

Chi Zhang

List of Publications by Year in descending order

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120
papers

5,996
citations

87888

38
h-index

85541

71
g-index

125
all docs

125
docs citations

125
times ranked

8181
citing authors

#	ARTICLE	IF	CITATIONS
1	PopLDdecay: a fast and effective tool for linkage disequilibrium decay analysis based on variant call format files. <i>Bioinformatics</i> , 2019, 35, 1786-1788.	4.1	818
2	SVMTriP: A Method to Predict Antigenic Epitopes Using Support Vector Machine to Integrate Tri-Peptide Similarity and Propensity. <i>PLoS ONE</i> , 2012, 7, e45152.	2.5	269
3	A Knowledge-Based Energy Function for Protein~Ligand, Protein~Protein, and Protein~DNA Complexes. <i>Journal of Medicinal Chemistry</i> , 2005, 48, 2325-2335.	6.4	264
4	Protein binding site prediction using an empirical scoring function. <i>Nucleic Acids Research</i> , 2006, 34, 3698-3707.	14.5	223
5	Regulation of miRNA abundance by RNA binding protein TOUGH in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12817-12821.	7.1	177
6	A physical reference state unifies the structure-derived potential of mean force for protein folding and binding. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 93-101.	2.6	176
7	An accurate, residue-level, pair potential of mean force for folding and binding based on the distance-scaled, ideal-gas reference state. <i>Protein Science</i> , 2004, 13, 400-411.	7.6	153
8	Heat stress yields a unique MADS box transcription factor in determining seed size and thermal sensitivity. <i>Plant Physiology</i> , 2016, 171, 606-622.	4.8	146
9	EPSVR and EPMeta: prediction of antigenic epitopes using support vector regression and multiple server results. <i>BMC Bioinformatics</i> , 2010, 11, 381.	2.6	140
10	PhosphoSVM: prediction of phosphorylation sites by integrating various protein sequence attributes with a support vector machine. <i>Amino Acids</i> , 2014, 46, 1459-1469.	2.7	132
11	Editing of an Alpha-Kafirin Gene Family Increases, Digestibility and Protein Quality in Sorghum. <i>Plant Physiology</i> , 2018, 177, 1425-1438.	4.8	128
12	PIWI Associated siRNAs and piRNAs Specifically Require the <i>Caenorhabditis elegans</i> HEN1 Ortholog henn-1. <i>PLoS Genetics</i> , 2012, 8, e1002616.	3.5	124
13	Identification of differentially expressed genes between sorghum genotypes with contrasting nitrogen stress tolerance by genome-wide transcriptional profiling. <i>BMC Genomics</i> , 2014, 15, 179.	2.8	118
14	Allelic variants of OsHKT1;1 underlie the divergence between indica and japonica subspecies of rice (<i>Oryza sativa</i>) for root sodium content. <i>PLoS Genetics</i> , 2017, 13, e1006823.	3.5	118
15	Accurate and efficient loop selections by the DFIRE-based all-atom statistical potential. <i>Protein Science</i> , 2004, 13, 391-399.	7.6	112
16	Conformational B-Cell Epitope Prediction on Antigen Protein Structures: A Review of Current Algorithms and Comparison with Common Binding Site Prediction Methods. <i>PLoS ONE</i> , 2013, 8, e62249.	2.5	101
17	Prediction of antigenic epitopes on protein surfaces by consensus scoring. <i>BMC Bioinformatics</i> , 2009, 10, 302.	2.6	99
18	Distinct <i>Pseudomonas</i> effectors use a cleavable transit peptide to target chloroplasts. <i>Plant Journal</i> , 2014, 77, 310-321.	5.7	92

