

Zhijun Li

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/634698/publications.pdf>

Version: 2024-02-01

21
papers

300
citations

840776

11
h-index

888059

17
g-index

22
all docs

22
docs citations

22
times ranked

476
citing authors

#	ARTICLE	IF	CITATIONS
1	Betulinic Acid Derivatives That Target gp120 and Inhibit Multiple Genetic Subtypes of Human Immunodeficiency Virus Type 1. <i>Antimicrobial Agents and Chemotherapy</i> , 2008, 52, 128-136.	3.2	39
2	A simple approach for protein structure discrimination based on the network pattern of conserved hydrophobic residues. <i>Protein Engineering, Design and Selection</i> , 2006, 19, 265-275.	2.1	36
3	Development of Allosteric BRAF Peptide Inhibitors Targeting the Dimer Interface of BRAF. <i>ACS Chemical Biology</i> , 2019, 14, 1471-1480.	3.4	34
4	PyMine: a PyMOL plugin to integrate and visualize data for drug discovery. <i>BMC Research Notes</i> , 2015, 8, 517.	1.4	33
5	Identification of a Diguanylate Cyclase and Its Role in <i>Porphyromonas gingivalis</i> Virulence. <i>Infection and Immunity</i> , 2014, 82, 2728-2735.	2.2	18
6	Non-peptide agonists and positive allosteric modulators of glucagon-like peptide-1 receptors: Alternative approaches for treatment of Type 2 diabetes. <i>British Journal of Pharmacology</i> , 2022, 179, 511-525.	5.4	18
7	Structure Optimization of Aloperine Derivatives as HIV-1 Entry Inhibitors. <i>ACS Medicinal Chemistry Letters</i> , 2017, 8, 1199-1203.	2.8	16
8	Structural Modeling and in Silico Screening of Potential Small-Molecule Allosteric Agonists of a Glucagon-like Peptide 1 Receptor. <i>ACS Omega</i> , 2019, 4, 961-970.	3.5	16
9	Network pattern of residue packing in helical membrane proteins and its application in membrane protein structure prediction. <i>Protein Engineering, Design and Selection</i> , 2008, 21, 55-64.	2.1	14
10	Developing a high-quality scoring function for membrane protein structures based on specific inter-residue interactions. <i>Journal of Computer-Aided Molecular Design</i> , 2012, 26, 301-309.	2.9	13
11	Characterization of the first fully human anti-TEM1 scFv in models of solid tumor imaging and immunotoxin-based therapy. <i>Cancer Immunology, Immunotherapy</i> , 2017, 66, 367-378.	4.2	12
12	Discovery of a potential positive allosteric modulator of glucagon-like peptide 1 receptor through virtual screening and experimental study. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 973-981.	2.9	10
13	Improving homology modeling of G-protein coupled receptors through multiple-template derived conserved inter-residue interactions. <i>Journal of Computer-Aided Molecular Design</i> , 2015, 29, 413-420.	2.9	9
14	Comparing four different approaches for the determination of inter-residue interactions provides insight for the structure prediction of helical membrane proteins. <i>Biopolymers</i> , 2009, 91, 547-556.	2.4	7
15	Conserved network properties of helical membrane protein structures and its implication for improving membrane protein homology modeling at the twilight zone. <i>Journal of Computer-Aided Molecular Design</i> , 2009, 23, 755-763.	2.9	7
16	Design and Synthesis of Quinolizidine Derivatives as Influenza Virus and HIV-1 Inhibitors. <i>Current Medicinal Chemistry</i> , 2021, 28, 4995-5003.	2.4	4
17	Splice Junction Identification using Long Short-Term Memory Neural Networks. <i>Current Genomics</i> , 2021, 22, 384-390.	1.6	3
18	2-Aminothiophene derivatives as a new class of positive allosteric modulators of glucagon-like peptide 1 receptor. <i>Chemical Biology and Drug Design</i> , 2022, 99, 857-867.	3.2	3

#	ARTICLE	IF	CITATIONS
19	Design, synthesis and biological evaluation of novel N-nitrophenyl derivatives based on the structure of acetoxyacid synthase. <i>Pesticide Biochemistry and Physiology</i> , 2018, 145, 100-107.	3.6	2
20	Is there a common allosteric binding site for G-protein coupled receptors?. <i>Journal of Computer-Aided Molecular Design</i> , 2022, 36, 405-413.	2.9	1
21	Rational design and construction of HER2 targeting recombinant human serum albumin. <i>FASEB Journal</i> , 2013, 27, 1b586.	0.5	0