

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	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
2	Isolating and cryopreserving pig skin cells for single-cell RNA sequencing study. <i>PLoS ONE</i> , 2022, 17, e0263869.	2.5	6
3	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
4	Using Quantitative Imaging for Personalized Medicine in Pancreatic Cancer: A Review of Radiomics and Deep Learning Applications. <i>Cancers</i> , 2022, 14, 1654.	3.7	27
5	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
6	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
7	<i>MLK4</i> -mediated phosphorylation of histone H3T3 promotes flowering by transcriptional silencing of <i>FLC/MAF</i> in <i>Arabidopsis thaliana</i> . <i>Plant Journal</i> , 2021, 105, 1400-1412.	5.7	9
8	Discovery and Characterization of Non-coding RNA Through Modern Genomics. , 2021, , 284-298.		0
9	Genome-wide discovery of natural variation in pre-mRNA splicing and prioritising causal alternative splicing to salt stress response in rice. <i>New Phytologist</i> , 2021, 230, 1273-1287.	7.3	20
10	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
11	Serrate-Associated Protein 1, a splicing-related protein, promotes miRNA biogenesis in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2021, 232, 1959-1973.	7.3	18
12	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
13	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
14	InMut-finder: a software tool for insertion identification in mutagenesis using Nanopore long reads. <i>BMC Genomics</i> , 2021, 22, 908.	2.8	1
15	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
16	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
17	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
18	Prediction of immunogenicity for humanized and full human therapeutic antibodies. <i>PLoS ONE</i> , 2020, 15, e0238150.	2.5	10

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19	MAC5, an RNA-binding protein, protects pri-miRNAs from SERRATE-dependent exoribonuclease activities. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23982-23990.	7.1	32
20	RGPDB: database of root-associated genes and promoters in maize, soybean, and sorghum. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	8
21	Characterization of the transcriptional divergence between the subspecies of cultivated rice (<i>Oryza</i>) Tj ETQq1 1 0.784314 rgBT /Over	2.8	16
22	<i>Zygnema circumcarinatum</i> UTEX 1559 chloroplast and mitochondrial genomes provide insight into land plant evolution. Journal of Experimental Botany, 2020, 71, 3361-3373.	4.8	9
23	Radiomics-Based Outcome Prediction for Pancreatic Cancer Following Stereotactic Body Radiotherapy. Cancers, 2020, 12, 1051.	3.7	38
24	<i>MADS78</i> and <i>MADS79</i> Are Essential Regulators of Early Seed Development in Rice. Plant Physiology, 2020, 182, 933-948.	4.8	49
25	SVMTriP: A Method to Predict B-Cell Linear Antigenic Epitopes. Methods in Molecular Biology, 2020, 2131, 299-307.	0.9	18
26	EPCEs and EPSVR: Prediction of B-Cell Antigenic Epitopes on Protein Surfaces with Conformational Information. Methods in Molecular Biology, 2020, 2131, 289-297.	0.9	2
27	Network-based feature selection reveals substructures of gene modules responding to salt stress in rice. Plant Direct, 2019, 3, e00154.	1.9	14
28	Manufacturing human pluripotent stem cell derived endothelial cells in scalable and cell-friendly microenvironments. Biomaterials Science, 2019, 7, 373-388.	5.4	12
29	Differentiating human pluripotent stem cells into vascular smooth muscle cells in three dimensional thermoreversible hydrogels. Biomaterials Science, 2019, 7, 347-361.	5.4	7
30	Radiomic feature stability across 4D respiratory phases and its impact on lung tumor prognosis prediction. PLoS ONE, 2019, 14, e0216480.	2.5	34
31	Mapping of transgenic alleles in soybean using a nanopore-based sequencing strategy. Journal of Experimental Botany, 2019, 70, 3825-3833.	4.8	24
32	Transcriptome analysis-identified long noncoding RNA CRNDE in maintaining endothelial cell proliferation, migration, and tube formation. Scientific Reports, 2019, 9, 19548.	3.3	6
33	Engineered Microenvironment for Manufacturing Human Pluripotent Stem Cell-Derived Vascular Smooth Muscle Cells. Stem Cell Reports, 2019, 12, 84-97.	4.8	25
34	Integrated generation of induced pluripotent stem cells in a low-cost device. Biomaterials, 2019, 189, 23-36.	11.4	28
35	PopLDdecay: a fast and effective tool for linkage disequilibrium decay analysis based on variant call format files. Bioinformatics, 2019, 35, 1786-1788.	4.1	818
36	Scalable Culturing of Primary Human Glioblastoma Tumor-Initiating Cells with a Cell-Friendly Culture System. Scientific Reports, 2018, 8, 3531.	3.3	27