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19	The <i>Pseudomonas syringae</i> type III effector <i>HopD1</i> suppresses effector-triggered immunity, localizes to the endoplasmic reticulum, and targets the <i>Arabidopsis</i> rabidopsis transcription factor <i>NTL9</i> . <i>New Phytologist</i> , 2014, 201, 1358-1370.	7.3	89
20	Fold recognition by concurrent use of solvent accessibility and residue depth. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 636-645.	2.6	87
21	Osmotic stress induces phosphorylation of histone H3 at threonine 3 in pericentromeric regions of <i>Arabidopsis thaliana</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8487-8492.	7.1	82
22	Synergistic and Independent Actions of Multiple Terminal Nucleotidyl Transferases in the 3' Tailing of Small RNAs in <i>Arabidopsis</i> . <i>PLoS Genetics</i> , 2015, 11, e1005091.	3.5	81
23	DFVF: database of fungal virulence factors. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas032-bas032.	3.0	80
24	Dehydration Stress Memory: Gene Networks Linked to Physiological Responses During Repeated Stresses of <i>Zea mays</i> . <i>Frontiers in Plant Science</i> , 2018, 9, 1058.	3.6	71
25	Genetic and Molecular Characterization of Submergence Response Identifies <i>Sub1a</i> as a Major Submergence Tolerance Locus in Maize. <i>PLoS ONE</i> , 2015, 10, e0120385.	2.5	66
26	Tracking the Sources of Antibiotic Resistance Genes in an Urban Stream during Wet Weather using Shotgun Metagenomic Analyses. <i>Environmental Science & Technology</i> , 2018, 52, 9033-9044.	10.0	66
27	<i>MAC3A</i> and <i>MAC3B</i> , Two Core Subunits of the <i>MOS4</i> -Associated Complex, Positively Influence miRNA Biogenesis. <i>Plant Cell</i> , 2018, 30, 481-494.	6.6	64
28	A simple reference state makes a significant improvement in near-native selections from structurally refined docking decoys. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 244-253.	2.6	59
29	Sharpening Low-Energy, Standard-Model Tests via Correlation Coefficients in Neutron β -Decay. <i>Physical Review Letters</i> , 2001, 86, 5666-5669.	7.8	58
30	Temperature Dependence of the Distribution of the First Passage Time: Results from Discontinuous Molecular Dynamics Simulations of an All-Atom Model of the Second β -Hairpin Fragment of Protein G. <i>Journal of the American Chemical Society</i> , 2003, 125, 6300-6305.	13.7	56
31	Fast and accurate prediction of protein side-chain conformations. <i>Bioinformatics</i> , 2011, 27, 2913-2914.	4.1	53
32	Mapping QTLs and association of differentially expressed gene transcripts for multiple agronomic traits under different nitrogen levels in sorghum. <i>BMC Plant Biology</i> , 2016, 16, 16.	3.6	51
33	What is a Desirable Statistical Energy Function for Proteins and How Can It Be Obtained?. <i>Cell Biochemistry and Biophysics</i> , 2006, 46, 165-174.	1.8	50
34	<i>MADS78</i> and <i>MADS79</i> Are Essential Regulators of Early Seed Development in Rice. <i>Plant Physiology</i> , 2020, 182, 933-948.	4.8	49
35	Identification of RNA silencing components in soybean and sorghum. <i>BMC Bioinformatics</i> , 2014, 15, 4.	2.6	46
36	Deletion Mutagenesis Identifies a Haploinsufficient Role for β -Zein in <i>opaque2</i> Endosperm Modification. <i>Plant Physiology</i> , 2014, 164, 119-130.	4.8	46

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37	Validation of QTL mapping and transcriptome profiling for identification of candidate genes associated with nitrogen stress tolerance in sorghum. <i>BMC Plant Biology</i> , 2017, 17, 123.	3.6	45
38	A Comprehensive Image-based Phenomic Analysis Reveals the Complex Genetic Architecture of Shoot Growth Dynamics in Rice (<i>Oryza sativa</i>). <i>Plant Genome</i> , 2017, 10, plantgenome2016.07.0064.	2.8	45
39	Automatic planning on hippocampal avoidance whole-brain radiotherapy. <i>Medical Dosimetry</i> , 2017, 42, 63-68.	0.9	42
40	The Dependence of All-Atom Statistical Potentials on Structural Training Database. <i>Biophysical Journal</i> , 2004, 86, 3349-3358.	0.5	41
41	SMA1, a homolog of the splicing factor Prp28, has a multifaceted role in miRNA biogenesis in <i>Arabidopsis</i> . <i>Nucleic Acids Research</i> , 2018, 46, 9148-9159.	14.5	38
42	Radiomics-Based Outcome Prediction for Pancreatic Cancer Following Stereotactic Body Radiotherapy. <i>Cancers</i> , 2020, 12, 1051.	3.7	38
43	STV1, a ribosomal protein, binds primary microRNA transcripts to promote their interaction with the processing complex in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1424-1429.	7.1	37
44	Evaluating potential risks of food allergy of novel food sources based on comparison of proteins predicted from genomes and compared to www.AllergenOnline.org. <i>Food and Chemical Toxicology</i> , 2021, 147, 111888.	3.6	35
45	Docking prediction using biological information, ZDOCK sampling technique, and clustering guided by the DFIRE statistical energy function. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 314-318.	2.6	34
46	LEAP: Highly accurate prediction of protein loop conformations by integrating coarse-grained sampling and optimized energy scores with all-atom refinement of backbone and side chains. <i>Journal of Computational Chemistry</i> , 2014, 35, 335-341.	3.3	34
47	Radiomic feature stability across 4D respiratory phases and its impact on lung tumor prognosis prediction. <i>PLoS ONE</i> , 2019, 14, e0216480.	2.5	34
48	MAC5, an RNA-binding protein, protects pri-miRNAs from SERRATE-dependent exoribonuclease activities. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23982-23990.	7.1	32
49	New aspects of iron-copper crosstalk uncovered by transcriptomic characterization of Col-0 and the copper uptake mutant <i>spl7</i> in <i>Arabidopsis thaliana</i> . <i>Metallomics</i> , 2018, 10, 1824-1840.	2.4	31
50	Genome-Wide Gene Expression in relation to Age in Large Laboratory Cohorts of <i>Drosophila melanogaster</i> . <i>Genetics Research International</i> , 2015, 2015, 1-19.	2.0	30
51	Proteomic profiling of maize opaque endosperm mutants reveals selective accumulation of lysine-enriched proteins. <i>Journal of Experimental Botany</i> , 2016, 67, 1381-1396.	4.8	30
52	Radiative neutron \hat{I}^2 -decay in effective field theory. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 2004, 593, 105-114.	4.1	29
53	Fuzzy clustering of CPP family in plants with evolution and interaction analyses. <i>BMC Bioinformatics</i> , 2013, 14, S10.	2.6	28
54	Scalable and physiologically relevant microenvironments for human pluripotent stem cell expansion and differentiation. <i>Biofabrication</i> , 2018, 10, 025006.	7.1	28

