

Jan DomaÅ„ski

List of Publications by Year in descending order

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Version: 2024-02-01

10
papers

1,008
citations

1039406

9
h-index

1473754

9
g-index

10
all docs

10
docs citations

10
times ranked

1181
citing authors

#	ARTICLE	IF	CITATIONS
1	Martini 3: a general purpose force field for coarse-grained molecular dynamics. <i>Nature Methods</i> , 2021, 18, 382-388.	9.0	557
2	Atomistic mechanism of transmembrane helix association. <i>PLoS Computational Biology</i> , 2020, 16, e1007919.	1.5	16
3	Multiple lipid binding sites determine the affinity of PH domains for phosphoinositide-containing membranes. <i>Science Advances</i> , 2020, 6, eaay5736.	4.7	44
4	Balancing Force Field Protein-Lipid Interactions To Capture Transmembrane Helix-Helix Association. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 1706-1715.	2.3	40
5	Interactions of the EphA2 Kinase Domain with PIPs in Membranes: Implications for Receptor Function. <i>Structure</i> , 2018, 26, 1025-1034.e2.	1.6	33
6	Convergence and Sampling in Determining Free Energy Landscapes for Membrane Protein Association. <i>Journal of Physical Chemistry B</i> , 2017, 121, 3364-3375.	1.2	93
7	Ligandbook: an online repository for small and drug-like molecule force field parameters. <i>Bioinformatics</i> , 2017, 33, 1747-1749.	1.8	17
8	Lipid-Loving ANTs: Molecular Simulations of Cardiolipin Interactions and the Organization of the Adenine Nucleotide Translocase in Model Mitochondrial Membranes. <i>Biochemistry</i> , 2016, 55, 6238-6249.	1.2	63
9	Studying Membrane Protein Folding by Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2015, 108, 92a.	0.2	0
10	Lipidbook: A Public Repository for Force-Field Parameters Used in Membrane Simulations. <i>Journal of Membrane Biology</i> , 2010, 236, 255-258.	1.0	145