

Carsten Kutzner

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

17
papers

13,272
citations

15
h-index

18
g-index

18
ext. papers

14,988
ext. citations

5.3
avg. IF

6.5
L-index

#	Paper	IF	Citations
17	GROMACS 4: Algorithms for Highly Efficient, Load-Balanced, and Scalable Molecular Simulation. <i>Journal of Chemical Theory and Computation</i> , 2008 , 4, 435-47	6.4	11706
16	Anatomy and dynamics of a supramolecular membrane protein cluster. <i>Science</i> , 2007 , 317, 1072-6	33.3	360
15	Tackling Exascale Software Challenges in Molecular Dynamics Simulations with GROMACS. <i>Lecture Notes in Computer Science</i> , 2015 , 3-27	0.9	329
14	Computational electrophysiology: the molecular dynamics of ion channel permeation and selectivity in atomistic detail. <i>Biophysical Journal</i> , 2011 , 101, 809-17	2.9	158
13	Best bang for your buck: GPU nodes for GROMACS biomolecular simulations. <i>Journal of Computational Chemistry</i> , 2015 , 36, 1990-2008	3.5	130
12	More bang for your buck: Improved use of GPU nodes for GROMACS 2018. <i>Journal of Computational Chemistry</i> , 2019 , 40, 2418-2431	3.5	122
11	Caught in the act: visualization of SNARE-mediated fusion events in molecular detail. <i>ChemBioChem</i> , 2011 , 12, 1049-55	3.8	109
10	Speeding up parallel GROMACS on high-latency networks. <i>Journal of Computational Chemistry</i> , 2007 , 28, 2075-84	3.5	98
9	effects of driving mechanisms in geodynamo models. <i>Geophysical Research Letters</i> , 2000 , 27, 29-32	4.9	71
8	Insights into the function of ion channels by computational electrophysiology simulations. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 1741-52	3.8	43
7	Automated cryo-EM structure refinement using correlation-driven molecular dynamics. <i>ELife</i> , 2019 , 8,	8.9	38
6	Keep It Flexible: Driving Macromolecular Rotary Motions in Atomistic Simulations with GROMACS. <i>Journal of Chemical Theory and Computation</i> , 2011 , 7, 1381-1393	6.4	33
5	GROMaB: A GROMACS-Based Toolset to Analyze Density Maps Derived from Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2019 , 116, 4-11	2.9	33
4	A GPU-Accelerated Fast Multipole Method for GROMACS: Performance and Accuracy. <i>Journal of Chemical Theory and Computation</i> , 2020 , 16, 6938-6949	6.4	21
3	Molecular dynamics in principal component space. <i>Journal of Physical Chemistry B</i> , 2012 , 116, 8350-4	3.4	17
2	GROMEX: A Scalable and Versatile Fast Multipole Method for Biomolecular Simulation. <i>Lecture Notes in Computational Science and Engineering</i> , 2020 , 517-543	0.3	2
1	A CUDA fast multipole method with highly efficient M2L far field evaluation. <i>International Journal of High Performance Computing Applications</i> , 2021 , 35, 97-117	1.8	1

