

# Volodymyr Babin

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

28

papers

1,808

citations

17

h-index

31

g-index

31

ext. papers

2,030

ext. citations

4.8

avg, IF

5.01

L-index

#	Paper	IF	Citations
28	The Adaptively Biased Molecular Dynamics method revisited: New capabilities and an application. <i>Journal of Physics: Conference Series</i> , <b>2015</b> , 640, 012020	0.3	8
27	Development of a "First Principles" Water Potential with Flexible Monomers. II: Trimer Potential Energy Surface, Third Virial Coefficient, and Small Clusters. <i>Journal of Chemical Theory and Computation</i> , <b>2014</b> , 10, 1599-607	6.4	230
26	Development of a "First-Principles" Water Potential with Flexible Monomers. III. Liquid Phase Properties. <i>Journal of Chemical Theory and Computation</i> , <b>2014</b> , 10, 2906-10	6.4	227
25	The curious case of the water hexamer: Cage vs. Prism. <i>Chemical Physics Letters</i> , <b>2013</b> , 580, 1-8	2.5	36
24	Recipes for free energy calculations in biomolecular systems. <i>Methods in Molecular Biology</i> , <b>2013</b> , 924, 313-37	1.4	5
23	A Critical Assessment of Two-Body and Three-Body Interactions in Water. <i>Journal of Chemical Theory and Computation</i> , <b>2013</b> , 9, 1103-14	6.4	111
22	Electrostatics interactions in classical simulations. <i>Methods in Molecular Biology</i> , <b>2013</b> , 924, 243-70	1.4	6
21	Development of a "First Principles" Water Potential with Flexible Monomers: Dimer Potential Energy Surface, VRT Spectrum, and Second Virial Coefficient. <i>Journal of Chemical Theory and Computation</i> , <b>2013</b> , 9, 5395-403	6.4	296
20	Binding polymorphism in the DNA bound state of the Pdx1 homeodomain. <i>PLoS Computational Biology</i> , <b>2013</b> , 9, e1003160	5	8
19	Reaction path ensemble of the B-Z-DNA transition: a comprehensive atomistic study. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 33-43	20.1	39
18	Toward a Universal Water Model: First Principles Simulations from the Dimer to the Liquid Phase. <i>Journal of Physical Chemistry Letters</i> , <b>2012</b> , 3, 3765-9	6.4	114
17	The water hexamer: cage, prism, or both. Full dimensional quantum simulations say both. <i>Journal of the American Chemical Society</i> , <b>2012</b> , 134, 11116-9	16.4	114
16	Are long-range structural correlations behind the aggregation phenomena of polyglutamine diseases?. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002501	5	14
15	A statistical analysis of the PPII propensity of amino acid guests in proline-rich peptides. <i>Biophysical Journal</i> , <b>2011</b> , 100, 1083-93	2.9	23
14	PPII propensity of multiple-guest amino acids in a proline-rich environment. <i>Journal of Physical Chemistry B</i> , <b>2011</b> , 115, 8645-56	3.4	15
13	The $\beta$ -sheet: a missing-in-action secondary structure?. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2011</b> , 79, 937-46	4.2	17
12	Conformational free energies of methyl-alpha-L-iduronic and methyl-beta-D-glucuronic acids in water. <i>Journal of Chemical Physics</i> , <b>2010</b> , 132, 104108	3.9	44

11	A classical molecular dynamics investigation of the free energy and structure of short polyproline conformers. <i>Journal of Chemical Physics</i> , <b>2010</b> , 133, 125104	3.9	29
10	Free energy and structure of polyproline peptides: An ab initio and classical molecular dynamics investigation. <i>International Journal of Quantum Chemistry</i> , <b>2010</b> , 110, 2865-2879	2.1	15
9	Conformations and free energy landscapes of polyproline peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 20746-51	11.5	80
8	Adaptively biased molecular dynamics: An umbrella sampling method with a time-dependent potential. <i>International Journal of Quantum Chemistry</i> , <b>2009</b> , 109, 3666-3678	2.1	27
7	Adaptively biased molecular dynamics for free energy calculations. <i>Journal of Chemical Physics</i> , <b>2008</b> , 128, 134101	3.9	138
6	Deprotonation of solvated formic acid: Car-Parrinello and metadynamics simulations. <i>Journal of Physical Chemistry B</i> , <b>2006</b> , 110, 2325-31	3.4	49
5	The free energy landscape of small peptides as obtained from metadynamics with umbrella sampling corrections. <i>Journal of Chemical Physics</i> , <b>2006</b> , 125, 204909	3.9	72
4	Molecular dynamics simulations of DNA with polarizable force fields: convergence of an ideal B-DNA structure to the crystallographic structure. <i>Journal of Physical Chemistry B</i> , <b>2006</b> , 110, 11571-81	3.4	62
3	Molecular dynamics simulations of polarizable DNA in crystal environment. <i>International Journal of Quantum Chemistry</i> , <b>2006</b> , 106, 3260-3269	2.1	12
2	Pattern formation in nonextensive thermodynamics: selection criterion based on the Renyi entropy production. <i>Journal of Chemical Physics</i> , <b>2005</b> , 122, 174105	3.9	4
1	Minimization of the Renyi entropy production in the stationary states of the Brownian process with matched death and birth rates. <i>Physical Review E</i> , <b>2004</b> , 69, 016110	2.4	8