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# Classical MD simulations of the IR spectra of amino acids with neutral residues in water. Reassignment of the band around 2300 cm⁻¹

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Aqueous solutions of glycine, phenylalanine and proline were studied using the classical MD simulations. The amino acids were described by Amber and OPLS-AA force fields. The SPC/E and TIP3P models were used for water. Pair correlation functions of the amino acids evaluated using the Amber-TIP3P scheme agree well with the experimental data. This scheme was used in the subsequent simulations. The IR spectrum was obtained from Fourier transform of the autocorrelation function of classical dipole moment of the amino acids. The theoretical frequencies of the IR-intensive bands of glycine in water, associated with N−H and C−H stretching, and N−H bending vibrations, agree with the experimental data. The appearance of band near 2300 cm⁻¹ is a characteristic feature of the theoretical IR spectra of aqueous glycine and phenylalanine. This band is associated with the stretching vibrations of the $NH_3+$ group forming strong $+N−H…O_w$ bonds with the adjacent water molecules. This band appears in the experimental IR spectrum of aqueous solution of glycine, and was treated as a combination band (Spectrochim. Acta A 61 (2005) 2741). In the theoretical IR spectrum of proline no band around 2300 cm⁻¹ was obtained. This difference could be explained by inability of the proline $NH_2+$ group to form strong $+N−H…O_w$ bonds with water molecules.

**Keyword**s: amino acids zwitter-ions, intermolecular H-bonds

# Расчёт ИК-спектров аминокислот с неполярными радикалами методом классической МД. Отнесение полосы в области 2300 см⁻¹

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ИК спектры водных растворов глицина, фенилаланина и пролина рассчитаны методом классической МД. При этом применялись силовые поля Amber и OPLS-AA, а вода описывалась моделями SPC/E и TIP3P. Найдено, что приближение Amber-TIP3P хорошо воспроизводит парные функции распределения расстояний азот – кислород молекул воды. ИК спектры получали посредством Фурье-преобразования автокорреляционной функции дипольного момента аминокислот. Расчетные значения частот ИК-активных полос, обусловленных валентными колебаниями N−H и С−H групп, согласуются с литературными данными. Полоса около 2300 cm⁻¹ существует в расчетных ИК спектрах глицина и фенилаланина. Она обусловлена валентными колебаниями группы $NH_3+$, образующей $+N−H…O_w$ связи с молекулами воды. Эта полоса отсутствует в расчетном ИК спектре пролина.

**Ключевые слова**: цвиттер-ионы аминокислот, межмолекулярные H-связи

### Introduction

The solvation of the simplest amino acids (AAs) as already been investigated with various theoretical methods in recent years, see e.g. Refs. 1-21 for an incomplete list. The microsolvation regime presents an extreme limit of environmental effects on the structure and relative stability of the neutral and zwitterionic forms of AAs [2-6]. This regime led to valuable insights into the hydrogen bond (H-bond) interactions with water molecules; however, it fails to describe the long-range electrostatic effects. The latter can be taken into account in terms of the discrete-continuum model [22, 23] or quantum mechanics-molecular mechanics simulations [7, 8, 24]. The discrete-continuum model is successfully used for evaluation of the vibrational frequencies of molecules in water [25]. A serious drawback of the model is the uncertainty in the minimal number of water molecules required to simulate the diluted aqueous solutions [26]. A few water molecules are usually included into the quantum-chemistry part of the peptide models in the quantum mechanics-molecular mechanics simulations [27-30]. This complicates the adequate description of the solvation because the average number of solvent molecules in the first solvation shell is around 20 for zwitterionic glycine and alanine [8, 9]. A more rigorous description of the solvation phenomenon can be obtained by using explicit solvent models. Classical molecular dynamics (MD) and Monte Carlo simulations [10-16], and the RISM integral equation method [17, 18] led to valuable insights the hydration structure of zwitterions hydrophilic groups. However, the obtained results are very sensitive to the force field used in the simulations [31, 32]. The DFT based on MD (AIMD) simulations [33, 34] are believed to give a reliable description of the local structural motifs [19] and solvation shell of AAs in water [20, 21]. It should be noted that AIMD simulations for modest system sizes (an AA residue/molecule and ~ 50 water molecules) are at present computationally demanding, and for larger sizes (an AA residue/molecule and ~ 1000 water molecules [12, 35]) are currently intractable.

