# Carsten Kutzner

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6567798/publications.pdf

Version: 2024-02-01

| 18 | 16,264 | 516710 16 | 839539 18 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 18 | 18 | 18 | 20359 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | GROMACS 4:â€‰ Algorithms for Highly Efficient, Load-Balanced, and Scalable Molecular Simulation. Journal of Chemical Theory and Computation, 2008, 4, 435-447. | 5.3 | 13,875 |
| 2 | Tackling Exascale Software Challenges in Molecular Dynamics Simulations with GROMACS. Lecture Notes in Computer Science, 2015, , 3-27. | 1.3 | 581 |
| 3 | Anatomy and Dynamics of a Supramolecular Membrane Protein Cluster. Science, 2007, 317, 1072-1076. | 12.6 | 405 |
| 4 | More bang for your buck: Improved use of GPU nodes for GROMACS 2018. Journal of Computational Chemistry, 2019, 40, 2418-2431. | 3.3 | 286 |
| 5 | Computational Electrophysiology: The Molecular Dynamics of Ion Channel Permeation and Selectivity in Atomistic Detail. Biophysical Journal, 2011, 101, 809-817. | 0.5 | 214 |
| 6 | Best bang for your buck: GPU nodes for <scp>GROMACS</scp> biomolecular simulations. Journal of Computational Chemistry, 2015, 36, 1990-2008. | 3.3 | 195 |
| 7 | Caught in the Act: Visualization of SNAREâ€Mediated Fusion Events in Molecular Detail. ChemBioChem, 2011, 12, 1049-1055. | 2.6 | 134 |
| 8 | Speeding up parallel GROMACS on high-latency networks. Journal of Computational Chemistry, 2007, 28, 2075-2084. | 3.3 | 107 |
| 9 | Automated cryo-EM structure refinement using correlation-driven molecular dynamics. ELife, 2019, 8, . | 6.0 | 83 |
| 10 | effects of driving mechanisms in geodynamo models. Geophysical Research Letters, 2000, 27, 29-32. | 4.0 | 78 |
| 11 | GROmaïs: A GROMACS-Based Toolset to Analyze Density Maps Derived from Molecular Dynamics Simulations. Biophysical Journal, 2019, 116, 4-11. | 0.5 | 73 |
| 12 | A GPU-Accelerated Fast Multipole Method for GROMACS: Performance and Accuracy. Journal of Chemical Theory and Computation, 2020, 16, 6938-6949. | 5.3 | 68 |
| 13 | Insights into the function of ion channels by computational electrophysiology simulations. Biochimica Et Biophysica Acta - Biomembranes, 2016, 1858, 1741-1752. | 2.6 | 60 |
| 14 | Keep It Flexible: Driving Macromolecular Rotary Motions in Atomistic Simulations with GROMACS. Journal of Chemical Theory and Computation, 2011, 7, 1381-1393. | 5.3 | 42 |
| 15 | GROMACS in the Cloud: A Global Supercomputer to Speed Up Alchemical Drug Design. Journal of Chemical Information and Modeling, 2022, 62, 1691-1711. | 5.4 | 37 |
| 16 | Molecular Dynamics in Principal Component Space. Journal of Physical Chemistry B, 2012, 116, 8350-8354. | 2.6 | 21 |
| 17 | A CUDA fast multipole method with highly efficient M2L far field evaluation. International Journal of High Performance Computing Applications, 2021, 35, 97-117. | 3.7 | 3 |
| 18 | GROMEX: A Scalable and Versatile Fast Multipole Method for Biomolecular Simulation. Lecture Notes in Computational Science and Engineering, 2020, , 517-543. | 0.3 | 2 |