

# Jan DomaÅ„ski

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7512793/publications.pdf>

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	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
3	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
4	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
5	Multiple lipid binding sites determine the affinity of PH domains for phosphoinositide-containing membranes. <i>Science Advances</i> , 2020, 6, eaay5736.	4.7	44
6	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
7	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
8	Ligandbook: an online repository for small and drug-like molecule force field parameters. <i>Bioinformatics</i> , 2017, 33, 1747-1749.	1.8	17
9	Atomistic mechanism of transmembrane helix association. <i>PLoS Computational Biology</i> , 2020, 16, e1007919.	1.5	16
10	Studying Membrane Protein Folding by Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2015, 108, 92a.	0.2	0