Vibrational spectroscopy has been applied for decades as a powerful probe of AAs, short peptides and protein secondary structures in hydrated media [36]. The major attention is usually focused on the analysis of the N−H stretching vibrations (> 3000 cm$^{-1}$) and the amide I, II and III bands (< 1800 cm$^{-1}$) [37 – 43]. The low-intensive band around 2200 cm$^{-1}$ was detected in the IR spectra of aqueous solutions of AAs with neutral residues [44 - 46]. It was tentatively assigned to the combination band [44, 46]. According to [47 - 51], the IR active band in the 2200–2400 frequency region is a typical feature of the systems with +N−H…O- fragments and short H-bonds. At the same time, in the AIMD study of aqueous solutions of glycine no band around 2300 cm$^{-1}$ was obtained (Table 3 in [20]). This can be explained as follows. It was shown for glycine in water [20], that perturbations of the geometric and electronic structure of the solvating water molecules are astonishingly small even in the first shell compared to bulk water. This conclusion conflicts with the results obtained very recently in the FTIR study of AAs hydration [15]. According to it, "The structural-energetic characteristic of these solute-affected water molecules shows that, on average, water affected by amino acids forms stronger and shorter H-bonds than those in pure water". This discrepancy may be explained by the use of the Perdew–Burke–Ernzerhof exchange correlation density functional [52] in the AIMD study [20]. According to [53, 54], DFT within the generalized gradient approximation poorly reproduces the experimental properties of liquid water. In the present study the IR spectra of aqueous solutions of AAs with neutral residues are evaluated using the classical MD simulations. The main attention is paid to the 1900 – 2500 frequency region.

## Experimental

In the present study a set of AAs with neutral residues is considered. It includes the simplest AA glycine; the AA with the bulky residue, phenylalanine; and proline which contains an unusual ring to the N-end amine group. These AAs contain only two functional groups, therefore un-ionized functional groups are absent in aqueous solutions. L forms of proline and phenylalanine are considered in the present study. For each aqueous AA the cubic cell consisted of a single AA and 1000 water molecules (corresponding to concentration of ~ 0.1 M). Such concentration is typical for aqueous solutions of AAs [55, 56].

MD simulations are conducted using the GROMACS code [57]. Amino acids are described by the Amber force field [58] together with the TIP3P water model [59]. It will be called as the Amber-TIP3P scheme below. To check the sensitivity of the results to force fields the OPLS all-atom force field [60, 61] together with the SPC/E water model [62], the OPLS-SPC/E scheme, is also considered. The equations of motion are integrated using the leap-frog algorithm with a time step of 0.5 fs. Simulations are performed at the constant temperature of 298 K employing the Berendsen thermostat [63] with the time constant of 0.5 ps. An atmospheric pressure of 1 bar is maintained by the Parrinello-Rahman barostat [64] with the coupling constant of 0.5 ps. A short-range nonbonded cutoff of 12 Å is used, and long-range electrostatics were calculated using the particle mesh Ewald method [65] (cutoff was equal to 14 Å). Equilibration of each model is performed for 10 ns in the *NPT* ensemble using the both force fields. The *NVT* simulations are used for the data collection. A time step is 0.5 fs and the trajectory length is 100 ps. The IR spectrum is obtained by the Fourier transformation of the dipole moment autocorrelation function derived of the classical dipole moment [66] and adjusted by the harmonic quantum correction factor [67]. Details of this procedure are given elsewhere [51]. A classical MD simulation gives a reasonable description of the IR spectrum of the liquid systems [68, 69], where a 0.5 fs time step is sufficient to produce reliable IR results for the ~ 2000 cm$^{-1}$ region [70].

