

Carsten Kutzner

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

16,264
citations

516710

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839539

18
g-index

18
all docs

18
docs citations

18
times ranked

20359
citing authors

#	ARTICLE	IF	CITATIONS
1	GROMACS in the Cloud: A Global Supercomputer to Speed Up Alchemical Drug Design. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1691-1711.	5.4	37
2	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.	3.7	3
3	A GPU-Accelerated Fast Multipole Method for GROMACS: Performance and Accuracy. <i>Journal of Chemical Theory and Computation</i> , 2020, 16, 6938-6949.	5.3	68
4	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
5	More bang for your buck: Improved use of GPU nodes for GROMACS 2018. <i>Journal of Computational Chemistry</i> , 2019, 40, 2418-2431.	3.3	286
6	GROMaïs: A GROMACS-Based Toolset to Analyze Density Maps Derived from Molecular Dynamics Simulations. <i>Biophysical Journal</i> , 2019, 116, 4-11.	0.5	73
7	Automated cryo-EM structure refinement using correlation-driven molecular dynamics. <i>ELife</i> , 2019, 8, .	6.0	83
8	Insights into the function of ion channels by computational electrophysiology simulations. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016, 1858, 1741-1752.	2.6	60
9	Best bang for your buck: GPU nodes for <scp>GROMACS</scp> biomolecular simulations. <i>Journal of Computational Chemistry</i> , 2015, 36, 1990-2008.	3.3	195
10	Tackling Exascale Software Challenges in Molecular Dynamics Simulations with GROMACS. <i>Lecture Notes in Computer Science</i> , 2015, , 3-27.	1.3	581
11	Molecular Dynamics in Principal Component Space. <i>Journal of Physical Chemistry B</i> , 2012, 116, 8350-8354.	2.6	21
12	Computational Electrophysiology: The Molecular Dynamics of Ion Channel Permeation and Selectivity in Atomistic Detail. <i>Biophysical Journal</i> , 2011, 101, 809-817.	0.5	214
13	Keep It Flexible: Driving Macromolecular Rotary Motions in Atomistic Simulations with GROMACS. <i>Journal of Chemical Theory and Computation</i> , 2011, 7, 1381-1393.	5.3	42
14	Caught in the Act: Visualization of SNARE-Mediated Fusion Events in Molecular Detail. <i>ChemBioChem</i> , 2011, 12, 1049-1055.	2.6	134
15	GROMACS 4: Algorithms for Highly Efficient, Load-Balanced, and Scalable Molecular Simulation. <i>Journal of Chemical Theory and Computation</i> , 2008, 4, 435-447.	5.3	13,875
16	Anatomy and Dynamics of a Supramolecular Membrane Protein Cluster. <i>Science</i> , 2007, 317, 1072-1076.	12.6	405
17	Speeding up parallel GROMACS on high-latency networks. <i>Journal of Computational Chemistry</i> , 2007, 28, 2075-2084.	3.3	107
18	effects of driving mechanisms in geodynamo models. <i>Geophysical Research Letters</i> , 2000, 27, 29-32.	4.0	78