

# Jian Zhan

## List of Publications by Year in descending order

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Version: 2024-02-01

24  
papers

1,345  
citations

623734

14  
h-index

642732

23  
g-index

27  
all docs

27  
docs citations

27  
times ranked

2795  
citing authors

#	ARTICLE	IF	CITATIONS
1	Self-Inhibitory Peptides Targeting the <i>Neisseria gonorrhoeae</i> MtrCDE Efflux Pump Increase Antibiotic Susceptibility. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0154221.	3.2	2
2	High-throughput split-protein profiling by combining transposon mutagenesis and regulated protein-protein interactions with deep sequencing. <i>International Journal of Biological Macromolecules</i> , 2022, 203, 543-552.	7.5	0
3	Probing RNA structures and functions by solvent accessibility: an overview from experimental and computational perspectives. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	13
4	Pairing a high-resolution statistical potential with a nucleobase-centric sampling algorithm for improving RNA model refinement. <i>Nature Communications</i> , 2021, 12, 2777.	12.8	33
5	RNAcmap: a fully automatic pipeline for predicting contact maps of RNAs by evolutionary coupling analysis. <i>Bioinformatics</i> , 2021, 37, 3494-3500.	4.1	27
6	<i>De novo</i> protein design by an energy function based on series expansion in distance and orientation dependence. <i>Bioinformatics</i> , 2021, 38, 86-93.	4.1	8
7	Repurposing clinically approved drugs for COVID-19 treatment targeting SARS-CoV-2 papain-like protease. <i>International Journal of Biological Macromolecules</i> , 2021, 188, 137-146.	7.5	32
8	Accurate inference of the full base-pairing structure of RNA by deep mutational scanning and covariation-induced deviation of activity. <i>Nucleic Acids Research</i> , 2020, 48, 1451-1465.	14.5	15
9	Digestive system is a potential route of COVID-19: an analysis of single-cell coexpression pattern of key proteins in viral entry process. <i>Gut</i> , 2020, 69, 1010-1018.	12.1	404
10	Predicting functional long non-coding RNAs validated by low throughput experiments. <i>RNA Biology</i> , 2019, 16, 1555-1564.	3.1	6
11	Self-derived structure-disrupting peptides targeting methionine aminopeptidase in pathogenic bacteria: a new strategy to generate antimicrobial peptides. <i>FASEB Journal</i> , 2019, 33, 2095-2104.	0.5	7
12	<i>B-factor</i> profile prediction for RNA flexibility using support vector machines. <i>Journal of Computational Chemistry</i> , 2018, 39, 407-411.	3.3	13
13	YesU from <i>Bacillus subtilis</i> preferentially binds fucosylated glycans. <i>Scientific Reports</i> , 2018, 8, 13139.	3.3	7
14	Real-time reliable determination of binding kinetics of DNA hybridization using a multi-channel graphene biosensor. <i>Nature Communications</i> , 2017, 8, 14902.	12.8	303
15	Genome-scale characterization of RNA tertiary structures and their functional impact by RNA solvent accessibility prediction. <i>Rna</i> , 2017, 23, 14-22.	3.5	28
16	Structural signatures of thermal adaptation of bacterial ribosomal RNA, transfer RNA, and messenger RNA. <i>PLoS ONE</i> , 2017, 12, e0184722.	2.5	15
17	Investigation the Possibility of Using Peptides with a Helical Repeating Pattern of Hydro-Phobic and Hydrophilic Residues to Inhibit IL-10. <i>PLoS ONE</i> , 2016, 11, e0153939.	2.5	14
18	SPOT-Ligand: Fast and effective structure-based virtual screening by binding homology search according to ligand and receptor similarity. <i>Journal of Computational Chemistry</i> , 2016, 37, 1734-1739.	3.3	15

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19	Optimal secretion of alkali-tolerant xylanase in <i>Bacillus subtilis</i> by signal peptide screening. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 8745-8756.	3.6	35
20	Direct prediction of profiles of sequences compatible with a protein structure by neural networks with fragment-based local and energy-based nonlocal profiles. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2565-2573.	2.6	46
21	Energy Functions in De Novo Protein Design: Current Challenges and Future Prospects. <i>Annual Review of Biophysics</i> , 2013, 42, 315-335.	10.0	75
22	A new size-independent score for pairwise protein structure alignment and its application to structure classification and nucleic acid binding prediction. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2080-2088.	2.6	69
23	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
24	Develop reusable and combinable designs for transcriptional logic gates. <i>Molecular Systems Biology</i> , 2010, 6, 388.	7.2	46