## Results and discussion

The considered systems are well equilibrated after 20 ns *NPT* simulations run. The drift of the total energy is less 0.05 kJ/mol. The frame from the end of the *NPT* equilibration with volume closest to the average is used to start the production simulation.

In accord with the literature data [32, 71], a pair correlation function $g(N…O_w)$ of a nitrogen site (N) with respect to the oxygen ($O_w$) sites of the water molecules evaluated for the glycine zwitterionic form is very sensitive to force fields. The first maximum of the $g(N…O_w)$ function of glycine in water is at 2.76 Å (OPLS-SPC/E) and 2.94 Å (Amber-TIP3P). The latter value is in accord with isotopic neutron diffraction experiments [72], where a similar mean N…$O_w$ distance of 2.93 +/- 0.03 Å was deducted based on the N…$O_w$ correlation. To find out the scheme that gives reasonable results for the considered systems, different pair correlation functions of proline in water were evaluated. This AA was chosen because its aqueous solution was studied by neutron diffraction (ND) [11, 73]. The computed values of the first maximum position of the computed pair correlation functions are compared with the available literature data in Table 1. The values evaluated using the Amber-TIP3P scheme for non-hydrogen atoms agree with the ND data much better, than those evaluated using the OPLS-SPC/E scheme. We conclude that simulations

using the Amber-TIP3P scheme describe the $g(N{\ldots}O_w)$ function of aqueous solutions of AAs, considered in the study, quite realistically.

Table 1. The computed values of the first maximum position of different pair correlation functions of aqueous solution of proline vs. the literature data (the units are Å)

| RDF [a] | OPLS-SPC/E | AMBER-TIP3P | ND [73] | RISM [74] |
|---|---|---|---|---|
| $N-O_W$ | 2.74 | 2.92 | 2.90 | 3.00 |
| $O_1-O_W$ | 2.62 | 2.72 | 2.80 | 3.10 |
| $O_2-O_W$ | 2.66 | 2.70 | 2.80 | 3.13 |
| $O_1-H_W$ | 1.64 | 1.78 | 1.80 | 1.75 |
| $O_2-H_W$ | 1.66 | 1.78 | 1.80 | 1.78 |

[a] N and $H_n$ denote the nitrogen and hydrogen sites of proline, while $O_W$ and $H_W$ denote the oxygen and hydrogen sites of the water molecules

The dipole correlation function of aqueous AAs is well converged. Computed IR spectrum of glycine in water evaluated using the Amber-TIP3P scheme is given in Fig. 1. A tentative assignment of the IR-intensive bands is given in Table 2. Obtained results enable us to make the following conclusions. The theoretical frequencies of the IR-intensive bands of glycine in water, associated with N−H and C−H stretching, and N−H bending vibrations, agree with the experimental data. Their frequencies systematically overestimated on 100-200 cm$^{-1}$. At the same time, the classical MD simulations do not give a correct description of amid II and III bands. The appearance of band near 2300 cm$^{-1}$ is a characteristic feature of the theoretical IR spectrum of glycine in water. This band is associated with the stretching vibrations of the NH$_3$+ group forming strong +N−H…O$_w$ bonds with the adjacent water molecules, see the next Section. In the theoretical IR spectrum of proline no band around 2300 cm$^{-1}$ was obtained (Fig. 1). Proline is the naturally occurring AA with a secondary α-amino group, which explains its more basic character with respect to many other α-AA [75]. We believe that the absence of this band in proline is explained by inability of the proline NH$_2$+ group to form strong +N−H…O$_w$ bonds with water molecules. In contrast to proline, the band around 2300 cm$^{-1}$ does exist in the theoretical IR spectrum of phenylalanine in water (Fig. 2).
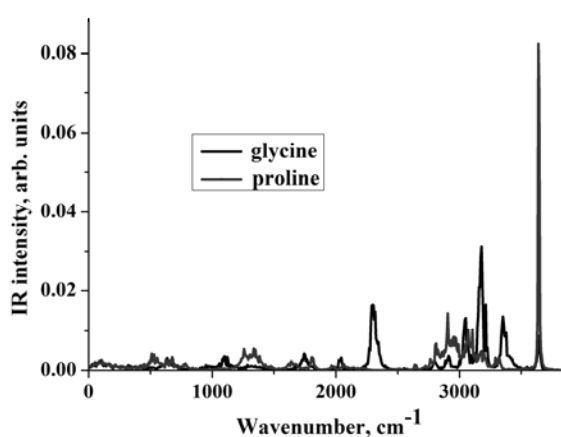


