Roland Schulz

List of Publications by Year
in descending order

14	21,341	840776 11	1125743 13
papers	citations	h-index	g-index

14	14	14	27504
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Bacillus subtilis Lipid Extract, A Branched-Chain Fatty Acid Model Membrane. Journal of Physical Chemistry Letters, 2017, 8, 4214-4217.	4.6	42
2	Mechanism of lignin inhibition of enzymatic biomass deconstruction. Biotechnology for Biofuels, 2015, 8, 217.	6.2	195
3	GROMACS: High performance molecular simulations through multi-level parallelism from laptops to supercomputers. SoftwareX, 2015, 1-2, 19-25.	2.6	14,414
4	Common processes drive the thermochemical pretreatment of lignocellulosic biomass. Green Chemistry, 2014, 16, 63-68.	9.0	198
5	Hydration Control of the Mechanical and Dynamical Properties of Cellulose. Biomacromolecules, 2014, 15, 4152-4159.	5.4	44
6	GROMACS 4.5: a high-throughput and highly parallel open source molecular simulation toolkit. Bioinformatics, 2013, 29, 845-854.	4.1	6,072
7	Initial Recognition of a Cellodextrin Chain in the Cellulose-Binding Tunnel May Affect Cellobiohydrolase Directional Specificity. Biophysical Journal, 2013, 104, 904-912.	0.5	33
8	Solvent-Driven Preferential Association of Lignin with Regions of Crystalline Cellulose in Molecular Dynamics Simulation. Biomacromolecules, 2013, 14, 3390-3398.	5.4	68
9	Molecular Simulation in the Energy Biosciences. RSC Biomolecular Sciences, 2012, , 87-114.	0.4	0
10	Enabling grandâ€canonical Monte Carlo: Extending the flexibility of GROMACS through the GromPy python interface module. Journal of Computational Chemistry, 2012, 33, 1207-1214.	3.3	4
11	Simulation Analysis of the Temperature Dependence of Lignin Structure and Dynamics. Journal of the American Chemical Society, 2011, 133, 20277-20287.	13.7	126
12	Taskâ€parallel message passing interface implementation of Autodock4 for docking of very large databases of compounds using highâ€performance superâ€computers. Journal of Computational Chemistry, 2011, 32, 1202-1209.	3.3	39
13	Instantaneous Normal Modes and the Protein Glass Transition. Biophysical Journal, 2009, 96, 476-484.	0.5	12
14	Scaling of Multimillion-Atom Biological Molecular Dynamics Simulation on a Petascale Supercomputer. Journal of Chemical Theory and Computation, 2009, 5, 2798-2808.	5.3	94