Zhijun Li

List of Publications by Year
in descending order

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21	300	840776 11	888059 17
papers	citations	h-index	g-index

22	22	22	476
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Nonâ€peptide agonists and positive allosteric modulators of glucagonâ€like peptideâ€1 receptors: Alternative approaches for treatment of Type 2 diabetes. British Journal of Pharmacology, 2022, 179, 511-525.	5.4	18
2	2â€Aminothiophene derivatives as a new class of positive allosteric modulators of glucagonâ€like peptide 1 receptor. Chemical Biology and Drug Design, 2022, 99, 857-867.	3.2	3
3	Is there a common allosteric binding site for G-protein coupled receptors?. Journal of Computer-Aided Molecular Design, 2022, 36, 405-413.	2.9	1
4	Design and Synthesis of Quinolizidine Derivatives as Influenza Virus and HIV-1 Inhibitors. Current Medicinal Chemistry, 2021, 28, 4995-5003.	2.4	4
5	Splice Junction Identification using Long Short-Term Memory Neural Networks. Current Genomics, 2021, 22, 384-390.	1.6	3
6	Development of Allosteric BRAF Peptide Inhibitors Targeting the Dimer Interface of BRAF. ACS Chemical Biology, 2019, 14, 1471-1480.	3.4	34
7	Discovery of a potential positive allosteric modulator of glucagon-like peptide 1 receptor through virtual screening and experimental study. Journal of Computer-Aided Molecular Design, 2019, 33, 973-981.	2.9	10
8	Structural Modeling and in Silico Screening of Potential Small-Molecule Allosteric Agonists of a Glucagon-like Peptide 1 Receptor. ACS Omega, 2019, 4, 961-970.	3.5	16
9	Design, synthesis and biological evaluation of novel N-nitrophenyl derivatives based on the structure of acetohydroxyacid synthase. Pesticide Biochemistry and Physiology, 2018, 145, 100-107.	3.6	2
10	Characterization of the first fully human anti-TEM1 scFv in models of solid tumor imaging and immunotoxin-based therapy. Cancer Immunology, Immunotherapy, 2017, 66, 367-378.	4.2	12
11	Structure Optimization of Aloperine Derivatives as HIV-1 Entry Inhibitors. ACS Medicinal Chemistry Letters, 2017, 8, 1199-1203.	2.8	16
12	PyMine: a PyMOL plugin to integrate and visualize data for drug discovery. BMC Research Notes, 2015, 8, 517.	1.4	33
13	Improving homology modeling of G-protein coupled receptors through multiple-template derived conserved inter-residue interactions. Journal of Computer-Aided Molecular Design, 2015, 29, 413-420.	2.9	9
14	Identification of a Diguanylate Cyclase and Its Role in Porphyromonas gingivalis Virulence. Infection and Immunity, 2014, 82, 2728-2735.	2.2	18
15	Rational design and construction of HER2 targeting recombinant human serum albumin. FASEB Journal, 2013, 27, lb586.	0.5	0
16	Developing a high-quality scoring function for membrane protein structures based on specific inter-residue interactions. Journal of Computer-Aided Molecular Design, 2012, 26, 301-309.	2.9	13
17	Comparing four different approaches for the determination of interâ€residue interactions provides insight for the structure prediction of helical membrane proteins. Biopolymers, 2009, 91, 547-556.	2.4	7
18	Conserved network properties of helical membrane protein structures and its implication for improving membrane protein homology modeling at the twilight zone. Journal of Computer-Aided Molecular Design, 2009, 23, 755-763.	2.9	7

#	Article	IF	Citations
19	Network pattern of residue packing in helical membrane proteins and its application in membrane protein structure prediction. Protein Engineering, Design and Selection, 2008, 21, 55-64.	2.1	14
20	Betulinic Acid Derivatives That Target gp120 and Inhibit Multiple Genetic Subtypes of Human Immunodeficiency Virus Type 1. Antimicrobial Agents and Chemotherapy, 2008, 52, 128-136.	3.2	39
21	A simple approach for protein structure discrimination based on the network pattern of conserved hydrophobic residues. Protein Engineering, Design and Selection, 2006, 19, 265-275.	2.1	36