Fig. 1. IR spectra of glycine and proline in water evaluated using the Amber-TIP3P scheme.

The computer simulation and the experimental correlation times for the bond rotations in NH$_3$+ groups in peptides and proteins suggest that their hydrogen bonding is highly dynamic with a subnanosecond lifetime. According to [76] lifetimes of H-bonds

between lysine side-chain amino groups in proteins and water molecules vary from 2 to 4 ps. Assuming that strong $^+$N–H…O$^-$ bonds forming by glycine and phenylalanine zwitterions with water molecules exist around 4 ps, we conclude that these bonds can be detected by IR spectroscopy.

Table 2. Comparison of the theoretical frequencies of the IR-intensive bands of glycine in water, evaluated using the Amber-TIP3P scheme, with the literature data (the units are $cm^{-1}$).

| This work | AIMD [20] | Exp. [44] | Tentative assignment |
|---|---|---|---|
| 3646 | - | - | "Free" N−H str. |
| 3352/3179 | 3064 +/- | -/3170 | Asymm. N−H str./Symm. N−H str. |
| 3045/2918 | 335 | -/2898 | Asymm. C−H str./Symm. C−H str. |
| 2304 | - | 2140 | Asymm. str. of the +N−H…O$_w$ moety |
| 2024 | - | - | CO$_2$ str. |
| 1750 | 1630 +/- 20 | 1615 | N−H bend. |
| - | 1535 +/- 60 | 1510 | NH$_3$ umbrella +C H$_2$ wagg. [b] |
| - | - | 1412 | C H$_2$ bend. [b] |
| - | 1350 +/- 10 | 1332 | C −C$_c$ str. +C$_c$−O$_c$ str. +C −H bend. [b] |
| - | 1295 +/- 10 | - | C H$_2$ wagg. [b] |
| 1110 | 1112 +/- 40 | 1111 | H−N−C bend. |

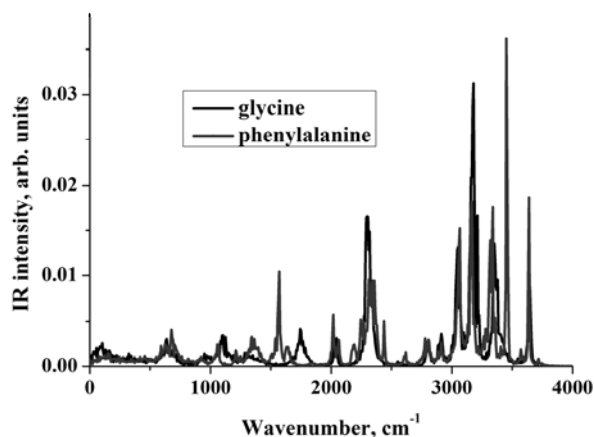[a] The designations introduced in Table 3 in [20]



Fig. 2. IR spectra of glycine and phenylalanine in water evaluated using the Amber-TIP3P scheme.

## Conclusions

The theoretical frequencies of the IR-intensive bands of glycine in water, associated with N−H and C−H stretching, and N−H bending vibrations, agree with the experimental data. The classical MD simulations do not give a correct description of amid II and III bands.

The appearance of band near 2300 $cm^{-1}$ is a characteristic feature of the theoretical IR spectra of glycine and phenylalanine in water. This band is associated with the stretching vibrations of the NH$_3$+ group forming strong +N−H…O$_w$ bonds with the adjacent water molecules. In the theoretical IR spectrum of aqueous solution of proline no band around 2300 $cm^{-1}$ was obtained. This difference could be explained by inability of the proline NH$_2$+ group to form strong +N−H…O$_w$ bonds with water molecules.

