

Berk Hess

List of Publications by Year in descending order

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46
papers

49,762
citations

172207

29
h-index

223531

46
g-index

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all docs

49
docs citations

49
times ranked

38304
citing authors

#	ARTICLE	IF	CITATIONS
1	GROMACS 4: Algorithms for Highly Efficient, Load-Balanced, and Scalable Molecular Simulation. <i>Journal of Chemical Theory and Computation</i> , 2008, 4, 435-447.	2.3	13,875
2	GROMACS: Fast, flexible, and free. <i>Journal of Computational Chemistry</i> , 2005, 26, 1701-1718.	1.5	13,676
3	LINCS: A linear constraint solver for molecular simulations. <i>Journal of Computational Chemistry</i> , 1997, 18, 1463-1472.	1.5	13,446
4	P-LINCS: A Parallel Linear Constraint Solver for Molecular Simulation. <i>Journal of Chemical Theory and Computation</i> , 2008, 4, 116-122.	2.3	2,976
5	Implementation of the CHARMM Force Field in GROMACS: Analysis of Protein Stability Effects from Correction Maps, Virtual Interaction Sites, and Water Models. <i>Journal of Chemical Theory and Computation</i> , 2010, 6, 459-466.	2.3	866
6	Improving efficiency of large time-scale molecular dynamics simulations of hydrogen-rich systems. <i>Journal of Computational Chemistry</i> , 1999, 20, 786-798.	1.5	779
7	Determining the shear viscosity of model liquids from molecular dynamics simulations. <i>Journal of Chemical Physics</i> , 2002, 116, 209.	1.2	620
8	A flexible algorithm for calculating pair interactions on SIMD architectures. <i>Computer Physics Communications</i> , 2013, 184, 2641-2650.	3.0	544
9	Hydration Thermodynamic Properties of Amino Acid Analogues: A Systematic Comparison of Biomolecular Force Fields and Water Models. <i>Journal of Physical Chemistry B</i> , 2006, 110, 17616-17626.	1.2	305
10	Similarities between principal components of protein dynamics and random diffusion. <i>Physical Review E</i> , 2000, 62, 8438-8448.	0.8	276
11	Heterogeneous parallelization and acceleration of molecular dynamics simulations in GROMACS. <i>Journal of Chemical Physics</i> , 2020, 153, 134110.	1.2	275
12	Photoactivation of the Photoactive Yellow Protein: Why Photon Absorption Triggers a Trans-to-Cis Isomerization of the Chromophore in the Protein. <i>Journal of the American Chemical Society</i> , 2004, 126, 4228-4233.	6.6	265
13	Cation specific binding with protein surface charges. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 13296-13300.	3.3	226
14	Reproducible Polypeptide Folding and Structure Prediction using Molecular Dynamics Simulations. <i>Journal of Molecular Biology</i> , 2005, 354, 173-183.	2.0	165
15	Lennard-Jones Lattice Summation in Bilayer Simulations Has Critical Effects on Surface Tension and Lipid Properties. <i>Journal of Chemical Theory and Computation</i> , 2013, 9, 3527-3537.	2.3	138
16	Osmotic coefficients of atomistic NaCl (aq) force fields. <i>Journal of Chemical Physics</i> , 2006, 124, 164509.	1.2	132
17	Analysis and Evaluation of Channel Models: Simulations of Alamethicin. <i>Biophysical Journal</i> , 2002, 83, 2393-2407.	0.2	123
18	Long time atomistic polymer trajectories from coarse grained simulations: bisphenol-A polycarbonate. <i>Soft Matter</i> , 2006, 2, 409-414.	1.2	123

