

Supplementary Material

**Similarities and differences in interaction of K⁺ and Na⁺ with
condensed ordered DNA. A molecular dynamics simulation study.**

Yuhua Cheng, Nikolay Korolev and Lars Nordenskiöld

Table 1S. General properties of the simulated systems.

System	Cell dimension, Å	Density, g/cm ³	Box volume, nm ³	Species concentration, M	Diffusion parameters: $D \cdot 10^{10}$, m ² /s ($\langle R \rangle$, Å)*
K/20	43.4×37.6×33.0	1.318	53.85	37.52 (H ₂ O) 2.001 (K ⁺) 0.125 (Cl ⁻)	7.0 (20.6) H ₂ O 3.52 (14.6) K ⁺ 3.0 (13.5) Cl ⁻
K/15	39.5×34.2×33.2	1.375	44.7	33.21 (H ₂ O) 2.214 (K ⁺)	4.35 (16.2) H ₂ O 1.76 (10.3) K ⁺
Na/20	42.8×37.1×32.9	1.326	52.2	38.39 (H ₂ O) 2.048 (Na ⁺) 0.128 (Cl ⁻)	5.5 (18.2) H ₂ O 1.33 (8.9) Na ⁺ 3.22 (10.3) Cl ⁻
Na/15	39.1×33.8×32.8	1.382	43.9	34.82 (H ₂ O) 2.321 (Na ⁺)	2.82 (13.0) H ₂ O 0.58 (5.93) Na ⁺
K/20-22 [¶]	45.9×39.8×29.4	1.320	53.72	37.11 (H ₂ O) 1.979 (K ⁺) 0.124 (Cl ⁻)	6.9 (20.4) H ₂ O 3.30 (14.1) K ⁺ 3.08 (13.6) Cl ⁻
K/15-22 [¶]	43.3×37.5×27.7	1.371	44.8	33.30 (H ₂ O) 2.220 (K ⁺)	4.30 (16.1) H ₂ O 1.90 (10.7) K ⁺
Na/20-22 [¶]	44.2×38.3×30.8 ₅	1.328	51.9	38.40 (H ₂ O) 2.045 (Na ⁺) 0.128 (Cl ⁻)	4.75 (17.0) H ₂ O 1.40 (9.2) Na ⁺ 2.05 (11.2) Cl ⁻
Na/15-22 [¶]	43.3×34.3×32.0	1.380	43.3	34.55 (H ₂ O) 2.303 (Na ⁺)	2.85 (13.1) H ₂ O 0.56 (5.8) Na ⁺

* D is diffusion coefficient; $\langle R \rangle$ is root mean square displacement calculated for 1 ns. [¶] 10 ns MD simulations with CHARMM22 force field, other conditions are similar to these of corresponding system simulated with the use of the CHARMM27 force field.

Experimental and MD simulation data for comparison

I. Low water content

1. Ref. (1); Experimental data on Na-DNA oriented fibers, NMR relaxation method: 85% relative humidity (RH), 13 H₂O/nucleotide, $D_{\text{wat}}=2.1 \cdot 10^{-10} \text{ m}^2/\text{s}$; 95% RH, 22 H₂O/nucleotide, $D_{\text{wat}}=5.3 \cdot 10^{-10} \text{ m}^2/\text{s}$.
2. Ref. (1); MD simulation data; CHARMM22 force field, water model SPC, Ref. (2). Na⁺, model Ref. (3), 15 H₂O/phosphate: $D_{\text{Na}}=0.55 \cdot 10^{-10} \text{ m}^2/\text{s}$, $D_{\text{wat}}=2.5 \cdot 10^{-10} \text{ m}^2/\text{s}$; 20 H₂O/phosphate: $D_{\text{Na}}=1.3 \cdot 10^{-10} \text{ m}^2/\text{s}$, $D_{\text{wat}}=4.6 \cdot 10^{-10} \text{ m}^2/\text{s}$.