## References

1. Aikens C.M., Gordon M.S., *J. Am. Chem. Soc.,* 2006, Vol. 128, pp. 12835-12850.
2. Rodziewicz P., Doltsinis N.L., Chem.Phys.Chem., 2007, Vol.8, pp. 1959 - 1968.
3. Bachrach S.M., *J. Phys. Chem. A,* 2008, Vol. 112, pp. 3722-3730.
4. Rai A.K., Fei W., Lu Z., Lin Z., *Theor. Chem. Acc.,* 2009, Vol. 124, pp. 37-47.
5. Jacquemin D., Michaux C., Perpete E.A., Frison G., *J. Phys. Chem. B*, 2011, Vol. 115, pp. 3604-3613.
6. Kim J.Y., Ahn D.S., Park S.W. et al., *RSC Adv.,*2014, Vol. 4, pp. 16352-16361.
7. Hugosson H.W., Laio A., Maurer P., Rothlisberger U., *J. Comput. Chem.,* 2006, Vol. 27, pp. 672-684.
8. Jalkanen K.J., Degtyarenko I.M., Nieminen R.M., Cao X., Nafie L.A., Zhu F., Barron L.D., *Theor. Chem. Acc.,* 2008, Vol.119, pp. 191-210.
9. Niskanen J., Murugan N.A., Rinkevicius Z., Vahtras O., Monti S., Carravetta V., Ågren H., *Phys. Chem. Chem. Phys.*, 2013, Vol. 15, pp. 244-254.
10. Chang J., Lenhoff A.M., Sandler S.I., *J. Phys. Chem. B*, 2007, Vol. 111, pp. 2098-2106.
11. Troitzsch R.Z., Martyna G. J., McLain S.E., Soper A.K., *J. Crain, J. Phys. Chem. B*, 2007, Vol.111, pp. 8210-8222.
12. Sterpone F., Stirnemann G., Hynes J.T., Laage D., *J. Phys. Chem. B*, 2010, Vol. 114, pp. 2083-2089.
13. Horn A.H.C., *J. Mol. Model.*, 2014, Vol. 20, pp. 2478-2592.
14. Amninder S. V. , Timothy S.G., Scott A.W., Allan M.T., William S.P., *Frontiers in Physics*, 2015, Vol. 3, pp. 1-15.
15. Panuszko A., Adamczak B., Czub J., Gojło E., *J. Stangret, Amino Acids*, 2015, Vol. 47, pp. 2265-2278.
16. Bastida A., Zuniga J., Requena A., Miguel B., Candela M.E., Soler M.A., *J. Phys. Chem. B*, 2016, Vol.120, pp. 348-357.
17. Fedotova M.V., Kruchinin S.E., *J. Mol. Liq.*, 2012, Vol. 169, pp. 1-7.
18. Fedotova M.V., Dmitrieva O.A., *Amino Acids*, 2015, Vol. 47, pp. 1015-1023.
19. Troitzsch R.Z., Tulip P.R., Crain J., Martyna G.J., *Biophys. J.*, Vol. 95, 2008, pp. 5014-5020.
20. Sun J., Bousquet D., Forbert H., Marx D., *J. Chem. Phys.*, 2010, Vol. 133, pp. 114508-114518.
