Sang-Jun Park

List of Publications by Citations

16 papers	636 citations	7 h-index	17 g-index
17 ext. papers	1,093 ext. citations	5.6 avg, IF	4.14 L-index

#	Paper	IF	Citations
16	CHARMM-GUI Membrane Builder for Complex Biological Membrane Simulations with Glycolipids and Lipoglycans. *Journal of Chemical Theory and Computation*, **2019**, 15, 775-786	6.4	152
15	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	3.4	131
14	CHARMM-GUI 10 years for biomolecular modeling and simulation. *Journal of Computational Chemistry*, **2017**, 38, 1114-1124	3.5	119
13	CHARMM-GUI Glycan Modeler for modeling and simulation of carbohydrates and glycoconjugates. *Glycobiology*, **2019**, 29, 320-331	5.8	101
12	Glycan Reader is improved to recognize most sugar types and chemical modifications in the Protein Data Bank. *Bioinformatics*, **2017**, 33, 3051-3057	7.2	59
11	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	6.4	26
10	CHARMM-GUI Polymer Builder for Modeling and Simulation of Synthetic Polymers. *Journal of Chemical Theory and Computation*, **2021**, 17, 2431-2443	6.4	12
9	Ligand-Binding-Site Refinement to Generate Reliable Holo Protein Structure Conformations from Apo Structures. *Journal of Chemical Information and Modeling*, **2021**, 61, 535-546	6.1	7
8	GlyMDB: Glycan Microarray Database and analysis toolset. *Bioinformatics*, **2020**, 36, 2438-2442	7.2	6
7	Additive CHARMM36 Force Field for Nonstandard Amino Acids. *Journal of Chemical Theory and Computation*, **2021**, 17, 3554-3570	6.4	5
6	A systematic analysis of protein-carbohydrate interactions in the Protein Data Bank. *Glycobiology*, **2021**, 31, 126-136	5.8	5
5	Developing a Fully-glycosylated Full-length SARS-CoV-2 Spike Protein Model in a Viral Membrane **2020**,		4
4	CHARMM-GUI Drude prepper for molecular dynamics simulation using the classical Drude polarizable force field. *Journal of Computational Chemistry*, **2021**,	3.5	4
3	CHARMM-GUI for Ligand Binding Site Prediction and Refinement. *Journal of Chemical Information and Modeling*, **2021**, 61, 3744-3751	6.1	2
2	Dynamic Interactions of Fully Glycosylated SARS-CoV-2 Spike Protein with Various Antibodies. *Journal of Chemical Theory and Computation*, **2021**, 17, 6559-6569	6.4	2
1	CHARMM-GUI for Template-Based Virtual Ligand Design in a Binding Site. *Journal of Chemical Information and Modeling*, **2021**, 61, 5336-5342	6.1	1