Jun Zeng

List of Publications by Year in descending order

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25 papers	566 citations	623734 14 h-index	677142 22 g-index
25 all docs	25 docs citations	25 times ranked	866 citing authors

#	Article	IF	Citations
1	A Novel Class of Anticancer Compounds Targets the Actin Cytoskeleton in Tumor Cells. Cancer Research, 2013, 73, 5169-5182.	0.9	155
2	Quantum Mechanical Quantification of Weakly Interacting Complexes of Peptides with Single-Walled Carbon Nanotubes. Journal of Chemical Theory and Computation, 2009, 5, 2879-2885.	5.3	38
3	Identification of Cancer-Targeted Tropomyosin Inhibitors and Their Synergy with Microtubule Drugs. Molecular Cancer Therapeutics, 2017, 16, 1555-1565.	4.1	38
4	Mini-Review: Computational Structure-Based Design of Inhibitors that Target Protein Surfaces. Combinatorial Chemistry and High Throughput Screening, 2000, 3, 355-362.	1.1	35
5	Electronic excitations of green fluorescent proteins: Protonation states of chromophore model compound in solutions. Journal of Computational Chemistry, 2005, 26, 1487-1496.	3.3	32
6	Predicting sequences and structures of MHC-binding peptides: a computational combinatorial approach. Journal of Computer-Aided Molecular Design, 2001, 15, 573-586.	2.9	31
7	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.	7.6	31
8	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.	3.0	31
9	Design of inhibitors of Rasâ€“Raf interaction using a computational combinatorial algorithm. Protein Engineering, Design and Selection, 2001, 14, 39-45.	2.1	26
10	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.	2.6	21
11	On-target action of anti-tropomyosin drugs regulates glucose metabolism. Scientific Reports, 2018, 8, 4604.	3.3	20
12	Molecular dynamics simulations of the Ras:Raf and Rap:Raf complexes. Proteins: Structure, Function and Bioinformatics, 1999, 35, 89-100.	2.6	17
13	Computational Identification of Antibody Epitopes on the Dengue Virus NS1 Protein. Molecules, 2017, 22, 607.	3.8	17
14	A method for computational combinatorial peptide design of inhibitors of Ras protein. Protein Engineering, Design and Selection, 1999, 12, 457-468.	2.1	16
15	Discovery of 2-(Î±-methylbenzylamino) pyrazines as potent Type II inhibitors of FMS. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 1206-1209.	2.2	13
16	Conformation of the Ras-binding domain of Raf studied by molecular dynamics and free energy simulations. , 1998, 31, 186-200.		9
17	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.	2.9	9
18	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

#	Article	IF	Citations
19	GPU Accelerated Quantum Virtual Screening: Application for the Natural Inhibitors of New Dehli Metalloprotein (NDM-1). Frontiers in Chemistry, 2018, 6, 564.	3.6	7
20	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.	2.5	6
21	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.	2.8	3
22	Peptide Bondtransâ€“cisIsomerization and Acylimine Formation in Chromophore Maturation of the Red Fluorescent Proteins. Journal of Physical Chemistry A, 2011, 115, 10129-10135.	2.5	3
23	Computational identification of antibody epitopes of human papillomavirus 16 (HPV16) L1 proteins. Journal of Theoretical and Computational Chemistry, 2018, 17, 1850017.	1.8	1
24	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
25	Computational Prediction of the Epitopes of HA1 Protein of Influenza Viruses to its Neutralizing Antibodies. Antibodies, 2019, 8, 2.	2.5	0