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37	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
38	Exome chip analyses identify genes affecting mortality after HLA-matched unrelated-donor blood and marrow transplantation. <i>Blood</i> , 2018, 131, 2490-2499.	1.4	21
39	MAC3A and MAC3B, Two Core Subunits of the MOS4-Associated Complex, Positively Influence miRNA Biogenesis. <i>Plant Cell</i> , 2018, 30, 481-494.	6.6	64
40	Scalable and physiologically relevant microenvironments for human pluripotent stem cell expansion and differentiation. <i>Biofabrication</i> , 2018, 10, 025006.	7.1	28
41	Deletion Mutagenesis and Identification of Causative Mutations in Maize. <i>Methods in Molecular Biology</i> , 2018, 1676, 97-108.	0.9	1
42	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
43	New aspects of iron-copper crosstalk uncovered by transcriptomic characterization of Col-0 and the copper uptake mutant <i>col-1</i> in <i>Arabidopsis thaliana</i> . <i>Metallomics</i> , 2018, 10, 1824-1840.	2.4	31
44	DAWDLE Interacts with DICER-LIKE Proteins to Mediate Small RNA Biogenesis. <i>Plant Physiology</i> , 2018, 177, 1142-1151.	4.8	25
45	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
46	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
47	Automated Expansion of Primary Human T Cells in Scalable and Cell-Friendly Hydrogel Microtubes for Adoptive Immunotherapy. <i>Advanced Healthcare Materials</i> , 2018, 7, e1701297.	7.6	19
48	A Scalable and Efficient Bioprocess for Manufacturing Human Pluripotent Stem Cell-Derived Endothelial Cells. <i>Stem Cell Reports</i> , 2018, 11, 454-469.	4.8	22
49	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
50	Hydrogel-Based Bioprocess for Scalable Manufacturing of Human Pluripotent Stem Cell-Derived Neural Stem Cells. <i>ACS Applied Materials & Interfaces</i> , 2018, 10, 29238-29250.	8.0	28
51	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
52	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
53	Automatic planning on hippocampal avoidance whole-brain radiotherapy. <i>Medical Dosimetry</i> , 2017, 42, 63-68.	0.9	42
54	Insect and plant-derived miRNAs in greenbug (<i>Schizaphis graminum</i>) and yellow sugarcane aphid (<i>Sipha</i>) Tj ETQq0 0.0 rgBT /Overlock 10	2.2	23

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55	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
56	A mapping-by-sequencing tool for searching causative genes in mutants. , 2017, , .		0
57	iVAR: Interactive visual analytics of radiomics features from large-scale medical images. , 2017, , .		4
58	NanoAsPipe: A transcriptome analysis and alternative splicing detection pipeline for MinION long-read RNA-seq. , 2017, , .		1
59	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
60	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
61	Identification of differential alternative splicing events with an adjusted beta-distribution model. , 2017, , .		1
62	A Comprehensive Imageâ€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
63	Genome-wide Discovery of Circular RNAs in the Leaf and Seedling Tissues of <i>Arabidopsis thaliana</i> . <i>Current Genomics</i> , 2017, 18, 360-365.	1.6	16
64	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
65	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
66	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
67	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
68	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
69	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
70	Genetic and Molecular Characterization of Submergence Response Identifies Subtol6 as a Major Submergence Tolerance Locus in Maize. <i>PLoS ONE</i> , 2015, 10, e0120385.	2.5	66
71	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
72	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

