## Yang Cao

## List of Publications by Year in descending order

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331670 276875 2,229 42 21 41 citations h-index g-index papers 44 44 44 4952 all docs docs citations times ranked citing authors

#	Article	IF	CITATIONS
1	Physiological functions of Atg6/Beclin 1: a unique autophagy-related protein. Cell Research, 2007, 17, 839-849.	12.0	492
2	CB-Dock: a web server for cavity detection-guided protein–ligand blind docking. Acta Pharmacologica Sinica, 2020, 41, 138-144.	6.1	377
3	CB-Dock2: improved protein–ligand blind docking by integrating cavity detection, docking and homologous template fitting. Nucleic Acids Research, 2022, 50, W159-W164.	14.5	219
4	Improved protein–ligand binding affinity prediction by using a curvature-dependent surface-area model. Bioinformatics, 2014, 30, 1674-1680.	4.1	126
5	TRUST4: immune repertoire reconstruction from bulk and single-cell RNA-seq data. Nature Methods, 2021, 18, 627-630.	19.0	126
6	Exploring the computational methods for protein-ligand binding site prediction. Computational and Structural Biotechnology Journal, 2020, 18, 417-426.	4.1	112
7	Lack of Salicylic Acid in Arabidopsis Protects Plants against Moderate Salt Stress. Zeitschrift Fur Naturforschung - Section C Journal of Biosciences, 2009, 64, 231-238.	1.4	69
8	In vivo reconstitution of autophagy in <i>Saccharomyces cerevisiae </i> . Journal of Cell Biology, 2008, 182, 703-713.	<b>5.</b> 2	61
9	Advances in RNA 3D Structure Modeling Using Experimental Data. Frontiers in Genetics, 2020, 11, 574485.	2.3	56
10	Improved side-chain modeling by coupling clash-detection guided iterative search with rotamer relaxation. Bioinformatics, 2011, 27, 785-790.	4.1	52
11	Versatility in acyltransferase activity completes chicoric acid biosynthesis in purple coneflower. Nature Communications, 2021, 12, 1563.	12.8	45
12	RNA-Puzzles toolkit: a computational resource of RNA 3D structure benchmark datasets, structure manipulation, and evaluation tools. Nucleic Acids Research, 2020, 48, 576-588.	14.5	44
13	FitDock: protein–ligand docking by template fitting. Briefings in Bioinformatics, 2022, 23, .	6.5	38
14	Atg26 is Not Involved in Autophagy-Related Pathways in <i>Saccharomyces cerevisiae</i> . Autophagy, 2007, 3, 17-20.	9.1	35
15	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
16	Quantifying side-chain conformational variations in protein structure. Scientific Reports, 2016, 6, 37024.	3.3	30
17	AbRSA: A robust tool for antibody numbering. Protein Science, 2019, 28, 1524-1531.	7.6	29
18	FBXL2 counteracts Grp94 to destabilize EGFR and inhibit EGFR-driven NSCLC growth. Nature Communications, 2021, 12, 5919.	12.8	29

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19	Exploring the Species Diversity of Edible Mushrooms in Yunnan, Southwestern China, by DNA Barcoding. Journal of Fungi (Basel, Switzerland), 2021, 7, 310.	3.5	23
20	Structure, Gene Flow, and Recombination among Geographic Populations of a Russula virescens Ally from Southwestern China. PLoS ONE, 2013, 8, e73174.	2.5	22
21	Classification and characterization of multigene family proteins of African swine fever viruses. Briefings in Bioinformatics, 2021, 22, .	6.5	22
22	Functional comparison of SARS-CoV-2 with closely related pangolin and bat coronaviruses. Cell Discovery, 2021, 7, 21.	6.7	20
23	A multiple <i>ATG</i> gene knockout strain for yeast two-hybrid analysis. Autophagy, 2009, 5, 699-705.	9.1	17
24	Novel and selective acetylcholinesterase inhibitors for Tetranychus cinnabarinus (Acari:) Tj ETQq0 0 0 rgBT /Over	ock 10 Tf	50 542 Td (To
25	Characteristics of Stenotrophomonas maltophilia infection in children in Sichuan, China, from 2010 to 2017. Medicine (United States), 2020, 99, e19250.	1.0	14
26	Rapid Estimation of Binding Activity of Influenza Virus Hemagglutinin to Human and Avian Receptors. PLoS ONE, 2011, 6, e18664.	2.5	13
27	A systematic analysis of miRNA markers and classification algorithms for forensic body fluid identification. Briefings in Bioinformatics, 2021, 22, .	6.5	13
28	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
29	Inhibition of Cdc42 is essential for Mig-6 suppression of cell migration induced by EGF. Oncotarget, 2016, 7, 49180-49193.	1.8	12
30	Prediction of antiviral drugs against African swine fever viruses based on protein–protein interaction analysis. PeerJ, 2020, 8, e8855.	2.0	11
31	DrugDevCovid19: An Atlas of Anti-COVID-19 Compounds Derived by Computer-Aided Drug Design. Molecules, 2022, 27, 683.	3.8	11
32	Comprehensive Characterizations of Immune Receptor Repertoire in Tumors and Cancer Immunotherapy Studies. Cancer Immunology Research, 2022, 10, 788-799.	3.4	10
33	LigMate: A Multifeature Integration Algorithm for Ligand-Similarity-Based Virtual Screening. Journal of Chemical Information and Modeling, 2020, 60, 6044-6053.	5.4	8
34	New insights into autophagy using a multiple knockout strain. Autophagy, 2008, 4, 1073-1075.	9.1	7
35	Cloning and Characterization of the Acetylcholinesterase $1$ Gene of Tetranychus cinnabarinus (Acari:) Tj ETQq $1\ 1$	0.784314 1.8	rgBT /Over <mark>lo</mark>
36	A homozygous G insertion in MPLKIP leads to TTDN1 with the hypergonadotropic hypogonadism symptom. BMC Medical Genetics, 2018, 19, 214.	2.1	5

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37	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
38	Antibody engineering improves neutralization activity against K417 spike mutant SARS-CoV-2 variants. Cell and Bioscience, 2022, 12, 63.	4.8	4
39	Evaluation of Protein–Ligand Docking by Cyscore. Methods in Molecular Biology, 2018, 1762, 233-243.	0.9	3
40	Acetylcholinesterase target sites for developing environmentally friendly insecticides against Tetranychus urticae (Acari: Tetranychidae). Experimental and Applied Acarology, 2021, 84, 419-431.	1.6	3
41	The complete mitochondrial genome of the edible Basidiomycete mushroom <i>Phlebopus Portentosus </i> Nitochondrial DNA Part B: Resources, 2017, 2, 696-697.	0.4	2
42	Computational Methods for scRNA-seq Analysis at Cell Level. , 2019, , .		0