21. Sun J., Niehues G., Forbert H., Decka D., Schwaab G., Marx D., Havenith M., *J. Am. Chem. Soc.*, 2014, Vol.136, pp. 5031-5038.
22. Tuñón I., Rinaldi D., Ruiz-López M.F., Rivail J.L., *J. Phys. Chem.*, 1995, Vol. 99, pp. 3798-3805.
23. Da Silva E.F., Svendsen H.F., Merz K.M., *J. Phys. Chem. A*, 2009, Vol. 113, pp. 6404-6409.
24. Brancato G., Barone V., Rega N., *Theor. Chem. Acc.,* 2007, Vol. 117, pp. 1001-1015.
25. Barone V., Carnimeo I., Scalmani G., *J. Chem. Theory Comput.*, 2013, Vol. 9, pp. 2052-2071.
26. Vener M. V., Shenderovich I. G., Rykounov A. A., *Theor. Chem. Acc.,* 2013, Vol. 132, pp. 1-9.
27. Lee Y.S., Krauss M., *J. Am. Chem. Soc.*, 2004, Vol. 126, pp. 2225–2230.
28. Mathias G., Marx D., *Proc. Natl. Acad. Sci. USA*, 2007, Vol. 104, pp. 6980–6985.
29. Kaliman I., Grigorenko B., Shadrina M., Nemukhin A., *Phys. Chem. Chem. Phys.*, 2009, Vol. 11, pp. 4804-4807.
30. Goyal P., Ghosh N., Phatak P., Clemens M., Gaus M. et al., *J. Am. Chem. Soc.*, 2011, Vol. 133, pp. 14981-14997.
31. Liang T., Walsh T. R., *Phys. Chem. Chem. Phys.,* 2006, Vol. 8, pp. 4410–4419.
32. Debiec K.T., Gronenborn A.M., Chong L.T., *J. Phys. Chem. B*, 2014, Vol. 118, pp. 6561–6569.
33. Iftimie R., Tuckerman M. E., *J. Chem. Phys.*, 2005, Vol. 122, pp. 214508 (1-11).
34. Gaigeot M.P., *Phys. Chem. Chem. Phys.*, 2010, Vol. 12, pp. 3336-3359.
35. Rocchi C., Bizzarri A.R., Cannistraro S., *Phys. Rev. E*, 1998, Vol. 57, pp. 3315-3325.
36. Barth A., *Biochim. Biophys. Acta*, 2007, Vol. 1767, pp. 1073-1101.
37. Wolpert M., Hellwig P., *Spectrochim. Acta A,* 2006, Vol. 64, pp. 987-1001.
38. Derbel N., Hernández B., Pflüger F., Liquier J., Geinguenaud F. et al., *J. Phys. Chem. B*, 2007, Vol. 111, pp.1470–1477.
39. Daněček P., Kapitán J., Baumruk V., Bednárová L. et al., *J. Chem. Phys.*, 2007, Vol. 126, pp. 224513 (1-13 ).
40. Chowdhry B.Z., Dines T.J., Jabeen S., Withnal R., *J. Phys. Chem. A*, 2008, Vol. 112, pp. 10333-10347.