II. Water solutions.

3. Ref. (4); experimental data for simple salt solution at infinite dilution,: $D_{\text{Na}}=13.3 \cdot 10^{-10} \text{ m}^2/\text{s}$; $D_{\text{K}}=19.6 \cdot 10^{-10} \text{ m}^2/\text{s}$; $D_{\text{wat}}=23 \cdot 10^{-10} \text{ m}^2/\text{s}$.
4. Ref. (5); MD simulations of water: water model, SPC, Ref. (2), $D_{\text{wat}}=(42.0 \pm 0.8) \cdot 10^{-10} \text{ m}^2/\text{s}$; water model SPC/E, Ref. (6), $D_{\text{wat}}=(27-28) \cdot 10^{-10} \text{ m}^2/\text{s}$; water model TIP3P original Ref. (7), $D_{\text{wat}}=(54-56) \cdot 10^{-10} \text{ m}^2/\text{s}$; water model TIP3P modified Ref. (8), $D_{\text{wat}}=(59.0 \pm 0.8) \cdot 10^{-10} \text{ m}^2/\text{s}$.
5. Ref. (9); MD simulation data for simple salt solution at infinite dilution (water model, SPC/E, Ref. (6), Na⁺, K⁺, Ref. (3)): $D_{\text{Na}}=(12.8 \pm 0.5) \cdot 10^{-10} \text{ m}^2/\text{s}$; $D_{\text{K}}=(18.3 \pm 1.3) \cdot 10^{-10} \text{ m}^2/\text{s}$.
6. Ref. (10), MD simulation of the DNA solution, (227 H₂O/DNA phosphate; Amber, parm99; water model, TIP3P; Na⁺ and K⁺ models, Ref. (11)): $D_{\text{Na}}=17 \cdot 10^{-10} \text{ m}^2/\text{s}$, $D_{\text{K}}=28 \cdot 10^{-10} \text{ m}^2/\text{s}$.
7. Ref. (12), MD simulation of the DNA solution, (180 H₂O/DNA phosphate; Amber, parm94, water model TIP3P; Na⁺, Ref. (11)): $D_{\text{Na}} \sim 10 \cdot 10^{-10} \text{ m}^2/\text{s}$.