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73	Serrate-Associated Protein 1, a splicing-related protein, promotes miRNA biogenesis in Arabidopsis. <i>New Phytologist</i> , 2021, 232, 1959-1973.	7.3	18
74	SVMTriP: A Method to Predict B-Cell Linear Antigenic Epitopes. <i>Methods in Molecular Biology</i> , 2020, 2131, 299-307.	0.9	18
75	Web-based toolkits for topology prediction of transmembrane helical proteins, fold recognition, structure and binding scoring, folding-kinetics analysis and comparative analysis of domain combinations. <i>Nucleic Acids Research</i> , 2005, 33, W193-W197.	14.5	17
76	Protein Loop Modeling with Optimized Backbone Potential Functions. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 1820-1827.	5.3	17
77	Endoplasmic reticulum stress pathway mediates the early heat stress response of developing rice seeds. <i>Plant, Cell and Environment</i> , 2021, 44, 2604-2624.	5.7	17
78	Target dose conversion modeling from pencil beam (PB) to Monte Carlo (MC) for lung SBRT. <i>Radiation Oncology</i> , 2016, 11, 83.	2.7	16
79	Characterization of the transcriptional divergence between the subspecies of cultivated rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Overl	2.8	16
80	Genome-wide Discovery of Circular RNAs in the Leaf and Seedling Tissues of Arabidopsis Thaliana. <i>Current Genomics</i> , 2017, 18, 360-365.	1.6	16
81	Perineural clonidine reduces p38 mitogen-activated protein kinase activation in sensory neurons. <i>NeuroReport</i> , 2006, 17, 1313-1317.	1.2	15
82	A Population of Deletion Mutants and an Integrated Mapping and Exome-seq Pipeline for Gene Discovery in Maize. <i>G3: Genes, Genomes, Genetics</i> , 2016, 6, 2385-2395.	1.8	14
83	Network-based feature selection reveals substructures of gene modules responding to salt stress in rice. <i>Plant Direct</i> , 2019, 3, e00154.	1.9	14
84	A novel function prediction approach using protein overlap networks. <i>BMC Systems Biology</i> , 2013, 7, 61.	3.0	13
85	Manufacturing human pluripotent stem cell derived endothelial cells in scalable and cell-friendly microenvironments. <i>Biomaterials Science</i> , 2019, 7, 373-388.	5.4	12
86	Template-based structure prediction and classification of transcription factors in <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2012, 21, 828-838.	7.6	11
87	Domain Graph of Arabidopsis Proteome by Comparative Analysis. <i>Journal of Proteome Research</i> , 2005, 4, 435-444.	3.7	10
88	Virus-host mucosal interactions during early SIV rectal transmission. <i>Virology</i> , 2014, 464-465, 406-414.	2.4	10
89	Prediction of immunogenicity for humanized and full human therapeutic antibodies. <i>PLoS ONE</i> , 2020, 15, e0238150.	2.5	10
90	Chemical and genetic variation in feral <i>Cannabis sativa</i> populations across the Nebraska climate gradient. <i>Phytochemistry</i> , 2022, 200, 113206.	2.9	10