41. Panuszko A., Smiechowski M., Stangret J., *J. Chem. Phys.*, 2010, Vol. 134, pp. 115104 (1-9).

42. Hernández B., Pflüger F., Adenier A. et al., *J. Phys. Chem. B*, 2010, Vol. 114, pp.15319-15330.

43. Moreno J.R.A., Moreno M.M.Q., Ureña F.P. et al., *Asymmetry*, 2012, Vol. 23, pp. 1084-1092.

44. Kumar S., Rai A.K., Singh V.B., Rai S.B., *Spectrochimica Acta Part A*, 2005, Vol. 61, pp. 2741-2746.

45. Kitadai N., Yokoyama T., Nakashima S., *J. Mol. Struct.*, 2010, Vol. 981, pp. 179-186.

46. Kumar S., *Elixir. Vib. Spec.*, 2011, Vol. 39, pp. 4996-4999.

47. Johnson S.L., Rumon K.A., *J. Phys. Chem.*, 1965, Vol. 69, pp. 74-86.

48. Kong S., Shenderovich I.G., Vener M.V., *J. Phys. Chem. A*, 2010, Vol. 114, pp. 2393-2399.

49. Mukherjee A., Tothadi S., Chakraborty S. et al., *Cryst. Eng. Comm.*, 2013, Vol. 15, pp. 4640-4654.

50. Chakraborty S., Ganguly S., Desiraju G.R., *Cryst. Eng. Comm.*, 2014, Vol. 16, pp. 4732-4741.

51. Vener M.V., Odinokov F.V., et al., *J. Chem. Phys.*, 2015, Vol. 142, pp. 215106 (1-9).

52. Perdew J.P., Burke K., Ernzerhof M., *Phys. Rev. Lett.,* 1996, Vol. 77, pp. 3865-3868.

53. Schwegler E., Grossman J.C., Gygi F., Galli G., *J. Chem. Phys.*, 2004, Vol. 121, pp. 5400-5409.

54. Jonchiere R., Seitsonen A.P. et al., *J. Chem. Phys.*, 2011, Vol. 135, pp. 154503 (1-10).

55. Needham T.E., Paruta A.N., Gerraughty R.J., *J. Pharm. Sci.*, 1971, Vol. 60, pp. 565-567.

56. Gomaa E.A., *American Journal of Biochemistry*, 2012, Vol. 2, pp. 25-28.

57. Berendsen H. J. C., Spoel D., Drunen R., *Comp. Phys. Comm.*, 1995, Vol. 91, pp. 43-56.

58. Lindorff-Larsen K., Piana S. et al., *Proteins*, 2010, Vol. 78, pp. 1950-1958.

59. Jorgensen W.L., Chandrasekhar J., Madura J.D. et al., *J. Chem. Phys*., 1983, Vol. 79, pp. 926-935.

60. Jorgensen W.L., Maxwell D.S., Tirado-Rives J., *J. Am. Chem. Soc.*, 1996, Vol. 118, pp. 11225-11236.

61. Kaminski G.A., Friesner R.A. et al., *J. Phys. Chem. B*, 2001, Vol. 105, pp. 6471-6474.

62. Berendsen H. J. C., Grigera J. R., Sraatsma T.P., *J. Phys. Chem.,* 1987, Vol. 91, pp. 6269-6271.

63. Berendsen H. J. C., Postma J. P. M., et al., *J. Chem. Phys*., 1984, Vol. 81, pp. 3684-3690.

64. Parrinello M., Rahman A., *J. Appl. Phys*., 1981, Vol. 52, pp. 7182-7190.

65. Perera U. L., Berkowitz M. L., Darden T. Et al., *J. Chem. Phys*., 1995, Vol. 103, pp. 8577-8593.

66. Bosma W.B., Fried L.E., Mukamel S., *J. Chem. Phys*., 1993, Vol. 98, pp. 4413-4421.

67. Vener M.V., Sauer J., *Phys. Chem. Chem. Phys*., 2005, Vol. 7, pp. 258-263.

68. Praprotnik M., Janezic D., Mavri J., *J. Phys. Chem. A*, 2004, Vol. 108, pp. 11056–11062.

69. Praprotnik M., Janeži D., *J. Chem. Phys*., 2005, Vol. 122, pp. 174103(1-10).

70. Yu. H., Cui Q., *J. Chem. Phys.,* 2007, Vol. 127, pp. 234504(1-8).

71. Andrews C.T., Elcock A.H., *J. Chem. Theory Comp*., 2013, Vol. 9, pp. 4585-4602.

72. Sugawara K., Kameda Y., Usuki T. et al., *Bull. Chem. Soc. Jpn*., 2000, Vol. 73, pp. 1967-1972.

73. McLain S.E., Soper A.K., Terry A.E., Watts A., *J. Phys. Chem*. B, 2007, Vol. 111, pp. 4568-4580.

74. Fedotova M.V., Dmitrieva O.A., *Russ. J. Phys. Chem. A*, Vol., 2014, Vol. 88, pp. 794-797.

75. Mary Y.S., Ushakumarib L., Harikumarc B., Varghesed H.T., Panickerb C.Y., *J. Iran Chem.* Soc., 2009, Vol. 6, pp. 138-144.

76. Esadze A., Li D.W., Wang T., Bruschweiler R., Iwahara J., *J. Am. Chem. Soc*., 2011, Vol. 133, pp. 909-919 .

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