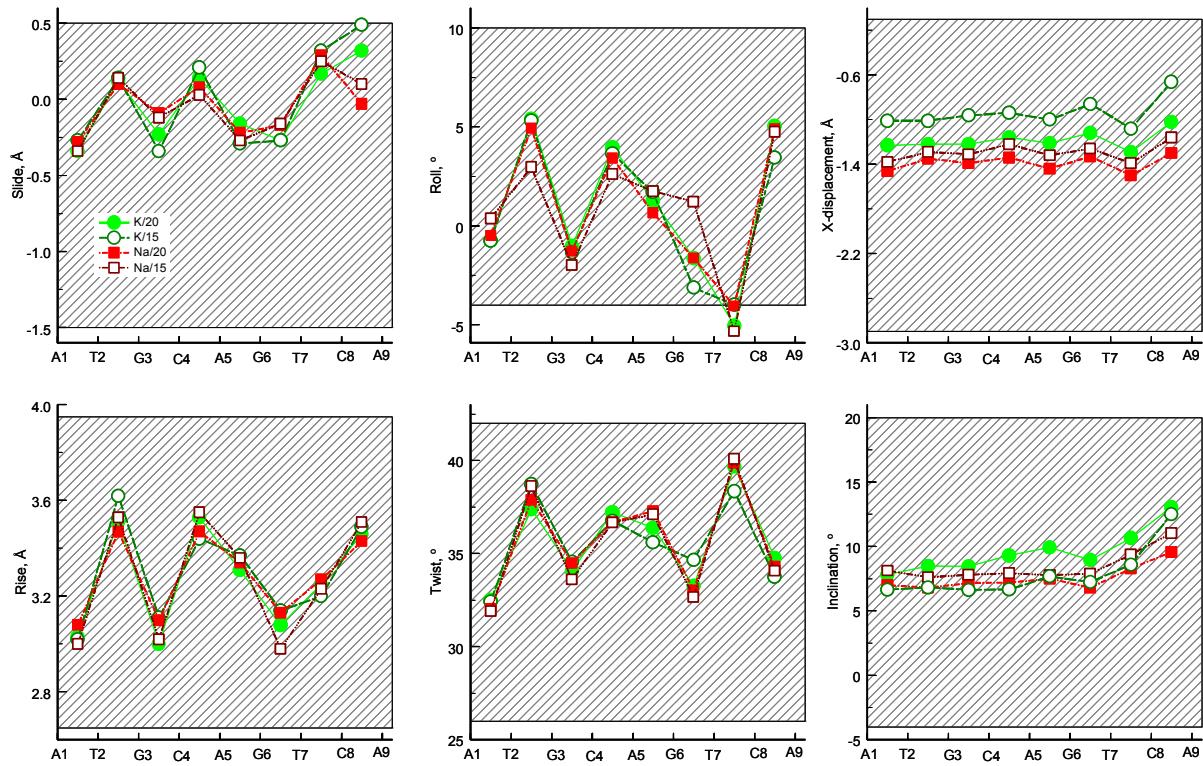


Figure 1S. Structural parameters (slide, roll, x-displacement, rise, twist, and inclination) of DNA base pair steps calculated by Curve5.2 (13) from averaged (over 20 ns and 3 decamers in the simulation cell) DNA structures of the four systems studied in the present work. The graphs show variation of the parameters in dependence of the DNA sequence. Shaded area shows regions typical for the B-DNA family found from analysis of X-ray crystallography data. The values of these six parameters are grouped in pairs (slide/rise, roll/twist, x-displacement/inclination) and displayed in Fig. 1 of the main text.

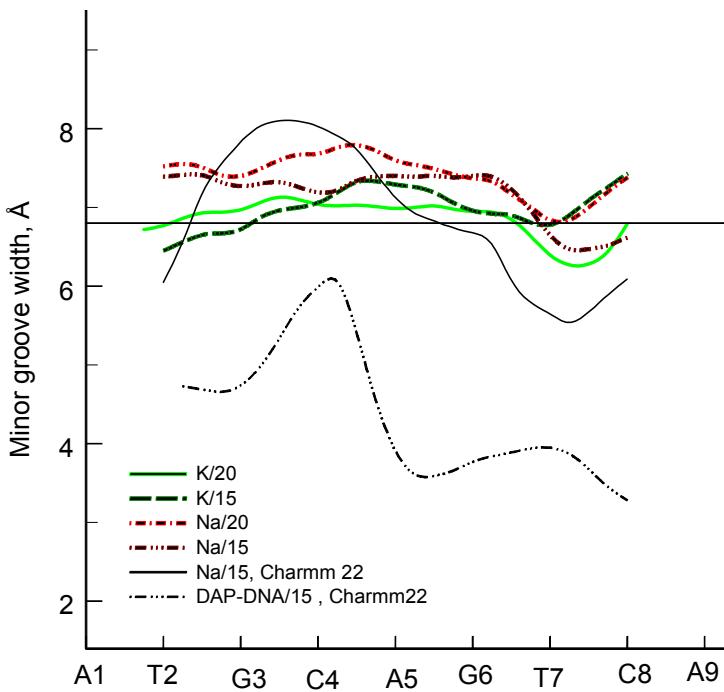


Figure 2S. Average minor groove width of the DNA sequence (*x*-axis) studied in the present work. For comparison, data is given from our earlier work (14) using Charmm22 force field calculated from a 6 ns simulation for the same DNA sequence and 15 H₂O/nucleotide with Na⁺ (thin black line) and the synthetic polyamine (diaminopropane²⁺, DAP, thin dot-dashed black line) as the DNA counterions. The DAP-DNA system shows an example of strong influence of the ligand binding on the DNA structure. **Horizontal bar shows the value of the minor groove width of the “ideal” B-DNA.**

Table 2S. Averaged occupancies and residence times (in ps) for water (Ow) and K⁺/Na⁺. Numbers separated by slash are average and longest residence time respectively.

