

Zied Gaieb

List of Publications by Citations

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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.

15
papers

742
citations

9
h-index

17
g-index

17
ext. papers

1,172
ext. citations

4.9
avg, IF

4.48
L-index

#	Paper	IF	Citations
15	Beyond Shielding: The Roles of Glycans in the SARS-CoV-2 Spike Protein. <i>ACS Central Science</i> , 2020 , 6, 1722-1734	16.8	340
14	D3R Grand Challenge 2: blind prediction of protein-ligand poses, affinity rankings, and relative binding free energies. <i>Journal of Computer-Aided Molecular Design</i> , 2018 , 32, 1-20	4.2	117
13	D3R Grand Challenge 3: blind prediction of protein-ligand poses and affinity rankings. <i>Journal of Computer-Aided Molecular Design</i> , 2019 , 33, 1-18	4.2	70
12	A multiscale coarse-grained model of the SARS-CoV-2 virion. <i>Biophysical Journal</i> , 2021 , 120, 1097-1104	2.9	54
11	The flexibility of ACE2 in the context of SARS-CoV-2 infection. <i>Biophysical Journal</i> , 2021 , 120, 1072-1084	2.9	52
10	D3R grand challenge 4: blind prediction of protein-ligand poses, affinity rankings, and relative binding free energies. <i>Journal of Computer-Aided Molecular Design</i> , 2020 , 34, 99-119	4.2	37
9	A potential interaction between the SARS-CoV-2 spike protein and nicotinic acetylcholine receptors. <i>Biophysical Journal</i> , 2021 , 120, 983-993	2.9	18
8	AI-Driven Multiscale Simulations Illuminate Mechanisms of SARS-CoV-2 Spike Dynamics 2020 ,		17
7	Molecular Mechanism of Biased Ligand Conformational Changes in CC Chemokine Receptor 7. <i>Journal of Chemical Information and Modeling</i> , 2016 , 56, 1808-22	6.1	11
6	Detection of Side Chain Rearrangements Mediating the Motions of Transmembrane Helices in Molecular Dynamics Simulations of G Protein-Coupled Receptors. <i>Computational and Structural Biotechnology Journal</i> , 2017 , 15, 131-137	6.8	7
5	Development of Dimethylisoxazole-Attached Imidazo[1,2-]pyridines as Potent and Selective CBP/P300 Inhibitors. <i>Journal of Medicinal Chemistry</i> , 2021 , 64, 5787-5801	8.3	6
4	An Analysis of Proteochemometric and Conformal Prediction Machine Learning Protein-Ligand Binding Affinity Models. <i>Frontiers in Molecular Biosciences</i> , 2020 , 7, 93	5.6	5
3	Conformational heterogeneity in CCR7 undergoes transitions to specific states upon ligand binding. <i>Journal of Molecular Graphics and Modelling</i> , 2017 , 74, 352-358	2.8	4
2	Electrostatic Interactions between Complement Regulator CD46(SCR1-2) and Adenovirus Ad11/Ad21 Fiber Protein Knob. <i>Molecular Biology International</i> , 2015 , 2015, 967465		1
1	Role of Electrostatic Hotspots in the Selectivity of Complement Control Proteins Toward Human and Bovine Complement Inhibition. <i>Frontiers in Molecular Biosciences</i> , 2021 , 8, 618068	5.6	1