Emiliano Brini

List of Publications by Year
in descending order

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21	1,062	840776	839539
papers	citations	11 h-index	18 g-index

21	21	21	1464
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Systematic coarse-graining methods for soft matter simulations â€“ a review. Soft Matter, 2013, 9, 2108-2119.	2.7	301
2	How Waterâ€™s Properties Are Encoded in Its Molecular Structure and Energies. Chemical Reviews, 2017, 117, 12385-12414.	47.7	284
3	Conditional reversible work method for molecular coarse graining applications. Physical Chemistry Chemical Physics, 2011, 13, 10468.	2.8	77
4	Grid-Based Backbone Correction to the ff12SB Protein Force Field for Implicit-Solvent Simulations. Journal of Chemical Theory and Computation, 2015, 11, 4770-4779.	5.3	76
5	Chemically transferable coarse-grained potentials from conditional reversible work calculations. Journal of Chemical Physics, 2012, 137, 154113.	3.0	58
6	Blind protein structure prediction using accelerated free-energy simulations. Science Advances, 2016, 2, e1601274.	10.3	57
7	Protein storytelling through physics. Science, 2020, 370, .	12.6	49
8	Shape Governs the Motion of Chemically Propelled Janus Swimmers. Journal of Physical Chemistry C, 2012, 116, 592-598.	3.1	47
9	Thermodynamic transferability of coarse-grained potentials for polymerâ€“additive systems. Physical Chemistry Chemical Physics, 2012, 14, 11896.	2.8	26
10	NMRâ€assisted protein structure prediction with MELDxMD. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1333-1340.	2.6	20
11	Predicting Protein Dimer Structures Using MELD Ã— MD. Journal of Chemical Theory and Computation, 2019, 15, 3381-3389.	5.3	15
12	Computing Ligands Bound to Proteins Using MELD-Accelerated MD. Journal of Chemical Theory and Computation, 2020, 16, 6377-6382.	5.3	15
13	Modeling betaâ€sheet peptideâ€protein interactions: Rosetta FlexPepDock in CAPRI rounds 38â€45. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1037-1049.	2.6	10
14	Sampling and refinement protocols for template-based macrocycle docking: 2018 D3R Grand Challenge 4. Journal of Computer-Aided Molecular Design, 2020, 34, 179-189.	2.9	8
15	Accelerating Protein Folding Molecular Dynamics Using Inter-Residue Distances from Machine Learning Servers. Journal of Chemical Theory and Computation, 2022, 18, 1929-1935.	5.3	8
16	ClusPro in rounds 38 to 45 of CAPRI: Toward combining templateâ€based methods with free docking. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1082-1090.	2.6	5
17	Adapting the semi-explicit assembly solvation model for estimating water-cyclohexane partitioning with the SAMPL5 molecules. Journal of Computer-Aided Molecular Design, 2016, 30, 1067-1077.	2.9	3
18	Accelerating Molecular Dynamics Enrichments of High-Affinity Ligands for Proteins. Journal of Chemical Theory and Computation, 2022, 18, 374-379.	5.3	2

#	Article	IF	Citations
19	Determining Protein Structures using Accelerated MD Simulations and Noisy Data. Biophysical Journal, 2020, 118, 141a.	0.5	1
20	Combining Physics and Knowledge in Blind Protein Structure Prediction. Biophysical Journal, 2016, 110, 345a.	0.5	0
21	Computing Poses of Ligands Bound to Proteins using MELD Accelerated Molecular Dynamics. Biophysical Journal, 2020, 118, 323a.	0.5	0