DNA site	Ow				K ⁺ or Na ⁺			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
Phosphate oxygen								
O1P Occupancy	2.59	2.82	2.61	2.68	0.24	0.17	0.35	0.22
Res. time	6.99/1278	5.56/1188	6.00/2520	5.95/2028	7.84/1566	5.88/510	58.3/11880	41.4/4752
O2P Occupancy	2.67	2.65	2.58	2.75	0.14	0.09	0.14	0.08
Res. time	7.54/1158	7.29/876	8.48/1482	7.35/1020	5.77/684	5.02/414	24.3/3744	18.8/1506
O3*	Occupancy	1.05	1.06	1.18	1.15	0.08	0.06	0.04
Res. time	3.36/648	3.09/372	3.99/1878	3.58/744	5.45/702	4.73/288	5.62/1392	3.58/894
O5*	Occupancy	0.29	0.32	0.38	0.36	0.03	0.02	0.01
Res. time	2.05/342	1.58/288	2.08/3612	1.81/732	3.55/678	3.54/2682	1.78/270	3.57/2328
Sugar								
O4*	Occupancy	1.00	1.14	1.32	1.19	0.24	0.17	0.05
Res. time	4.90/1404	4.64/888	5.76/5628	5.63/2742	14.0/3702	13.1/1722	16.2/7240	17.9/2328
Minor groove								
TO2 Occupancy	0.87	1.05	1.54	1.61	0.47	0.31	0.10	0.14
Res. time	3.49/1098	3.74/498	5.23/2046	5.14/1518	16.5/2532	15.2/1278	28.0/2868	27.9/2484
CO2 Occupancy	1.09	1.11	1.22	1.22	0.21	0.16	0.04	0.04
Res. time	5.57/714	5.00/1380	6.41/4734	6.44/1938	8.78/2004	8.56/1440	9.60/768	9.86/990
AN3 Occupancy	0.89	0.94	1.08	1.08	0.30	0.20	0.03	0.05
Res. time	5.05/834	6.11/672	9.27/5196	8.23/3396	32.8/4194	25.5/1884	10.0/696	23.6/1896
GN3 Occupancy	1.04	1.07	1.13	1.15	0.15	0.12	0.03	0.03
Res. time	6.91/858	6.89/1188	7.75/2994	7.94/1500	12.07/1770	7.82/774	27.1/2160	13.9/1356

Continuation of Table 2S

DNA site	Ow				K^+ or Na^+			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
Major groove								
AN7 Occupancy	0.95	0.95	1.09	1.09	0.22	0.19	0.09	0.09
Res. time	5.28/438	5.46/438	5.29/852	5.12/618	22.5/2700	16.8/1080	38.3/2406	44.6/1452
GN7 Occupancy	0.98	1.11	1.27	1.31	0.28	0.26	0.05	0.06
Res. time	4.02/696	3.67/444	4.72/840	4.61/576	23.5/1038	25.1/1398	22.1/708	19.5/1020
GO6 Occupancy	0.95	0.95	1.40	1.43	0.30	0.27	0.05	0.05
Res. time	3.97/252	3.95/270	5.49/948	5.46/1278	32.65/2946	32.75/2856	16.0/654	12.0/588
TO4 Occupancy	1.05	1.00	1.38	1.26	0.14	0.17	0.01	0.01
Res. time	3.76/228	3.73/240	4.31/612	4.24/582	8.44/996	9.15/1110	5.15/174	5.87/258
K^+/Na^+ Occupancy	7.28	7.56	5.295	5.47				
Res. time	7.06/3120	5.98/1280	19.9/5820	18.3/2920				

MD simulation results on K^+/Na^+ – Ow coordination number and residence time:

Data for comparison: Ref. (9); MD simulation data for simple salt solution at infinite dilution (water model, SPC/E, Ref. (6), Na^+ , K^+ , Ref. (3)): K^+ - Ow occupancy 7.1, $RT_{av} = 14.3$ ps; Na^+ - Ow occupancy 5.8, $RT_{av} = 22.4$ ps. (In the cited work, values of RT_{av} were calculated assuming 2 ps delay time; delay time used in the present work was 1 ps).

