

Benjamin R Jagger

List of Publications by Year in descending order

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Version: 2024-02-01

10
papers

217
citations

1684188

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h-index

1474206

9
g-index

14
all docs

14
docs citations

14
times ranked

294
citing authors

#	ARTICLE	IF	CITATIONS
1	SEKR: Simulation Enabled Estimation of Kinetic Rates, A Computational Tool to Estimate Molecular Kinetics and Its Application to Trypsinâ€“Benzamidine Binding. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3597-3606.	2.6	84
2	Predicting Ligand Binding Kinetics Using a Markovian Milestoning with Voronoi Tessellations Multiscale Approach. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 5348-5357.	5.3	37
3	Quantitative Ranking of Ligand Binding Kinetics with a Multiscale Milestoning Simulation Approach. <i>Journal of Physical Chemistry Letters</i> , 2018, 9, 4941-4948.	4.6	35
4	Multiscale simulation approaches to modeling drugâ€“protein binding. <i>Current Opinion in Structural Biology</i> , 2020, 61, 213-221.	5.7	29
5	Ranking of Ligand Binding Kinetics Using a Weighted Ensemble Approach and Comparison with a Multiscale Milestoning Approach. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 5340-5352.	5.4	21
6	Distinguishing the Protonation State of the Histidine Ligand to the Oxidized Ironâ€“Sulfur Cluster from the MitoNEET Family of Proteins. <i>ChemPhysChem</i> , 2017, 18, 39-41.	2.1	3
7	Distinguishing Protonation States of Histidine Ligands to the Oxidized Rieske Ironâ€“Sulfur Cluster through ¹⁵ N Vibrational Frequency Shifts. <i>ChemPhysChem</i> , 2016, 17, 216-220.	2.1	2
8	SEKR: Simulation Enabled Estimation of Kinetic Rates, A Multiscale Approach for the Calculation of Protein-Ligand Association and Dissociation Kinetics. <i>Biophysical Journal</i> , 2018, 114, 42a.	0.5	2
9	Computational Predictions of Drug-Protein Binding Kinetics with a Hybrid Molecular Dynamics, Brownian Dynamics, and Milestoning Approach. <i>Biophysical Journal</i> , 2019, 116, 562a.	0.5	2
10	Benchmarking ensemble docking methods in D3R Grand Challenge 4. <i>Journal of Computer-Aided Molecular Design</i> , 2022, 36, 87-99.	2.9	0