

Sang-Jun Park

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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 for Template-Based Virtual Ligand Design in a Binding Site. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 5336-5342	6.1	1
15	Structure, Dynamics, Receptor Binding, and Antibody Binding of the Fully Glycosylated Full-Length SARS-CoV-2 Spike Protein in a Viral Membrane. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 2479-2487	6.4	26
14	CHARMM-GUI Polymer Builder for Modeling and Simulation of Synthetic Polymers. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 2431-2443	6.4	12
13	Additive CHARMM36 Force Field for Nonstandard Amino Acids. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 3554-3570	6.4	5
12	A systematic analysis of protein-carbohydrate interactions in the Protein Data Bank. <i>Glycobiology</i> , 2021 , 31, 126-136	5.8	5
11	Ligand-Binding-Site Refinement to Generate Reliable Holo Protein Structure Conformations from Apo Structures. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 535-546	6.1	7
10	CHARMM-GUI for Ligand Binding Site Prediction and Refinement. <i>Journal of Chemical Information and Modeling</i> , 2021 , 61, 3744-3751	6.1	2
9	Dynamic Interactions of Fully Glycosylated SARS-CoV-2 Spike Protein with Various Antibodies. <i>Journal of Chemical Theory and Computation</i> , 2021 , 17, 6559-6569	6.4	2
8	CHARMM-GUI Drude prepper for molecular dynamics simulation using the classical Drude polarizable force field. <i>Journal of Computational Chemistry</i> , 2021 ,	3.5	4
7	Developing a Fully Glycosylated Full-Length SARS-CoV-2 Spike Protein Model in a Viral Membrane. <i>Journal of Physical Chemistry B</i> , 2020 , 124, 7128-7137	3.4	131
6	Developing a Fully-glycosylated Full-length SARS-CoV-2 Spike Protein Model in a Viral Membrane 2020 ,		4
5	GlyMDB: Glycan Microarray Database and analysis toolset. <i>Bioinformatics</i> , 2020 , 36, 2438-2442	7.2	6
4	CHARMM-GUI Glycan Modeler for modeling and simulation of carbohydrates and glycoconjugates. <i>Glycobiology</i> , 2019 , 29, 320-331	5.8	101
3	CHARMM-GUI Membrane Builder for Complex Biological Membrane Simulations with Glycolipids and Lipoglycans. <i>Journal of Chemical Theory and Computation</i> , 2019 , 15, 775-786	6.4	152
2	Glycan Reader is improved to recognize most sugar types and chemical modifications in the Protein Data Bank. <i>Bioinformatics</i> , 2017 , 33, 3051-3057	7.2	59
1	CHARMM-GUI 10 years for biomolecular modeling and simulation. <i>Journal of Computational Chemistry</i> , 2017 , 38, 1114-1124	3.5	119