Jumin Lee

List of Publications by Year in descending order

31 papers	7,223 citations	331538 21 h-index	414303 32 g-index
34 all docs	34 docs citations	34 times ranked	7941 citing authors

#	Article	IF	Citations
1	CHARMM-GUI Input Generator for NAMD, GROMACS, AMBER, OpenMM, and CHARMM/OpenMM Simulations Using the CHARMM36 Additive Force Field. Journal of Chemical Theory and Computation, 2016, 12, 405-413.	2.3	2,567
2	CHARMM-GUIMembrane Buildertoward realistic biological membrane simulations. Journal of Computational Chemistry, 2014, 35, 1997-2004.	1.5	1,802
3	CHARMM-GUI Membrane Builder for Complex Biological Membrane Simulations with Glycolipids and Lipoglycans. Journal of Chemical Theory and Computation, 2019, 15, 775-786.	2.3	388
4	CHARMM-GUI Martini Maker for Coarse-Grained Simulations with the Martini Force Field. Journal of Chemical Theory and Computation, 2015, 11, 4486-4494.	2.3	340
5	CHARMM-GUI ligand reader and modeler for CHARMM force field generation of small molecules. Journal of Computational Chemistry, 2017, 38, 1879-1886.	1.5	311
6	Developing a Fully Glycosylated Full-Length SARS-CoV-2 Spike Protein Model in a Viral Membrane. Journal of Physical Chemistry B, 2020, 124, 7128-7137.	1.2	240
7	CHARMMâ€GUI 10 years for biomolecular modeling and simulation. Journal of Computational Chemistry, 2017, 38, 1114-1124.	1.5	224
8	CHARMM-GUIGlycan Modelerfor modeling and simulation of carbohydrates and glycoconjugates. Glycobiology, 2019, 29, 320-331.	1.3	222
9	CHARMM-GUI supports the Amber force fields. Journal of Chemical Physics, 2020, 153, 035103.	1.2	175
10	CHARMMâ€GUI Martini Maker for modeling and simulation of complex bacterial membranes with lipopolysaccharides. Journal of Computational Chemistry, 2017, 38, 2354-2363.	1.5	150
11	Glycan Reader is improved to recognize most sugar types and chemical modifications in the Protein Data Bank. Bioinformatics, 2017, 33, 3051-3057.	1.8	94
12	CHARMM-GUI HMMM Builder for Membrane Simulations with the Highly Mobile Membrane-Mimetic Model. Biophysical Journal, 2015, 109, 2012-2022.	0.2	89
13	CHARMM-GUI Input Generator for NAMD, Gromacs, Amber, Openmm, and CHARMM/OpenMM Simulations using the CHARMM36 Additive Force Field. Biophysical Journal, 2016, 110, 641a.	0.2	63
14	CHARMM-GUI Supports Hydrogen Mass Repartitioning and Different Protonation States of Phosphates in Lipopolysaccharides. Journal of Chemical Information and Modeling, 2021, 61, 831-839.	2.5	59
15	CHARMM-GUI Polymer Builder for Modeling and Simulation of Synthetic Polymers. Journal of Chemical Theory and Computation, 2021, 17, 2431-2443.	2.3	58
16	CHARMM-GUI Free Energy Calculator for Absolute and Relative Ligand Solvation and Binding Free Energy Simulations. Journal of Chemical Theory and Computation, 2020, 16, 7207-7218.	2.3	57
17	CHARMM-GUI Nanomaterial Modeler for Modeling and Simulation of Nanomaterial Systems. Journal of Chemical Theory and Computation, 2022, 18, 479-493.	2.3	53
18	CHARMMâ€GUI Nanodisc Builder for modeling and simulation of various nanodisc systems. Journal of Computational Chemistry, 2019, 40, 893-899.	1.5	42

#	Article	IF	Citations
19	Additive CHARMM36 Force Field for Nonstandard Amino Acids. Journal of Chemical Theory and Computation, 2021, 17, 3554-3570.	2.3	39
20	The Structure of a Sugar Transporter of the Glucose EIIC Superfamily Provides Insight into the Elevator Mechanism of Membrane Transport. Structure, 2016, 24, 956-964.	1.6	37
21	Comparative Molecular Dynamics Simulation Studies of Realistic Eukaryotic, Prokaryotic, and Archaeal Membranes. Journal of Chemical Information and Modeling, 2022, 62, 1036-1051.	2.5	32
22	Modeling and Simulation of Bacterial Outer Membranes with Lipopolysaccharides and Enterobacterial Common Antigen. Journal of Physical Chemistry B, 2020, 124, 5948-5956.	1.2	26
23	CHARMM-GUI Membrane Builder for Lipid Nanoparticles with Ionizable Cationic Lipids and PEGylated Lipids. Journal of Chemical Information and Modeling, 2021, 61, 5192-5202.	2.5	25
24	CHARMM-GUI MDFF/xMDFF Utilizer for Molecular Dynamics Flexible Fitting Simulations in Various Environments. Journal of Physical Chemistry B, 2017, 121, 3718-3723.	1.2	24
25	CHARMM-GUI Free Energy Calculator for Practical Ligand Binding Free Energy Simulations with AMBER. Journal of Chemical Information and Modeling, 2021, 61, 4145-4151.	2.5	24
26	<scp>CHARMMâ€GUI</scp> Drude prepper for molecular dynamics simulation using the classical Drude polarizable force field. Journal of Computational Chemistry, 2022, 43, 359-375.	1.5	24
27	CHARMMâ€GUI DEER facilitator for spinâ€pair distance distribution calculations and preparation of restrainedâ€ensemble molecular dynamics simulations. Journal of Computational Chemistry, 2020, 41, 415-420.	1.5	19
28	Modeling of Specific Lipopolysaccharide Binding Sites on a Gram-Negative Porin. Journal of Physical Chemistry B, 2019, 123, 5700-5708.	1.2	11
29	Molecular Simulation and Biochemical Studies Support an Elevator-type Transport Mechanism inÂEIIC. Biophysical Journal, 2017, 112, 2249-2252.	0.2	7
30	Preferred conformations of lipooligosaccharides and oligosaccharides of Moraxella catarrhalis. Glycobiology, 2020, 30, 86-94.	1.3	6
31	Structure, Dynamics, and Interactions of GPI-Anchored Human Glypican-1 with Heparan Sulfates in a Membrane. Glycobiology, 2021, 31, 593-602.	1.3	6