

Sandro Bottaro

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.

40
papers

1,494
citations

21
h-index

38
g-index

49
ext. papers

2,163
ext. citations

10.4
avg, IF

5.95
L-index

#	Paper	IF	Citations
40	MEDTEC Students against Coronavirus: Investigating the Role of Hemostatic Genes in the Predisposition to COVID-19 Severity. <i>Journal of Personalized Medicine</i> , 2021 , 11,	3.6	1
39	Conformational Ensembles of Noncoding Elements in the SARS-CoV-2 Genome from Molecular Dynamics Simulations. <i>Journal of the American Chemical Society</i> , 2021 , 143, 8333-8343	16.4	2
38	Integrating NMR and simulations reveals motions in the UUCG tetraloop. <i>Nucleic Acids Research</i> , 2020 , 48, 5839-5848	20.1	5
37	Combining molecular dynamics simulations with small-angle X-ray and neutron scattering data to study multi-domain proteins in solution. <i>PLoS Computational Biology</i> , 2020 , 16, e1007870	5	39
36	Structure and dynamics of a nanodisc by integrating NMR, SAXS and SANS experiments with molecular dynamics simulations. <i>ELife</i> , 2020 , 9,	8.9	20
35	How to learn from inconsistencies: Integrating molecular simulations with experimental data. <i>Progress in Molecular Biology and Translational Science</i> , 2020 , 170, 123-176	4	35
34	Integrating Molecular Simulation and Experimental Data: A Bayesian/Maximum Entropy Reweighting Approach. <i>Methods in Molecular Biology</i> , 2020 , 2112, 219-240	1.4	60
33	Combining molecular dynamics simulations with small-angle X-ray and neutron scattering data to study multi-domain proteins in solution 2020 , 16, e1007870		
32	Combining molecular dynamics simulations with small-angle X-ray and neutron scattering data to study multi-domain proteins in solution 2020 , 16, e1007870		
31	Combining molecular dynamics simulations with small-angle X-ray and neutron scattering data to study multi-domain proteins in solution 2020 , 16, e1007870		
30	Combining molecular dynamics simulations with small-angle X-ray and neutron scattering data to study multi-domain proteins in solution 2020 , 16, e1007870		
29	Fitting Corrections to an RNA Force Field Using Experimental Data. <i>Journal of Chemical Theory and Computation</i> , 2019 , 15, 3425-3431	6.4	31
28	Promoting transparency and reproducibility in enhanced molecular simulations. <i>Nature Methods</i> , 2019 , 16, 670-673	21.6	271
27	Barnaba: software for analysis of nucleic acid structures and trajectories. <i>Rna</i> , 2019 , 25, 219-231	5.8	21
26	Effects and limitations of a nucleobase-driven backmapping procedure for nucleic acids using steered molecular dynamics. <i>Biochemical and Biophysical Research Communications</i> , 2018 , 498, 352-358	3.4	4
25	A nucleobase-centered coarse-grained representation for structure prediction of RNA motifs. <i>Nucleic Acids Research</i> , 2018 , 46, 1674-1683	20.1	17
24	RNA Structural Dynamics As Captured by Molecular Simulations: A Comprehensive Overview. <i>Chemical Reviews</i> , 2018 , 118, 4177-4338	68.1	235

23	Biophysical experiments and biomolecular simulations: A perfect match?. <i>Science</i> , 2018 , 361, 355-360	33.3	110
22	Conformational ensembles of RNA oligonucleotides from integrating NMR and molecular simulations. <i>Science Advances</i> , 2018 , 4, eaar8521	14.3	59
21	Mapping the Universe of RNA Tetraloop Folds. <i>Biophysical Journal</i> , 2017 , 113, 257-267	2.9	24
20	Computer Folding of RNA Tetraloops: Identification of Key Force Field Deficiencies. <i>Journal of Chemical Theory and Computation</i> , 2016 , 12, 4534-48	6.4	77
19	RNA folding pathways in stop motion. <i>Nucleic Acids Research</i> , 2016 , 44, 5883-91	20.1	29
18	Empirical Corrections to the Amber RNA Force Field with Target Metadynamics. <i>Journal of Chemical Theory and Computation</i> , 2016 , 12, 2790-8	6.4	42
17	Free Energy Landscape of GAGA and UUCG RNA Tetraloops. <i>Journal of Physical Chemistry Letters</i> , 2016 , 7, 4032-4038	6.4	49
16	Accurate multiple time step in biased molecular simulations. <i>Journal of Chemical Theory and Computation</i> , 2015 , 11, 139-46	6.4	21
15	Kissing loop interaction in adenine riboswitch: insights from umbrella sampling simulations. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 9, S6	3.6	26
14	Elastic network models for RNA: a comparative assessment with molecular dynamics and SHAPE experiments. <i>Nucleic Acids Research</i> , 2015 , 43, 7260-9	20.1	28
13	The role of nucleobase interactions in RNA structure and dynamics. <i>Nucleic Acids Research</i> , 2014 , 42, 13306-14	20.1	75
12	Formulation of probabilistic models of protein structure in atomic detail using the reference ratio method. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 288-99	4.2	8
11	PHAISTOS: a framework for Markov chain Monte Carlo simulation and inference of protein structure. <i>Journal of Computational Chemistry</i> , 2013 , 34, 1697-705	3.5	31
10	Variational Optimization of an All-Atom Implicit Solvent Force Field to Match Explicit Solvent Simulation Data. <i>Journal of Chemical Theory and Computation</i> , 2013 , 9, 5641-5652	6.4	38
9	An efficient null model for conformational fluctuations in proteins. <i>Structure</i> , 2012 , 20, 1028-39	5.2	7
8	Subtle Monte Carlo Updates in Dense Molecular Systems. <i>Journal of Chemical Theory and Computation</i> , 2012 , 8, 695-702	6.4	21
7	Generative probabilistic models extend the scope of inferential structure determination. <i>Journal of Magnetic Resonance</i> , 2011 , 213, 182-6	3	15
6	Potentials of mean force for protein structure prediction vindicated, formalized and generalized. <i>PLoS ONE</i> , 2010 , 5, e13714	3.7	51

5	Accuracy of the pseudopotential approximation in ab initio theoretical spectroscopies. <i>Physical Review B</i> , 2008 , 78,	3-3	23
4	Combining molecular dynamics simulations with small-angle X-ray and neutron scattering data to study multi-domain proteins in solution		2
3	Conformational Ensemble of RNA Oligonucleotides from Reweighted Molecular Simulations		2
2	Integrating Molecular Simulation and Experimental Data: A Bayesian/Maximum Entropy reweighting approach		11
1	Structure and dynamics of a nanodisc by integrating NMR, SAXS and SANS experiments with molecular dynamics simulations		1