Table 3S. Occupancies and average and longest (in parentheses) residence times (in ps) of K⁺/Na⁺ and water (Ow) near electronegative sites of the DNA bases.

TO2

DNA site	K ⁺ or Na ⁺				Ow			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
T2 Occupancy	0.65	0.39	0.10	0.14	0.90	1.13	1.57	1.60
Res. time	11.2 (1566)	11.5 (804)	23.7 (942)	26.0 (1806)	3.45 (444)	3.59 (348)	5.18 (1188)	5.13 (1224)
T7 Occupancy	0.50	0.34	0.23	0.13	0.84	1.02	1.67	1.49
Res. time	31.5 (2532)	20.9 (1074)	92.0 (3180)	29.4 (1434)	3.08 (288)	3.59 (498)	4.98 (2046)	4.99 (1086)
T11 Occupancy	0.48	0.31	0.05	0.04	0.78	0.99	1.37	1.35
Res. time	31.6 (2130)	28.7 (1278)	17.0 (1182)	17.4 (1074)	3.05 (942)	3.23 (330)	5.31 (1428)	4.71 (846)
T15 Occupancy	0.40	0.18	0.06	0.20	0.90	1.16	1.41	1.37
Res. time	22.6 (2502)	20.6 (852)	26.4 (816)	36.5 (2496)	3.54 (720)	4.12 (390)	5.74 (870)	5.15 (972)
T19 Occupancy	0.33	0.33	0.12	0.18	1.17	1.19	1.81	1.46
Res. time	10.0 (1788)	11.6 (960)	15.9 (1146)	22.9 (1806)	4.46 (1098)	4.28 (396)	5.16 (918)	4.66 (600)

CO2

DNA site	K ⁺ or Na ⁺				Ow			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
C4 Occupancy	0.08	0.06	0.00	0.01	0.94	0.98	0.92	1.09
Res.time	10.80(474)	8.79(252)	5.68(78)	6.78(96)	5.14(348)	5.22(414)	5.82(1476)	6.36(1572)
C8 Occupancy	0.38	0.32	0.09	0.07	0.97	0.98	1.37	1.55
Res.time	8.87(942)	9.60(1440)	7.34(702)	9.27(750)	4.56(480)	3.89(246)	6.87(4734)	6.90(2010)
C14 Occupancy	0.21	0.18	0.03	0.09	1.17	1.17	1.33	1.23
Res.time	7.29(1998)	8.90(810)	14.33(570)	25.71(990)	6.65(360)	5.74(402)	6.11(1974)	6.55(1284)
C17 Occupancy	0.10	0.09	0.03	0.01	0.95	1.01	0.96	1.07
Res.time	22.67(678)	16.49(516)	19.17(768)	4.55(72)	5.35(318)	5.24(318)	5.94(624)	6.40(678)
C20 Occupancy	0.31	0.20	0.02	0.04	1.02	1.28	1.48	1.28
Res.time	7.38(744)	6.65(474)	14.10(294)	8.26(210)	4.36(468)	5.01(1380)	6.94(3966)	6.27(1056)

