

Yang Cao

List of Publications by Year in descending order

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Version: 2024-02-01

42
papers

2,229
citations

331670

21
h-index

276875

41
g-index

44
all docs

44
docs citations

44
times ranked

4952
citing authors

#	ARTICLE	IF	CITATIONS
1	DrugDevCovid19: An Atlas of Anti-COVID-19 Compounds Derived by Computer-Aided Drug Design. <i>Molecules</i> , 2022, 27, 683.	3.8	11
2	FitDock: protein–ligand docking by template fitting. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	38
3	CB-Dock2: improved protein–ligand blind docking by integrating cavity detection, docking and homologous template fitting. <i>Nucleic Acids Research</i> , 2022, 50, W159-W164.	14.5	219
4	Antibody engineering improves neutralization activity against K417 spike mutant SARS-CoV-2 variants. <i>Cell and Bioscience</i> , 2022, 12, 63.	4.8	4
5	Comprehensive Characterizations of Immune Receptor Repertoire in Tumors and Cancer Immunotherapy Studies. <i>Cancer Immunology Research</i> , 2022, 10, 788-799.	3.4	10
6	Classification and characterization of multigene family proteins of African swine fever viruses. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	22
7	Versatility in acyltransferase activity completes chicoric acid biosynthesis in purple coneflower. <i>Nature Communications</i> , 2021, 12, 1563.	12.8	45
8	Functional comparison of SARS-CoV-2 with closely related pangolin and bat coronaviruses. <i>Cell Discovery</i> , 2021, 7, 21.	6.7	20
9	Acetylcholinesterase target sites for developing environmentally friendly insecticides against <i>Tetranychus urticae</i> (Acari: Tetranychidae). <i>Experimental and Applied Acarology</i> , 2021, 84, 419-431.	1.6	3
10	Exploring the Species Diversity of Edible Mushrooms in Yunnan, Southwestern China, by DNA Barcoding. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 310.	3.5	23
11	TRUST4: immune repertoire reconstruction from bulk and single-cell RNA-seq data. <i>Nature Methods</i> , 2021, 18, 627-630.	19.0	126
12	A systematic analysis of miRNA markers and classification algorithms for forensic body fluid identification. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	13
13	FBXL2 counteracts Grp94 to destabilize EGFR and inhibit EGFR-driven NSCLC growth. <i>Nature Communications</i> , 2021, 12, 5919.	12.8	29
14	RNA-Puzzles toolkit: a computational resource of RNA 3D structure benchmark datasets, structure manipulation, and evaluation tools. <i>Nucleic Acids Research</i> , 2020, 48, 576-588.	14.5	44
15	CB-Dock: a web server for cavity detection-guided protein–ligand blind docking. <i>Acta Pharmacologica Sinica</i> , 2020, 41, 138-144.	6.1	377
16	LigMate: A Multifeature Integration Algorithm for Ligand-Similarity-Based Virtual Screening. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 6044-6053.	5.4	8
17	Advances in RNA 3D Structure Modeling Using Experimental Data. <i>Frontiers in Genetics</i> , 2020, 11, 574485.	2.3	56
18	Characteristics of <i>Stenotrophomonas maltophilia</i> infection in children in Sichuan, China, from 2010 to 2017. <i>Medicine (United States)</i> , 2020, 99, e19250.	1.0	14

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19	Exploring the computational methods for protein-ligand binding site prediction. Computational and Structural Biotechnology Journal, 2020, 18, 417-426.	4.1	112
20	The bacterial deubiquitinase Ceg23 regulates the association of Lys-63-linked polyubiquitin molecules on the Legionella phagosome. Journal of Biological Chemistry, 2020, 295, 1646-1657.	3.4	33
21	Prediction of antiviral drugs against African swine fever viruses based on protein-protein interaction analysis. PeerJ, 2020, 8, e8855.	2.0	11
22	AbRSA: A robust tool for antibody numbering. Protein Science, 2019, 28, 1524-1531.	7.6	29
23	Computational Methods for scRNA-seq Analysis at Cell Level. , 2019, , .		0
24	Evaluation of Protein-Ligand Docking by Cyscore. Methods in Molecular Biology, 2018, 1762, 233-243.	0.9	3
25	A homozygous G insertion in MPLKIP leads to TTDN1 with the hypergonadotropic hypogonadism symptom. BMC Medical Genetics, 2018, 19, 214.	2.1	5
26	Affinity maturation of an antibody for the UV-induced DNA lesions 6,4 pyrimidine-pyrimidones. Applied Microbiology and Biotechnology, 2018, 102, 6409-6424.	3.6	5
27	Screening for Novel Small-Molecule Inhibitors Targeting the Assembly of Influenza Virus Polymerase Complex by a Bimolecular Luminescence Complementation-Based Reporter System. Journal of Virology, 2017, 91, .	3.4	12
28	The complete mitochondrial genome of the edible Basidiomycete mushroom <i>Phlebopus portentosus</i> . Mitochondrial DNA Part B: Resources, 2017, 2, 696-697.	0.4	2
29	Quantifying side-chain conformational variations in protein structure. Scientific Reports, 2016, 6, 37024.	3.3	30
30	Inhibition of Cdc42 is essential for Mig-6 suppression of cell migration induced by EGF. Oncotarget, 2016, 7, 49180-49193.	1.8	12
31	Cloning and Characterization of the Acetylcholinesterase1 Gene of Tetranychus cinnabarinus (Acari: Tj ETQq1 1 0.784314 rgBT /Overlock 1.8 5		
32	Novel and selective acetylcholinesterase inhibitors for Tetranychus cinnabarinus (Acari: Tj ETQq0 0 0 rgBT /Overlock 1.0 Tf 50.222 Td (Tj ETQq0 0 0 2.7 14		
33	Improved protein-ligand binding affinity prediction by using a curvature-dependent surface-area model. Bioinformatics, 2014, 30, 1674-1680.	4.1	126
34	Structure, Gene Flow, and Recombination among Geographic Populations of a <i>Russula virescens</i> Ally from Southwestern China. PLoS ONE, 2013, 8, e73174.	2.5	22
35	Rapid Estimation of Binding Activity of Influenza Virus Hemagglutinin to Human and Avian Receptors. PLoS ONE, 2011, 6, e18664.	2.5	13
36	Improved side-chain modeling by coupling clash-detection guided iterative search with rotamer relaxation. Bioinformatics, 2011, 27, 785-790.	4.1	52

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37	A multiple <i>ATG</i> gene knockout strain for yeast two-hybrid analysis. <i>Autophagy</i> , 2009, 5, 699-705.	9.1	17
38	Lack of Salicylic Acid in <i>Arabidopsis</i> Protects Plants against Moderate Salt Stress. <i>Zeitschrift Fur Naturforschung - Section C Journal of Biosciences</i> , 2009, 64, 231-238.	1.4	69
39	New insights into autophagy using a multiple knockout strain. <i>Autophagy</i> , 2008, 4, 1073-1075.	9.1	7
40	In vivo reconstitution of autophagy in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 2008, 182, 703-713.	5.2	61
41	<i>Atg26</i> is Not Involved in Autophagy-Related Pathways in <i>Saccharomyces cerevisiae</i> . <i>Autophagy</i> , 2007, 3, 17-20.	9.1	35
42	Physiological functions of <i>Atg6/Beclin 1</i> : a unique autophagy-related protein. <i>Cell Research</i> , 2007, 17, 839-849.	12.0	492