

Joseph A Morrone

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1701232/publications.pdf>

Version: 2024-02-01

24
papers

1,300
citations

361413

20
h-index

610901

24
g-index

24
all docs

24
docs citations

24
times ranked

1670
citing authors

#	ARTICLE	IF	CITATIONS
1	Ab initio molecular dynamics study of proton mobility in liquid methanol. <i>Journal of Chemical Physics</i> , 2002, 117, 4403-4413.	3.0	135
2	Advances in free-energy-based simulations of protein folding and ligand binding. <i>Current Opinion in Structural Biology</i> , 2016, 36, 25-31.	5.7	121
3	Ab Initio Molecular Dynamics Simulation of the Structure and Proton Transport Dynamics of Methanolâ€”Water Solutionsâ€”. <i>Journal of Physical Chemistry B</i> , 2006, 110, 3712-3720.	2.6	101
4	Quantum fluctuations can promote or inhibit glassâ€”formation. <i>Nature Physics</i> , 2011, 7, 134-137.	16.7	84
5	Role of water and steric constraints in the kinetics of cavityâ€”ligand unbinding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 12015-12019.	7.1	74
6	Computed Binding of Peptides to Proteins with MELD-Accelerated Molecular Dynamics. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 870-876.	5.3	68
7	Proton momentum distribution in water: an open path integral molecular dynamics study. <i>Journal of Chemical Physics</i> , 2007, 126, 234504.	3.0	66
8	Tunneling and delocalization effects in hydrogen bonded systems: A study in position and momentum space. <i>Journal of Chemical Physics</i> , 2009, 130, 204511.	3.0	65
9	Combining Docking Pose Rank and Structure with Deep Learning Improves Proteinâ€”Ligand Binding Mode Prediction over a Baseline Docking Approach. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 4170-4179.	5.4	64
10	Molecular Dynamics with Multiple Time Scales: How to Avoid Pitfalls. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 1798-1804.	5.3	57
11	Blind protein structure prediction using accelerated free-energy simulations. <i>Science Advances</i> , 2016, 2, e1601274.	10.3	57
12	Interplay between Hydrodynamics and the Free Energy Surface in the Assembly of Nanoscale Hydrophobes. <i>Journal of Physical Chemistry B</i> , 2012, 116, 378-389.	2.6	52
13	Displaced Path Integral Formulation for the Momentum Distribution of Quantum Particles. <i>Physical Review Letters</i> , 2010, 105, 110602.	7.8	49
14	Molecular Simulations Identify Binding Poses and Approximate Affinities of Stapled Î±-Helical Peptides to MDM2 and MDMX. <i>Journal of Chemical Theory and Computation</i> , 2017, 13, 863-869.	5.3	49
15	Correlated Tunneling in Hydrogen Bonds. <i>Journal of Statistical Physics</i> , 2011, 145, 365-384.	1.2	45
16	How hydrophobic drying forces impact the kinetics of molecular recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 13277-13282.	7.1	45
17	Structure and Dynamics of Acetonitrile Confined in a Silica Nanopore. <i>Journal of Physical Chemistry C</i> , 2012, 116, 9582-9593.	3.1	38
18	Are Hydrodynamic Interactions Important in the Kinetics of Hydrophobic Collapse?. <i>Journal of Physical Chemistry B</i> , 2012, 116, 11537-11544.	2.6	29

#	ARTICLE	IF	CITATIONS
19	Binding Specificity Determines the Cytochrome P450 3A4 Mediated Enantioselective Metabolism of Metconazole. <i>Journal of Physical Chemistry B</i> , 2018, 122, 1176-1184.	2.6	29
20	Long range interactions on wires: A reciprocal space based formalism. <i>Journal of Chemical Physics</i> , 2004, 121, 11949-11956.	3.0	24
21	A simple quantum mechanical/molecular mechanical (QM/MM) model for methanol. <i>Chemical Physics Letters</i> , 2003, 370, 406-411.	2.6	17
22	Accelerating physical simulations of proteins by leveraging external knowledge. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2017, 7, e1309.	14.6	16
23	Simplified, interpretable graph convolutional neural networks for small molecule activity prediction. <i>Journal of Computer-Aided Molecular Design</i> , 2022, 36, 391-404.	2.9	10
24	Analysis of Training and Seed Bias in Small Molecules Generated with a Conditional Graph-Based Variational Autoencoder—Insights for Practical AI-Driven Molecule Generation. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 801-816.	5.4	5