AN3

GN3

DNA site	K^+ or Na^+				Ow			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
G3 Occupancy	0.12	0.09	0.01	0.01	1.04	1.12	1.23	1.20
	Res.time	10.4 (1152)	6.91 (426)	16.5 (288)	10.4 (168)	7.52 (858)	7.08 (516)	8.30 (1512)
G6 Occupancy	0.15	0.10	0.02	0.02	1.03	1.08	1.26	1.26
	Res.time	10.9 (1770)	9.93 (372)	22.3 (360)	34.1 (774)	8.34 (696)	8.55 (582)	8.42 (2994)
G10 Occupancy	0.07	0.16	0.06	0.04	1.09	0.95	1.14	1.08
	Res.time	12.5 (870)	14.3 (600)	63.9 (2160)	21.5 (1356)	6.58 (780)	6.56 (984)	5.98 (1536)
G12 Occupancy	0.30	0.10	0.01	0.02	0.83	1.05	1.07	1.15
	Res.time	16.0 (924)	10.3 (444)	9.25 (84)	13.7 (222)	6.20 (732)	6.02 (1188)	7.51 (1710)
G16 Occupancy	0.11	0.11	0.07	0.05	1.23	1.12	1.13	1.17
	Res.time	7.10 (504)	8.06 (738)	43.8 (1458)	25.9 (726)	6.82 (810)	6.63 (582)	7.76 (1740)

GN7

G06

DNA site	K^+ or Na^+				Ow			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
G3 Occupancy	0.12	0.11	0.00	0.02	1.60	1.46	1.38	1.66
	Res.time	20.5 (786)	14.9 456)	7.46 (144)	9.15 (216)	6.01 (414)	5.71 (294)	5.80 (402)
G6 Occupancy	0.51	0.45	0.17	0.10	0.58	0.73	1.34	1.43
	Res.time	37.6 (1326)	40.8 (1296)	18.6 (654)	23.0 (528)	2.82 (180)	2.68 (150)	4.87 (816)
G10 Occupancy	0.61	0.57	0.05	0.12	0.54	0.58	1.36	1.60
	Res.time	105 (2946)	89.5 (2856)	12.5 (342)	10.8 (588)	2.58 (150)	2.66 (108)	5.37 (696)
G12 Occupancy	0.12	0.10	0.01	0.01	1.18	1.05	1.32	1.29
	Res.time	11.7 (774)	15.1 (732)	7.09 (96)	14.4 (168)	5.38 (252)	5.48 (270)	5.84 (444)
G16 Occupancy	0.11	0.11	0.01	0.01	1.36	1.43	1.71	1.51
	Res.time	14.2 (414)	13.8 (414)	14.5 (138)	5.64 (132)	5.64 (306)	5.68 (360)	5.95 (498)

AN7

DNA site	K^+ or Na^+				Ow			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
A1 Occupancy	0.02	0.03	0.06	0.01	1.10	1.05	1.11	1.10
	Res.time	20.4 (318)	26.5 (330)	107 (654)	84.3 (558)	6.21 (372)	6.82 (480)	6.67 (672)
A5 Occupancy	0.46	0.36	0.21	0.15	0.88	0.92	1.18	1.19
	Res.time	22.3 (780)	16.9 (900)	29.4 (2406)	45.9 (1242)	3.48 (234)	3.58 (252)	3.83 (852)
A9 Occupancy	0.57	0.49	0.13	0.22	0.77	0.84	1.19	0.93
	Res.time	23.4 (2058)	15.9 (972)	50.7 (2010)	35.6 (936)	2.90 (240)	3.19 (234)	3.47 (540)
A13 Occupancy	0.01	n.a.	0.03	0.05	1.13	1.13	1.04	1.05
	Res.time	26.0 (282)	n.a.	129 (1500)	101 (1452)	4.94 (438)	5.04 (402)	6.95 (570)
A18 Occupancy	0.03	0.07	0.03	0.02	1.07	1.01	1.07	1.09
	Res.time	22.9 (486)	55.4 (1080)	109 (1368)	71.0 (492)	7.27 (444)	6.81 (438)	8.35 (546)

