Jun Zeng

List of Publications by Year
in descending order

25	566	623188 14	676716 22
papers	citations	h-index	g-index

25	25	25	866
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	A small molecule inhibitor of PCSK9 that antagonizes LDL receptor binding via interaction with a cryptic PCSK9 binding groove. Bioorganic and Medicinal Chemistry, 2020, 28, 115344.	1.4	31
2	Computational Prediction of the Epitopes of HA1 Protein of Influenza Viruses to its Neutralizing Antibodies. Antibodies, 2019, 8, 2.	1.2	0
3	Computational identification of antibody epitopes of human papillomavirus 16 (HPV16) L1 proteins. Journal of Theoretical and Computational Chemistry, 2018, 17, 1850017.	1.8	1
4	On-target action of anti-tropomyosin drugs regulates glucose metabolism. Scientific Reports, 2018, 8, 4604.	1.6	20
5	GPU Accelerated Quantum Virtual Screening: Application for the Natural Inhibitors of New Dehli Metalloprotein (NDM-1). Frontiers in Chemistry, 2018, 6, 564.	1.8	7
6	Design of peptide inhibitors of human papillomavirus 16 (HPV16) transcriptional regulator E1â€“E2 formation. Journal of Theoretical and Computational Chemistry, 2017, 16, 1750026.	1.8	0
7	Identification of Cancer-Targeted Tropomyosin Inhibitors and Their Synergy with Microtubule Drugs. Molecular Cancer Therapeutics, 2017, 16, 1555-1565.	1.9	38
8	Computational Identification of Antibody Epitopes on the Dengue Virus NS1 Protein. Molecules, 2017, 22, 607.	1.7	17
9	Antibody Recognition of Shiga Toxins (Stxs): Computational Identification of the Epitopes of Stx2 Subunit A to the Antibodies 11E10 and S2C4. PLoS ONE, 2014, 9, e88191.	1.1	6
10	Computational identification of epitopes in the glycoproteins of novel bunyavirus (SFTS virus) recognized by a human monoclonal antibody (MAb 4-5). Journal of Computer-Aided Molecular Design, 2013, 27, 539-550.	1.3	9
11	A Novel Class of Anticancer Compounds Targets the Actin Cytoskeleton in Tumor Cells. Cancer Research, 2013, 73, 5169-5182.	0.4	155
12	Peptide Bondtransâ€“cisIsomerization and Acylimine Formation in Chromophore Maturation of the Red Fluorescent Proteins. Journal of Physical Chemistry A, 2011, 115, 10129-10135.	1.1	3
13	Discovery of 2-(Î±-methylbenzylamino) pyrazines as potent Type II inhibitors of FMS. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 1206-1209.	1.0	13
14	Quantum Mechanical Quantification of Weakly Interacting Complexes of Peptides with Single-Walled Carbon Nanotubes. Journal of Chemical Theory and Computation, 2009, 5, 2879-2885.	2.3	38
15	The 559-to-600 nm shift observed in red fluorescent protein eqFP611 is attributed to cisâ€“trans isomerization of the chromophore in an anionic protein pocket. Physical Chemistry Chemical Physics, 2009, 11, 6042.	1.3	3
16	Electronic Excitations of Green Fluorescent Proteins:â€‰ Modeling Solvatochromatic Shifts of Red Fluorescent Protein Chromophore Model Compound in Aqueous Solutions. Journal of Physical Chemistry B, 2007, 111, 14055-14063.	1.2	21
17	ELECTRONIC EXCITATIONS OF GREEN FLUORESCENT PROTEINS: MODELING SOLVATOCHROMATIC SHIFTS OF CHROMOPHORE MODEL COMPOUNDS IN SOLUTIONS. Journal of Theoretical and Computational Chemistry, 2006, 05, 375-390.	1.8	7
18	Electronic excitations of green fluorescent proteins: Protonation states of chromophore model compound in solutions. Journal of Computational Chemistry, 2005, 26, 1487-1496.	1.5	32

#	Article	IF	Citations
19	Predicting sequences and structures of MHC-binding peptides: a computational combinatorial approach. Journal of Computer-Aided Molecular Design, 2001, 15, 573-586.	1.3	31
20	Design of inhibitors of Rasâ€“Raf interaction using a computational combinatorial algorithm. Protein Engineering, Design and Selection, 2001, 14, 39-45.	1.0	26
21	Mini-Review: Computational Structure-Based Design of Inhibitors that Target Protein Surfaces. Combinatorial Chemistry and High Throughput Screening, 2000, 3, 355-362.	0.6	35
22	A method for computational combinatorial peptide design of inhibitors of Ras protein. Protein Engineering, Design and Selection, 1999, 12, 457-468.	1.0	16
23	Molecular dynamics simulations of the Ras:Raf and Rap:Raf complexes. Proteins: Structure, Function and Bioinformatics, 1999, 35, 89-100.	1.5	17
24	Proteinâ€protein recognition: An experimental and computational study of the R89K mutation in Raf and its effect on Ras binding. Protein Science, 1999, 8, 50-64.	3.1	31
25	Conformation of the Ras-binding domain of Raf studied by molecular dynamics and free energy simulations. , 1998, 31, 186-200.		9