

Zhaoqian Su

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.

28

papers

168

citations

8

h-index

12

g-index

33

ext. papers

240

ext. citations

4.8

avg, IF

3.95

L-index

#	Paper	IF	Citations
28	Understanding the functional role of membrane confinements in TNF-mediated signaling by multiscale simulations.. <i>Communications Biology</i> , 2022 , 5, 228	6.7	0
27	A computational study of co-inhibitory immune complex assembly at the interface between T cells and antigen presenting cells. <i>PLoS Computational Biology</i> , 2021 , 17, e1008825	5	0
26	Characterizing the function of domain linkers in regulating the dynamics of multi-domain fusion proteins by microsecond molecular dynamics simulations and artificial intelligence. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021 , 89, 884-895	4.2	
25	Methane Clathrate Formation is Catalyzed and Kinetically Inhibited by the Same Molecule: Two Facets of Methanol. <i>Journal of Physical Chemistry B</i> , 2021 , 125, 4162-4168	3.4	1
24	Mechanistic dissection of spatial organization in NF- κ B signaling pathways by hybrid simulations. <i>Integrative Biology (United Kingdom)</i> , 2021 , 13, 109-120	3.7	1
23	Computational Simulation of Holin S105 in Membrane Bilayer and Its Dimerization Through a Helix-Turn-Helix Motif. <i>Journal of Membrane Biology</i> , 2021 , 254, 397-407	2.3	0
22	Understanding the impacts of cellular environments on ligand binding of membrane receptors by computational simulations. <i>Journal of Chemical Physics</i> , 2021 , 154, 055101	3.9	1
21	Coarse-grained simulations of phase separation driven by DNA and its sensor protein cGAS. <i>Archives of Biochemistry and Biophysics</i> , 2021 , 710, 109001	4.1	2
20	A structural-based machine learning method to classify binding affinities between TCR and peptide-MHC complexes. <i>Molecular Immunology</i> , 2021 , 139, 76-86	4.3	0
19	A multiscale study on the mechanisms of spatial organization in ligand-receptor interactions on cell surfaces. <i>Computational and Structural Biotechnology Journal</i> , 2021 , 19, 1620-1634	6.8	2
18	Understanding the Targeting Mechanisms of Multi-Specific Biologics in Immunotherapy with Multiscale Modeling. <i>iScience</i> , 2020 , 23, 101835	6.1	1
17	A Systematic Test of Receptor Binding Kinetics for Ligands in Tumor Necrosis Factor Superfamily by Computational Simulations. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	5
16	A computational model for understanding the oligomerization mechanisms of TNF receptor superfamily. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 258-270	6.8	10
15	Cadherin clusters stabilized by a combination of specific and nonspecific cis-interactions. <i>ELife</i> , 2020 , 9,	8.9	13
14	Computational simulations of TNF receptor oligomerization on plasma membrane. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 698-709	4.2	4
13	Multiscale simulation unravel the kinetic mechanisms of inflammasome assembly. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2020 , 1867, 118612	4.9	4
12	Understanding the Impacts of Conformational Dynamics on the Regulation of Protein-Protein Association by a Multiscale Simulation Method. <i>Journal of Chemical Theory and Computation</i> , 2020 , 16, 5323-5333	6.4	2

11	Using Coarse-Grained Simulations to Characterize the Mechanisms of Protein-Protein Association. <i>Biomolecules</i> , 2020 , 10,	5.9	3
10	Understand the Functions of Scaffold Proteins in Cell Signaling by a Mesoscopic Simulation Method. <i>Biophysical Journal</i> , 2020 , 119, 2116-2126	2.9	1
9	Computational studies of protein-protein dissociation by statistical potential and coarse-grained simulations: a case study on interactions between colicin E9 endonuclease and immunity proteins. <i>Physical Chemistry Chemical Physics</i> , 2019 , 21, 2463-2471	3.6	7
8	Thermodynamic Stability of Polar and Nonpolar Amyloid Fibrils. <i>Journal of Chemical Theory and Computation</i> , 2019 , 15, 3868-3874	6.4	10
7	Individual and combined effects of urea and trimethylamine N-oxide (TMAO) on protein structures. <i>Journal of Molecular Liquids</i> , 2019 , 293, 111443	6	5
6	Effects of Trimethylamine- N-oxide (TMAO) on Hydrophobic and Charged Interactions. <i>Journal of Physical Chemistry B</i> , 2018 , 122, 5557-5566	3.4	14
5	Molecular interactions accounting for protein denaturation by urea. <i>Journal of Molecular Liquids</i> , 2017 , 228, 168-175	6	19
4	Effects of Trimethylamine-N-oxide on the Conformation of Peptides and its Implications for Proteins. <i>Physical Review Letters</i> , 2017 , 119, 108102	7.4	36
3	Thermodynamics of A β 16-21 dissociation from a fibril: Enthalpy, entropy, and volumetric properties. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015 , 83, 1963-72	4.2	4
2	Driving β strands into fibrils. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 10830-6	3.4	14
1	Steady state minority carrier lifetime and defect level occupation in thin film CdTe solar cells. <i>Thin Solid Films</i> , 2014 , 558, 391-399	2.2	9