

Brian K Radak

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1738611/publications.pdf>

Version: 2024-02-01

25
papers

2,521
citations

567281

15
h-index

552781

26
g-index

28
all docs

28
docs citations

28
times ranked

3081
citing authors

#	ARTICLE	IF	CITATIONS
1	Scalable molecular dynamics on CPU and GPU architectures with NAMD. <i>Journal of Chemical Physics</i> , 2020, 153, 044130.	3.0	1,548
2	Alchemical Binding Free Energy Calculations in AMBER20: Advances and Best Practices for Drug Discovery. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5595-5623.	5.4	177
3	Constant-pH Molecular Dynamics Simulations for Large Biomolecular Systems. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 5933-5944.	5.3	139
4	Rigorous Free Energy Simulations in Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 4153-4169.	5.4	114
5	A New Maximum Likelihood Approach for Free Energy Profile Construction from Molecular Simulations. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 153-164.	5.3	76
6	Experimental and computational analysis of the transition state for ribonuclease A-catalyzed RNA 2'- <i>O</i> -transphosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13002-13007.	7.1	62
7	Roadmaps through Free Energy Landscapes Calculated Using the Multidimensional vFEP Approach. <i>Journal of Chemical Theory and Computation</i> , 2014, 10, 24-34.	5.3	58
8	A Variational Linear-Scaling Framework to Build Practical, Efficient Next-Generation Orbital-Based Quantum Force Fields. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 1417-1427.	5.3	55
9	Boosting Free-Energy Perturbation Calculations with GPU-Accelerated NAMD. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5301-5307.	5.4	37
10	Improved Alchemical Free Energy Calculations with Optimized Smoothstep Softcore Potentials. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 5512-5525.	5.3	35
11	Enhanced configurational sampling with hybrid non-equilibrium molecular dynamicsâ€“Monte Carlo propagator. <i>Journal of Chemical Physics</i> , 2018, 148, 014101.	3.0	26
12	A Two-Metal-Ion-Mediated Conformational Switching Pathway for HDV Ribozyme Activation. <i>ACS Catalysis</i> , 2016, 6, 1853-1869.	11.2	24
13	Accounting for the Central Role of Interfacial Water in Proteinâ€™Ligand Binding Free Energy Calculations. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 7883-7894.	5.3	24
14	Molecular Simulations of RNA 2'- <i>O</i> -Transesterification Reaction Models in Solution. <i>Journal of Physical Chemistry B</i> , 2013, 117, 94-103.	2.6	21
15	Assessment of metal-assisted nucleophile activation in the hepatitis delta virus ribozyme from molecular simulation and 3D-RISM. <i>Rna</i> , 2015, 21, 1566-1577.	3.5	18
16	Multiscale Methods for Computational RNA Enzymology. <i>Methods in Enzymology</i> , 2015, 553, 335-374.	1.0	16
17	Fast Equilibration of Water between Buried Sites and the Bulk by Molecular Dynamics with Parallel Monte Carlo Water Moves on Graphical Processing Units. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 7366-7372.	5.3	16
18	Efficiency in nonequilibrium molecular dynamics Monte Carlo simulations. <i>Journal of Chemical Physics</i> , 2016, 145, 134109.	3.0	15

#	ARTICLE	IF	CITATIONS
19	Modeling Reactive Scattering of F_2 at a Liquid Squalane Interface: A Hybrid QM/MM Molecular Dynamics Study. <i>Journal of Physical Chemistry A</i> , 2009, 113, 7218-7226.	2.5	13
20	A Multidimensional B-Spline Correction for Accurate Modeling Sugar Puckering in QM/MM Simulations. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 3975-3984.	5.3	12
21	Characterization of the Three-Dimensional Free Energy Manifold for the Uracil Ribonucleoside from Asynchronous Replica Exchange Simulations. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 373-377.	5.3	10
22	A generalized linear response framework for expanded ensemble and replica exchange simulations. <i>Journal of Chemical Physics</i> , 2018, 149, 072315.	3.0	7
23	Precise Binding Free Energy Calculations for Multiple Molecules Using an Optimal Measurement Network of Pairwise Differences. <i>Journal of Chemical Theory and Computation</i> , 2022, 18, 650-663.	5.3	7
24	Modeling Ion Channels Using Poisson-Nernst-Planck Theory as an Integrated Approach To Introducing Nanotechnology Concepts: The PNP Cyclic Peptide Ion Channel Model. <i>Journal of Chemical Education</i> , 2008, 85, 744.	2.3	2
25	Finite-sample bias in free energy bridge estimators. <i>Journal of Chemical Physics</i> , 2019, 151, 034105.	3.0	1