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91	Amyloid precursor protein is a restriction factor that protects against Zika virus infection in mammalian brains. <i>Journal of Biological Chemistry</i> , 2020, 295, 17114-17127.	3.4	9
92	<i>Zygnema circumcarinatum</i> UTEX 1559 chloroplast and mitochondrial genomes provide insight into land plant evolution. <i>Journal of Experimental Botany</i> , 2020, 71, 3361-3373.	4.8	9
93	MLK4-mediated phosphorylation of histone H3T3 promotes flowering by transcriptional silencing of FLC/MAF in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2021, 105, 1400-1412.	5.7	9
94	Protein loop selection using orientation-dependent force fields derived by parameter optimization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 2260-2267.	2.6	8
95	Deletion of maize RDM4 suggests a role in endosperm maturation as well as vegetative and stress-responsive growth. <i>Journal of Experimental Botany</i> , 2020, 71, 5880-5895.	4.8	8
96	RGPDB: database of root-associated genes and promoters in maize, soybean, and sorghum. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	8
97	An Exome-seq Based Tool for Mapping and Selection of Candidate Genes in Maize Deletion Mutants. <i>Genomics, Proteomics and Bioinformatics</i> , 2018, 16, 439-450.	6.9	7
98	Differentiating human pluripotent stem cells into vascular smooth muscle cells in three dimensional thermoreversible hydrogels. <i>Biomaterials Science</i> , 2019, 7, 347-361.	5.4	7
99	Identification of a EML4-ALK exon 19 fusion variant in lung adenocarcinoma and alectinib resistance. <i>Lung Cancer</i> , 2021, 160, 32-35.	2.0	7
100	The UDP-glycosyltransferase MtUGT84A1 regulates anthocyanin accumulation and plant growth via JA signaling in <i>Medicago truncatula</i> . <i>Environmental and Experimental Botany</i> , 2022, 201, 104972.	4.2	7
101	Differential Expression Analysis in RNA-Seq by a Naive Bayes Classifier with Local Normalization. <i>BioMed Research International</i> , 2015, 2015, 1-9.	1.9	6
102	Prediction of Protein Phosphorylation Sites by Integrating Secondary Structure Information and Other One-Dimensional Structural Properties. <i>Methods in Molecular Biology</i> , 2017, 1484, 265-274.	0.9	6
103	Transcriptome analysis-identified long noncoding RNA CRNDE in maintaining endothelial cell proliferation, migration, and tube formation. <i>Scientific Reports</i> , 2019, 9, 19548.	3.3	6
104	Isolating and cryopreserving pig skin cells for single-cell RNA sequencing study. <i>PLoS ONE</i> , 2022, 17, e0263869.	2.5	6
105	Uneven size distribution of mammalian genes in the number of tissues expressed and in the number of co-expressed genes. <i>Human Molecular Genetics</i> , 2006, 15, 1313-1318.	2.9	4
106	iVAR: Interactive visual analytics of radiomics features from large-scale medical images. , 2017, , .		4
107	Pervasive misannotation of microexons that are evolutionarily conserved and crucial for gene function in plants. <i>Nature Communications</i> , 2022, 13, 820.	12.8	4
108	Application of statistical and computational methodology to predict brainstem dosimetry for trigeminal neuralgia stereotactic radiosurgery. <i>Medical Physics</i> , 2018, 45, 1822-1831.	3.0	3

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109	Glycosyl rotation and distortion by key residues in Endocellulase Cel6A from <i>Thermobifida fusca</i> . <i>Glycobiology</i> , 2014, 24, 247-251.	2.5	2
110	TGCnA: temporal gene coexpression network analysis using a low-rank plus sparse framework. <i>Journal of Applied Statistics</i> , 2020, 47, 1064-1083.	1.3	2
111	EPCES and EPSVR: Prediction of B-Cell Antigenic Epitopes on Protein Surfaces with Conformational Information. <i>Methods in Molecular Biology</i> , 2020, 2131, 289-297.	0.9	2
112	NanoAsPipe: A transcriptome analysis and alternative splicing detection pipeline for MinION long-read RNA-seq. , 2017, , .		1
113	Identification of differential alternative splicing events with an adjusted beta-distribution model. , 2017, , .		1
114	Deletion Mutagenesis and Identification of Causative Mutations in Maize. <i>Methods in Molecular Biology</i> , 2018, 1676, 97-108.	0.9	1
115	InMut-finder: a software tool for insertion identification in mutagenesis using Nanopore long reads. <i>BMC Genomics</i> , 2021, 22, 908.	2.8	1
116	A dataset for assessing temporal changes in gene expression during the aging process of adult <i>Drosophila melanogaster</i> . <i>Data in Brief</i> , 2016, 7, 1652-1657.	1.0	0
117	A mapping-by-sequencing tool for searching causative genes in mutants. , 2017, , .		0
118	Discovery and Characterization of Non-coding RNA Through Modern Genomics. , 2021, , 284-298.		0
119	Radiative neutron beta-decay in effective field theory. <i>Journal of Research of the National Institute of Standards and Technology</i> , 2005, 110, 411.	1.2	0
120	FDDM1 and FDDM2, Two SGS3-like Proteins, Function as a Complex to Affect DNA Methylation in <i>Arabidopsis</i> . <i>Genes</i> , 2022, 13, 339.	2.4	0