding and the high values of the macromolecular surface/volume ratio, the properties of water are influenced by hydrophilic/hydrophobic interactions [25]. Water molecules, because they are electric dipoles, are attracted and oriented in the electric fields produced by polar or charged domains of macromolecules. In the region of apolar domains, which have little interaction with water, water molecules organise themselves in special structures, in order to compensate for the absence of equilibrium that exists at the frontier. In all cases, this water adopts a very different structure from that of bulk water. Similarities with water in model systems (Vycor, carbon powder, at low hydration) are observed.

6. Conclusion

From the present results, it appears that the structure and the dynamics of water are deeply perturbed when hydrophilic or hydrophobic interactions, or both, are developed in a medium. From the more recent findings, combining various techniques and molecular dynamics simulations, one gets the following picture of confined water. Water, in the vicinity of a hydrophilic surface, is in a state equivalent to bulk water at a lower

temperature. As previously demonstrated, the structure and dynamics of confined water depend on the degree of hydration of the sample. In particular, at room temperature, interfacial water shows a slow dynamics similar to that of bulk water at a temperature 30 K lower, such that it behaves like bulk supercooled water.

In order to understand the microscopic origin of the confinement and slowing down of motions of water molecules and the exact role played in this context, the theory of kinetic glass transition in dense supercooled liquids [12,19] has been recently used. This theory leads to some description of the dynamics of confined water in terms of correlated jump diffusion [10] instead of jump diffusion [37]. This description looks consistent with molecular dynamics simulations of supercooled water [18] and has been confirmed by high-resolution quasi-elastic neutron scattering experiments of water from hydrated Vycor [41] and from hydrated C-phycocyanin protein [13].

This more sophisticated way shows a large distribution of residence times for water molecules in the cage formed by the neighbouring molecules, which is a more realistic view than the sharp separation of water molecules into two classes, according to their mobility [8]. Short-time dynamics results about hydrated myoglobin have been recently interpreted by using this same theory of kinetic glass transition in dense supercooled liquids [30].

References

- [1] L. Almasy, P. Banki, M.-C. Bellissent-Funel, M. Bokor, L. Cser, G. Jancso, K. Tompa, J.-M. Zanotti, QENS and NMR studies of 3-picoline-water solutions, *Appl. Phys. A* 74 (2002) S516–S518.
- [2] M.-C. Bellissent-Funel, Status of experiments probing the dynamics of water in confinement, *Eur. Phys. J. E* 12 (2003) 83–92.
- [3] M.-C. Bellissent-Funel, J. Teixeira, Structural and dynamic properties of bulk and confined water, in: L. Rey, J.-C. May (Eds.), *Freeze-Drying/Lyophilization of Pharmaceutical and Biological Products*, Marcel Dekker, New York, 1998, pp. 53–77.
- [4] M.-C. Bellissent-Funel, J. Teixeira, L. Bosio, Structure of high-density amorphous water. II: Neutron scattering study, *J. Chem. Phys.* 87 (1987) 2231–2235.
- [5] M.-C. Bellissent-Funel, L. Bosio, J. Lal, Structural study of water confined in porous glass by neutron scattering, *J. Chem. Phys.* 98 (1993) 4246–4252.