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19	Direct-Space Corrections Enable Fast and Accurate Lorentz-Berthelot Combination Rule Lennard-Jones Lattice Summation. <i>Journal of Chemical Theory and Computation</i> , 2015, 11, 5737-5746.	2.3	112
20	Modeling Multibody Effects in Ionic Solutions with a Concentration Dependent Dielectric Permittivity. <i>Physical Review Letters</i> , 2006, 96, 147801.	2.9	110
21	Competing Adsorption between Hydrated Peptides and Water onto Metal Surfaces: From Electronic to Conformational Properties. <i>Journal of the American Chemical Society</i> , 2008, 130, 13460-13464.	6.6	68
22	Dynamics and Structure of Ln(III)-Aqua Ions: A Comparative Molecular Dynamics Study Using ab Initio Based Flexible and Polarizable Model Potentials. <i>Journal of Physical Chemistry B</i> , 2009, 113, 7270-7281.	1.2	62
23	310-Helix Conformation Facilitates the Transition of a Voltage Sensor S4 Segment toward the Down State. <i>Biophysical Journal</i> , 2011, 100, 1446-1454.	0.2	54
24	An application of flexible constraints in Monte Carlo simulations of the isobaric-isothermal ensemble of liquid water and ice Ih with the polarizable and flexible mobile charge densities in harmonic oscillators model. <i>Journal of Chemical Physics</i> , 2004, 120, 11133-11143.	1.2	53
25	Ion Pairing in Aqueous Electrolyte Solutions with Biologically Relevant Anions. <i>Journal of Physical Chemistry B</i> , 2011, 115, 3734-3739.	1.2	46
26	GROMACS—the road ahead. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2011, 1, 710-715.	6.2	43
27	Molecular origin of contact line friction in dynamic wetting. <i>Physical Review Fluids</i> , 2018, 3, .	1.0	40
28	Fast-Growth Thermodynamic Integration: Calculating Excess Chemical Potentials of Additive Molecules in Polymer Microstructures. <i>Macromolecules</i> , 2008, 41, 2283-2289.	2.2	34
29	Flexible constraints: An adiabatic treatment of quantum degrees of freedom, with application to the flexible and polarizable mobile charge densities in harmonic oscillators model for water. <i>Journal of Chemical Physics</i> , 2002, 116, 9602-9610.	1.2	31
30	Sequence dependency of canonical base pair opening in the DNA double helix. <i>PLoS Computational Biology</i> , 2017, 13, e1005463.	1.5	31
31	Algorithm improvements for molecular dynamics simulations. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2011, 1, 93-108.	6.2	30
32	Driving Forces for Adsorption of Amphiphilic Peptides to the Air-Water Interface. <i>Journal of Physical Chemistry B</i> , 2010, 114, 11093-11101.	1.2	28
33	Further investigation on the validity of Stokes-Einstein behaviour at the molecular level. <i>Chemical Physics Letters</i> , 2001, 334, 337-342.	1.2	27
34	Ten simple rules on how to create open access and reproducible molecular simulations of biological systems. <i>PLoS Computational Biology</i> , 2019, 15, e1006649.	1.5	25
35	Water-substrate physico-chemistry in wetting dynamics. <i>Journal of Fluid Mechanics</i> , 2015, 781, 695-711.	1.4	23
36	Modeling Solubilities of Additives in Polymer Microstructures: Single-Step Perturbation Method Based on a Soft-Cavity Reference State. <i>Macromolecules</i> , 2008, 41, 5055-5061.	2.2	22

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37	Riemann metric approach to optimal sampling of multidimensional free-energy landscapes. <i>Physical Review E</i> , 2018, 98, 023312.	0.8	18
38	Predictive Modeling of Phenol Chemical Potentials in Molten Bisphenol A Polycarbonate over a Broad Temperature Range. <i>Macromolecules</i> , 2008, 41, 7281-7283.	2.2	16
39	The accelerated weight histogram method for alchemical free energy calculations. <i>Journal of Chemical Physics</i> , 2021, 154, 204103.	1.2	15
40	Probing microscopic material properties inside simulated membranes through spatially resolved three-dimensional local pressure fields and surface tensions. <i>Chemistry and Physics of Lipids</i> , 2013, 169, 106-112.	1.5	11
41	Regularizing the fast multipole method for use in molecular simulation. <i>Journal of Chemical Physics</i> , 2019, 151, 234113.	1.2	10
42	Nanoscale sheared droplet: volume-of-fluid, phase-field and no-slip molecular dynamics. <i>Journal of Fluid Mechanics</i> , 2022, 940, .	1.4	10
43	Stability of Hydrophobically Modified Poly(p-phenylenesulfonate) Bundles As Observed by Molecular Dynamics Simulation. <i>Macromolecules</i> , 2007, 40, 1703-1707.	2.2	9
44	Chain packing in polycarbonate glasses. <i>Journal of Chemical Physics</i> , 2010, 132, 104901.	1.2	6
45	Interaction of Water with N,N'-1,2-Ethanediy-bis(6-hydroxy-hexanamide) Crystals: A Simulation Study. <i>Journal of Physical Chemistry B</i> , 2009, 113, 627-631.	1.2	3
46	Electrowetting diminishes contact line friction in molecular wetting. <i>Physical Review Fluids</i> , 2020, 5, .	1.0	3