Zhaoqian Su

List of Publications by Citations

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	Effects of Trimethylamine-N-oxide on the Conformation of Peptides and its Implications for Proteins. *Physical Review Letters*, **2017**, 119, 108102	7.4	36
27	Molecular interactions accounting for protein denaturation by urea. *Journal of Molecular Liquids*, **2017**, 228, 168-175	6	19
26	Effects of Trimethylamine- N-oxide (TMAO) on Hydrophobic and Charged Interactions. *Journal of Physical Chemistry B*, **2018**, 122, 5557-5566	3.4	14
25	Driving β-strands into fibrils. *Journal of Physical Chemistry B*, **2014**, 118, 10830-6	3.4	14
24	Cadherin clusters stabilized by a combination of specific and nonspecific cis-interactions. *ELife*, **2020**, 9,	8.9	13
23	Thermodynamic Stability of Polar and Nonpolar Amyloid Fibrils. *Journal of Chemical Theory and Computation*, **2019**, 15, 3868-3874	6.4	10
22	A computational model for understanding the oligomerization mechanisms of TNF receptor superfamily. *Computational and Structural Biotechnology Journal*, **2020**, 18, 258-270	6.8	10
21	Steady state minority carrier lifetime and defect level occupation in thin film CdTe solar cells. *Thin Solid Films*, **2014**, 558, 391-399	2.2	9
20	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. *Physical Chemistry Chemical Physics*, **2019**, 21, 2463-2471	3.6	7
19	A Systematic Test of Receptor Binding Kinetics for Ligands in Tumor Necrosis Factor Superfamily by Computational Simulations. *International Journal of Molecular Sciences*, **2020**, 21,	6.3	5
18	Individual and combined effects of urea and trimethylamine N-oxide (TMAO) on protein structures. *Journal of Molecular Liquids*, **2019**, 293, 111443	6	5
17	Thermodynamics of Aβ16-21 dissociation from a fibril: Enthalpy, entropy, and volumetric properties. *Proteins: Structure, Function and Bioinformatics*, **2015**, 83, 1963-72	4.2	4
16	Computational simulations of TNF receptor oligomerization on plasma membrane. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 698-709	4.2	4
15	Multiscale simulation unravel the kinetic mechanisms of inflammasome assembly. *Biochimica Et Biophysica Acta - Molecular Cell Research*, **2020**, 1867, 118612	4.9	4
14	Using Coarse-Grained Simulations to Characterize the Mechanisms of Protein-Protein Association. *Biomolecules*, **2020**, 10,	5.9	3
13	Understanding the Impacts of Conformational Dynamics on the Regulation of Protein-Protein Association by a Multiscale Simulation Method. *Journal of Chemical Theory and Computation*, **2020**, 16, 5323-5333	6.4	2
12	Coarse-grained simulations of phase separation driven by DNA and its sensor protein cGAS. *Archives of Biochemistry and Biophysics*, **2021**, 710, 109001	4.1	2

List of Publications

11	A multiscale study on the mechanisms of spatial organization in ligand-receptor interactions on cell surfaces. *Computational and Structural Biotechnology Journal*, **2021**, 19, 1620-1634	6.8	2
10	Understanding the Targeting Mechanisms of Multi-Specific Biologics in Immunotherapy with Multiscale Modeling. *IScience*, **2020**, 23, 101835	6.1	1
9	Understand the Functions of Scaffold Proteins in Cell Signaling by a Mesoscopic Simulation Method. *Biophysical Journal*, **2020**, 119, 2116-2126	2.9	1
8	Methane Clathrate Formation is Catalyzed and Kinetically Inhibited by the Same Molecule: Two Facets of Methanol. *Journal of Physical Chemistry B*, **2021**, 125, 4162-4168	3.4	1
7	Mechanistic dissection of spatial organization in NF-B signaling pathways by hybrid simulations. *Integrative Biology (United Kingdom)*, **2021**, 13, 109-120	3.7	1
6	Understanding the impacts of cellular environments on ligand binding of membrane receptors by computational simulations. *Journal of Chemical Physics*, **2021**, 154, 055101	3.9	1
5	A computational study of co-inhibitory immune complex assembly at the interface between T cells and antigen presenting cells. *PLoS Computational Biology*, **2021**, 17, e1008825	5	0
4	Computational Simulation of Holin S105 in Membrane Bilayer and Its Dimerization Through a Helix-Turn-Helix Motif. *Journal of Membrane Biology*, **2021**, 254, 397-407	2.3	0
3	A structural-based machine learning method to classify binding affinities between TCR and peptide-MHC complexes. *Molecular Immunology*, **2021**, 139, 76-86	4.3	0
2	Understanding the functional role of membrane confinements in TNF-mediated signaling by multiscale simulations.. *Communications Biology*, **2022**, 5, 228	6.7	0
1	Characterizing the function of domain linkers in regulating the dynamics of multi-domain fusion proteins by microsecond molecular dynamics simulations and artificial intelligence. *Proteins: Structure, Function and Bioinformatics*, **2021**, 89, 884-895	4.2	