Sang-Jun Park

List of Publications by Year
in descending order

15	1,432	840585 11	996849 15
papers	citations	h-index	g-index

17	17	17	2159
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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
2	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
3	CHARMMâ€GUI 10 years for biomolecular modeling and simulation. Journal of Computational Chemistry, 2017, 38, 1114-1124.	1.5	224
4	CHARMM-GUIGlycan Modelerfor modeling and simulation of carbohydrates and glycoconjugates. Glycobiology, 2019, 29, 320-331.	1.3	222
5	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
6	Structure, Dynamics, Receptor Binding, and Antibody Binding of the Fully Glycosylated Full-Length SARS-CoV-2 Spike Protein in a Viral Membrane. Journal of Chemical Theory and Computation, 2021, 17, 2479-2487.	2.3	62
7	CHARMM-GUI Polymer Builder for Modeling and Simulation of Synthetic Polymers. Journal of Chemical Theory and Computation, 2021, 17, 2431-2443.	2.3	58
8	Additive CHARMM36 Force Field for Nonstandard Amino Acids. Journal of Chemical Theory and Computation, 2021, 17, 3554-3570.	2.3	39
9	<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
10	Ligand-Binding-Site Refinement to Generate Reliable Holo Protein Structure Conformations from Apo Structures. Journal of Chemical Information and Modeling, 2021, 61, 535-546.	2.5	19
11	GlyMDB: Glycan Microarray Database and analysis toolset. Bioinformatics, 2020, 36, 2438-2442.	1.8	14
12	A systematic analysis of proteinâ€“carbohydrate interactions in the Protein Data Bank. Glycobiology, 2021, 31, 126-136.	1.3	13
13	Dynamic Interactions of Fully Glycosylated SARS-CoV-2 Spike Protein with Various Antibodies. Journal of Chemical Theory and Computation, 2021, 17, 6559-6569.	2.3	13
14	CHARMM-GUI LBS Finder & Refiner for Ligand Binding Site Prediction and Refinement. Journal of Chemical Information and Modeling, 2021, 61, 3744-3751.	2.5	9
15	CHARMM-GUI Ligand Designer for Template-Based Virtual Ligand Design in a Binding Site. Journal of Chemical Information and Modeling, 2021, 61, 5336-5342.	2.5	8