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73	Synergistic and Independent Actions of Multiple Terminal Nucleotidyl Transferases in the 3' Tailing of Small RNAs in Arabidopsis. PLoS Genetics, 2015, 11, e1005091.	3.5	81
74	Osmotic stress induces phosphorylation of histone H3 at threonine 3 in pericentromeric regions of <i>Arabidopsis thaliana</i> . Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 8487-8492.	7.1	82
75	Virus-host mucosal interactions during early SIV rectal transmission. Virology, 2014, 464-465, 406-414.	2.4	10
76	Glycosyl rotation and distortion by key residues in Endocellulase Cel6A from <i>Thermobifida fusca</i> . Glycobiology, 2014, 24, 247-251.	2.5	2
77	Distinct <i>Pseudomonas</i> type III effectors use a cleavable transit peptide to target chloroplasts. Plant Journal, 2014, 77, 310-321.	5.7	92
78	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> transcription factor <i>NTL9</i> . New Phytologist, 2014, 201, 1358-1370.	7.3	89
79	Identification of RNA silencing components in soybean and sorghum. BMC Bioinformatics, 2014, 15, 4.	2.6	46
80	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. Journal of Computational Chemistry, 2014, 35, 335-341.	3.3	34
81	Identification of differentially expressed genes between sorghum genotypes with contrasting nitrogen stress tolerance by genome-wide transcriptional profiling. BMC Genomics, 2014, 15, 179.	2.8	118
82	PhosphoSVM: prediction of phosphorylation sites by integrating various protein sequence attributes with a support vector machine. Amino Acids, 2014, 46, 1459-1469.	2.7	132
83	Deletion Mutagenesis Identifies a Haploinsufficient Role for β -Zein in <i>opaque2</i> Endosperm Modification. Plant Physiology, 2014, 164, 119-130.	4.8	46
84	A novel function prediction approach using protein overlap networks. BMC Systems Biology, 2013, 7, 61.	3.0	13
85	Fuzzy clustering of CPP family in plants with evolution and interaction analyses. BMC Bioinformatics, 2013, 14, S10.	2.6	28
86	Conformational B-Cell Epitope Prediction on Antigen Protein Structures: A Review of Current Algorithms and Comparison with Common Binding Site Prediction Methods. PLoS ONE, 2013, 8, e62249.	2.5	101
87	DFVF: database of fungal virulence factors. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas032-bas032.	3.0	80
88	PIWI Associated siRNAs and piRNAs Specifically Require the <i>Caenorhabditis elegans</i> HEN1 Ortholog <i>henn-1</i> . PLoS Genetics, 2012, 8, e1002616.	3.5	124
89	Pyrophosphate-Dependent Fructose-6-Phosphate 1-Phosphotransferase Induction and Attenuation of Hsp Gene Expression during Endosperm Modification in Quality Protein Maize. Plant Physiology, 2012, 158, 917-929.	4.8	26
90	The DNA- and RNA-binding protein FACTOR of DNA METHYLATION1 requires XH domain-mediated complex formation for its function in RNA-directed DNA methylation. Plant Journal, 2012, 72, 491-500.	5.7	21

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91	Protein Loop Modeling with Optimized Backbone Potential Functions. <i>Journal of Chemical Theory and Computation</i> , 2012, 8, 1820-1827.	5.3	17
92	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
93	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
94	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
95	L1pred: A Sequence-Based Prediction Tool for Catalytic Residues in Enzymes with the L1-logreg Classifier. <i>PLoS ONE</i> , 2012, 7, e35666.	2.5	24
96	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
97	Fast and accurate prediction of protein side-chain conformations. <i>Bioinformatics</i> , 2011, 27, 2913-2914.	4.1	53
98	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
99	Prediction of antigenic epitopes on protein surfaces by consensus scoring. <i>BMC Bioinformatics</i> , 2009, 10, 302.	2.6	99
100	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
101	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
102	Fast and Accurate Method for Identifying High-Quality Protein-Interaction Modules by Clique Merging and Its Application to Yeast. <i>Journal of Proteome Research</i> , 2006, 5, 801-807.	3.7	22
103	Perineural clonidine reduces p38 mitogen-activated protein kinase activation in sensory neurons. <i>NeuroReport</i> , 2006, 17, 1313-1317.	1.2	15
104	QBES: Predicting real values of solvent accessibility from sequences by efficient, constrained energy optimization. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006, 63, 961-966.	2.6	18
105	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
106	Protein binding site prediction using an empirical scoring function. <i>Nucleic Acids Research</i> , 2006, 34, 3698-3707.	14.5	223
107	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
108	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

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109	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
110	Domain Graph of Arabidopsis Proteome by Comparative Analysis. <i>Journal of Proteome Research</i> , 2005, 4, 435-444.	3.7	10
111	Protein flexibility prediction by an all-atom mean-field statistical theory. <i>Protein Science</i> , 2005, 14, 1772-1777.	7.6	19
112	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
113	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
114	Accurate and efficient loop selections by the DFIRE-based all-atom statistical potential. <i>Protein Science</i> , 2004, 13, 391-399.	7.6	112
115	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
116	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
117	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
118	The Dependence of All-Atom Statistical Potentials on Structural Training Database. <i>Biophysical Journal</i> , 2004, 86, 3349-3358.	0.5	41
119	Temperature Dependence of the Distribution of the First Passage Time: Results from Discontinuous Molecular Dynamics Simulations of an All-Atom Model of the Second \hat{I}^2 -Hairpin Fragment of Protein G. <i>Journal of the American Chemical Society</i> , 2003, 125, 6300-6305.	13.7	56
120	Sharpening Low-Energy, Standard-Model Tests via Correlation Coefficients in Neutron \hat{I}^2 Decay. <i>Physical Review Letters</i> , 2001, 86, 5666-5669.	7.8	58