T04

DNA site	K ⁺ or Na ⁺				Ow			
	K/15	K/20	Na/15	Na/20	K/15	K/20	Na/15	Na/20
T2 Occupancy	0.03	0.05	0.01	0.01	1.06	1.25	1.25	1.28
	Res.time	5.24 (126)	5.70 (168)	4.65 (60)	6.31 (198)	3.38 (162)	3.43 (150)	3.76 (414)
T7 Occupancy	0.24	0.27	0.06	0.03	1.55	1.66	1.87	1.88
	Res.time	7.66 (300)	8.88 (240)	8.97 (870)	6.44 (258)	5.33 (240)	5.31 (342)	5.70 (774)
T11 Occupancy	0.00	0.00	n.a.	0.00	0.61	0.78	0.94	0.96
	Res.time	4.00 (156)	1.84 (30)	n.a.	8.50 (138)	3.28 (156)	3.16 (144)	3.39 (288)
T15 Occupancy	0.00	0.01	0.00	n.a.	0.87	0.85	1.01	0.95
	Res.time	1.59 (42)	2.49 (72)	6.93 (84)	n.a.	3.85 (174)	4.22 (240)	4.53 (372)
T19 Occupancy	0.47	0.48	0.01	0.02	1.03	0.98	1.93	1.58
	Res.time	12.4 (1008)	13.7 (1110)	3.88 (90)	4.89 (132)	3.52 (168)	3.11 (222)	5.09 (528)

References

1. Korolev, N., Lyubartsev, A.P., Laaksonen, A. and Nordenskiöld, L. (2003) A molecular dynamics simulation study of oriented DNA with polyamine and sodium counterions: diffusion and averaged binding of water and cations. *Nucleic Acids Res.*, **31**, 5971-5981.
2. Toukan, K. and Rahman, A. (1985) Molecular-dynamics study of atomic motions in water. *Phys.Rev.B*, **31**, 2643-2648.
3. Smith, D.E. and Dang, L.X. (1994) Computer-simulations of NaCl association in polarizable water. *J.Chem.Phys.*, **100**, 3757-3766.
4. Harned, H.S. and Robinson, R.A. (1968) The International Encyclopedia of Physical Chemistry and Chemical Physics. Pergamon Press, Oxford.
5. Mark, P. and Nilsson, L. (2001) Structure and dynamics of the TIP3P, SPC, and SPC/E water models at 298 K. *J.Phys.Chem.A*, **105**, 9954-9960.
6. Berendsen, H.J.C., Grigera, J.R. and Straatsma, T.P. (1987) The missing term in effective pair potentials. *J.Phys.Chem.*, **91**, 6269-6271.
7. Jorgensen, W.L., Chandrasekhar, J., Madura, J.D., Impey, R.W. and Klein, M.L. (1987) Comparison of simple potential functions for simulating liquid water. *J.Chem.Phys.*, **79**, 926-935.
8. Neria, E., Fischer, S. and Karplus, M. (1996) Simulation of activation free energies in molecular systems. *J.Chem.Phys.*, **105**, 1902-1921.
9. Koneshan, S., Rasaiah, J.C., Lynden-Bell, R.M. and Lee, S.H. (1998) Solvent structure, dynamics, and ion mobility in aqueous solutions at 25° C. *J.Phys.Chem.B*, **102**, 4193-4204.
10. Varnai, P. and Zakrzewska, K. (2004) DNA and its counterions: a molecular dynamics study. *Nucleic Acids Res.*, **32**, 4269-4280.
11. Aqvist, J. (1990) Ion-water interaction potentials derived from free energy perturbation simulations. *J.Phys.Chem.*, **94**, 8021-8024.
12. Ponomarev, S.Y., Thayer, K.M. and Beveridge, D.L. (2004) Ion motion in molecular dynamics simulations on DNA. *Proc.Natl.Acad.Sci.U.S.A.*, **101**, 14771-14775.
13. Stofer, E. and Lavery, R. (1994) Measuring the geometry of DNA grooves. *Biopolymers*, **34**, 337-346.
14. Korolev, N., Lyubartsev, A.P., Laaksonen, A. and Nordenskiöld, L. (2004) A molecular dynamics simulation study of polyamine- and sodium-DNA. Interplay between polyamine binding and DNA structure. *Eur.Biophys.J.*, **33**, 671-682.