

Vojtech Mlynsky

List of Publications by Year in descending order

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687363

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#	ARTICLE	IF	CITATIONS
1	Toward Convergence in Folding Simulations of RNA Tetraloops: Comparison of Enhanced Sampling Techniques and Effects of Force Field Modifications. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 2642-2656.	5.3	34
2	Automatic Learning of Hydrogen-Bond Fixes in the AMBER RNA Force Field. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 4490-4502.	5.3	21
3	W-RESP: Well-Restrained Electrostatic Potential-Derived Charges. Revisiting the Charge Derivation Model. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 3495-3509.	5.3	18
4	Short-Range Imbalances in the AMBER Lennard-Jones Potential for (Deoxy)Ribose-Nucleobase Lone-Pair-Contacts in Nucleic Acids. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 5644-5657.	5.4	5
5	UUCG RNA Tetraloop as a Formidable Force-Field Challenge for MD Simulations. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 7601-7617.	5.3	29
6	Fine-Tuning of the AMBER RNA Force Field with a New Term Adjusting Interactions of Terminal Nucleotides. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 3936-3946.	5.3	39
7	Improving the Performance of the Amber RNA Force Field by Tuning the Hydrogen-Bonding Interactions. <i>Journal of Chemical Theory and Computation</i> , 2019, 15, 3288-3305.	5.3	97
8	Exploring RNA structure and dynamics through enhanced sampling simulations. <i>Current Opinion in Structural Biology</i> , 2018, 49, 63-71.	5.7	47
9	Molecular Dynamics Simulations Reveal an Interplay between SHAPE Reagent Binding and RNA Flexibility. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 313-318.	4.6	30
10	Understanding in-line probing experiments by modeling cleavage of nonreactive RNA nucleotides. <i>Rna</i> , 2017, 23, 712-720.	3.5	10
11	Mapping the Chemical Space of the RNA Cleavage and Its Implications for Ribozyme Catalysis. <i>Journal of Physical Chemistry B</i> , 2017, 121, 10828-10840.	2.6	4
12	The role of an active site Mg ²⁺ in HDV ribozyme self-cleavage: insights from QM/MM calculations. <i>Physical Chemistry Chemical Physics</i> , 2015, 17, 670-679.	2.8	28
13	Reactive Conformation of the Active Site in the Hairpin Ribozyme Achieved by Molecular Dynamics Simulations with μ/σ Force Field Reparametrizations. <i>Journal of Physical Chemistry B</i> , 2015, 119, 4220-4229.	2.6	45
14	Comparison of ab Initio, DFT, and Semiempirical QM/MM Approaches for Description of Catalytic Mechanism of Hairpin Ribozyme. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 1608-1622.	5.3	56
15	QM/MM Studies of Hairpin Ribozyme Self-Cleavage Suggest the Feasibility of Multiple Competing Reaction Mechanisms. <i>Journal of Physical Chemistry B</i> , 2011, 115, 13911-13924.	2.6	33
16	Extensive Molecular Dynamics Simulations Showing That Canonical G8 and Protonated A38H ⁺ Forms Are Most Consistent with Crystal Structures of Hairpin Ribozyme. <i>Journal of Physical Chemistry B</i> , 2010, 114, 6642-6652.	2.6	81