- [6] M.-C. Bellissent-Funel, J. Lal, K.F. Bradley, S.H. Chen, Neutron structure factors of in-vivo deuterated amorphous protein C-phycocyanin, *Biophys. J.* 64 (1993) 1542–1549.
- [7] M.-C. Bellissent-Funel, R. Sridi-Dorbez, L. Bosio, X-ray and neutron scattering studies of the structure of water at a hydrophobic surface, *J. Chem. Phys.* 104 (1996) 10023–10029.
- [8] M.-C. Bellissent-Funel, J.-M. Zanotti, S.H. Chen, Slow dynamics of water molecules on surface of a globular protein, *Faraday Discuss.* 103 (1996) 281–294.
- [9] J.T. Cabral, A. Luzar, J. Teixeira, M.-C. Bellissent-Funel, Single-particle dynamics in DMSO-water eutectic mixture by neutron scattering, *J. Chem. Phys.* 113 (2000) 8736–8745.
- [10] S.H. Chen, P. Gallo, M.-C. Bellissent-Funel, Slow dynamics of water in supercooled states and near hydrophilic surfaces, in: M. Giordano, D. Leporini, M.-P. Tosi (Eds.), *Non-Equilibrium Phenomena in Supercooled Fluids, Glasses and Materials*, World Scientific Publication, Singapore, 1996, pp. 186–194.
- [11] M.F. Colombo, D.C. Rau, V.A. Parsegian, Protein solvation in allosteric regulation: A water effect on hemoglobin, *Science* 256 (1992) 655–659.
- [12] H.Z. Cummins, G. Li, W.M. Du, W.M. Hernandez, Relaxational dynamics in supercooled liquids – Experimental tests of the mode-coupling theory, *Physica A* 204 (1994) 169–201.
- [13] S. Dellerue, M.-C. Bellissent-Funel, Relaxational dynamics of water molecules at protein surface, *Chem. Phys.* 258 (2000) 315–325.
- [14] J.-C. Dore, F. Coveney, M.-C. Bellissent-Funel, in: W.S. Howells, K. Soper (Eds.), *Recent Developments in the Physics of Fluids*, Adam Hilger, 1992, p. 299.
- [15] W. Drost-Hansen, The occurrence and extent of vicinal water, in: F. Franks, M. Mathias (Eds.), *Biophysics of Water*, Wiley and Sons, New York, 1982, pp. 163–169.
- [16] J.E. Enderby, Diffraction studies of aqueous ionic solutions, in: M.-C. Bellissent-Funel, G.W. Neilson (Eds.), *The Physics and Chemistry of Aqueous Ionic Solutions*, D. Reidel, Dordrecht, The Netherlands, C205, 1987, pp. 129–145, and references therein.
- [17] E. Fratini, A. Faraone, P. Baglioni, M.-C. Bellissent-Funel, S.H. Chen, Dynamic scaling of QENS spectra of glassy water in aging cement paste, *Physica A* 304 (2002) 1–10.
- [18] P. Gallo, F. Sciortino, P. Tartaglia, S.H. Chen, Slow dynamics of water molecules in supercooled water, *Phys. Rev. Lett.* 76 (1996) 2730–2733.
- [19] W. Gotze, L. Sjogren, Relaxation processes in supercooled liquids, *Rep. Prog. Phys.* 55 (1992) 241–376.
- [20] A.U. Konstantin, J.A. Ripmeester, A complex clathrate hydrate structure showing bimodal guest hydration, *Nature* 397 (1999) 420–423.
- [21] I. Köper, Influence du tréhalose sur la dynamique de la C-phycocyanine : une étude par diffusion quasiélastique de neutrons, PhD Thesis, University Paris-6, France, 2002.
- [22] Y. Kuroda, S. Kittaka, S. Takahara, T. Yamaguchi, M.-C. Bellissent-Funel, Characterization of the state of two-dimensionally condensed water on hydroxylated chromium (III) oxide surface through FT-IR, quasielastic neutron scattering and dielectric relaxation measurements, *J. Phys. Chem. B* 103 (1999) 11064–11073.
- [23] P. Linse, Molecular dynamics study of the aqueous core of a reversed ionic micelle, *J. Chem. Phys.* 90 (1989) 4992–5004.
- [24] V. Lounnas, B. M. Pettitt, G.N. Phillips Jr., A global model of the protein-solvent interface, *Biophys. J.* 66 (1994) 601–614.
- [25] P. Mentré, *L'eau dans la cellule. Une interface hétérogène et dynamique des macromolécules*, Masson, Paris, 1995.
- [26] G.D. Rose, A.R. Geselowitz, G.J. Lesser, R.H. Lee, M.H. Zehfus, Hydrophobicity of amino acids. Residues in globular proteins, *Science* 229 (1985) 834–838.
- [27] P.J. Rossky, Structure and dynamics of water at interfaces, in: M.-C. Bellissent-Funel, J.-C. Dore (Eds.), *Hydrogen-Bond Networks*, Kluwer Academic Publishers, The Netherlands, Dordrecht, C435, 1994, pp. 337–338.
- [28] J.A. Rupley, G. Careri, Protein hydration and function, *Adv. Prot. Chem.* 41 (1991) 37–172.
- [29] J.A. Rupley, E. Gratton, G. Careri, Water and globular proteins, *Trends Biochem. Sci.* 8 (1983) 18–22.
- [30] M. Settles, W. Doster, Anomalous diffusion of adsorbed water: A neutron scattering study of hydrated myoglobin, *Faraday Discuss.* 103 (1996) 269–279.
- [31] J.C. Smith, Protein dynamics: comparison of simulations with inelastic neutron scattering experiments, *Q. Rev. Biophys.* 24 (1991) 227–291.
- [32] A.K. Soper, Structural Studies of water near an interface, in: J.-C. Dore, J. Teixeira (Eds.), *Hydrogen-Bonded Liquids*, Kluwer Academic, Dordrecht, C329, 1991, pp. 147–158, and references therein.
- [33] A.K. Soper, A. Luzar, Orientation of water molecules around small polar and nonpolar groups in Solution: A neutron diffraction and computer simulation study, *J. Phys. Chem.* 100 (1996) 1357–1367.
- [34] P.J. Steinbach, B.R. Brooks, Protein hydration elucidated by molecular dynamics simulation, *Proc. Natl Acad. Sci. USA* 90 (1993) 9135–9139.
- [35] S. Takahara, S. Kittaka, T. Mori, Y. Kuroda, T. Yamaguchi, K. Shibata, Neutron scattering study on the dynamics of water molecules adsorbed on SrF₂ and ZnO surfaces, *J. Phys. Chem. B* 106 (2002) 5689–5694.
- [36] Y. Tardy, L. Mercury, C. Roquin, P. Vieillard, Le concept d'eau *ice-like*: hydratation-déshydratation des sels, hydroxydes, zéolites, argiles et matières organiques vivantes ou inertes, *C. R. Acad. Sci. Paris, Ser. Ila* 329 (1999) 377–388.
- [37] J. Teixeira, M.-C. Bellissent-Funel, S.H. Chen, A.J. Dianoux, Experimental determination of the nature of diffusive motions of water molecules at low temperatures, *Phys. Rev. A* 31 (1985) 1913–1917.
- [38] P.M. Wiggins, Water structure in polymer membranes, *Prog. Polym. Sci.* 13 (1988) 1–35.
- [39] P.M. Wiggins, B.A.E. MacClement, Two states of water found in hydrophobic clefts: Their possible contribution to mechanisms of action of pumps and other enzymes, *Int. Rev. Cytol.* 108 (1987) 249–304.
- [40] M.A. Winnik, A. Yekta, Associative polymers in aqueous solution, *Curr. Opin. Colloid Interface Sci.* 2 (1997) 424–436.
- [41] J.-M. Zanotti, M.-C. Bellissent-Funel, S.H. Chen, Relaxational dynamics of supercooled water in porous glass, *Phys. Rev. E* 59 (1999) 3084–3093.